



Full wwPDB EM Validation Report ⓘ

Apr 15, 2026 – 02:08 AM UTC

PDB ID : 9QT4 / pdb_00009qt4
EMDB ID : EMD-53346
Title : CryoEM structure of Arabidopsis TIR-NLR WRR4A tetramer in complex with effector CCG40 (focused refinement)
Authors : Zhao, H.; Lukyanova, N.; Selvaraj, M.; Jones, J.
Deposited on : 2025-04-07
Resolution : 4.00 Å(reported)
Based on initial model : .

This is a Full wwPDB EM Validation Report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

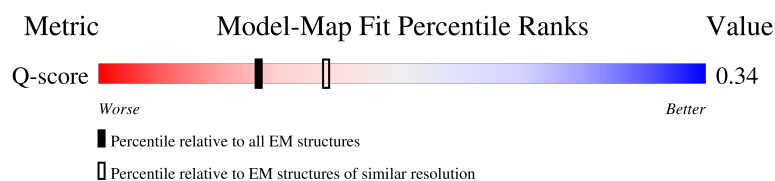
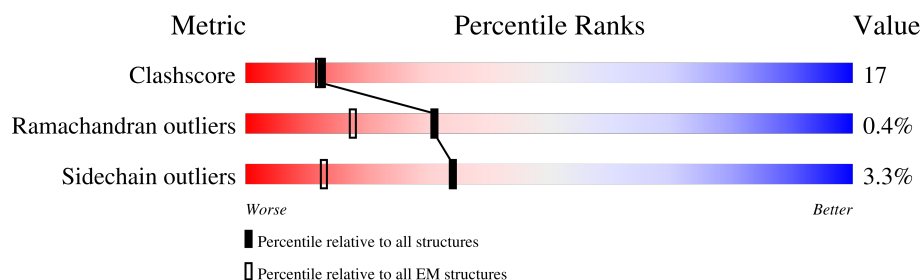
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 4.00 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



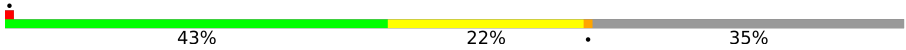
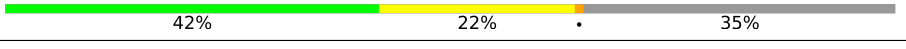
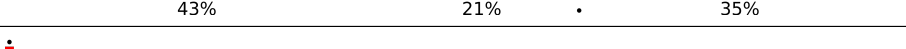
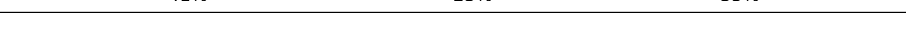
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
Q-score	-	25397	7587 (3.50 - 4.50)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the EM map (all-atom inclusion $< 40\%$). The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	P	216	
1	Q	216	
1	R	216	
1	S	216	

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Mol	Chain	Length	Quality of chain
2	A	1007	
2	B	1007	
2	C	1007	
2	D	1007	

2 Entry composition [i](#)

There are 2 unique types of molecules in this entry. The entry contains 23228 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a protein called CCG40.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	P	77	Total	C	N	O	S	0	0
			583	362	101	115	5		
1	Q	77	Total	C	N	O	S	0	0
			583	362	101	115	5		
1	R	77	Total	C	N	O	S	0	0
			583	362	101	115	5		
1	S	77	Total	C	N	O	S	0	0
			583	362	101	115	5		

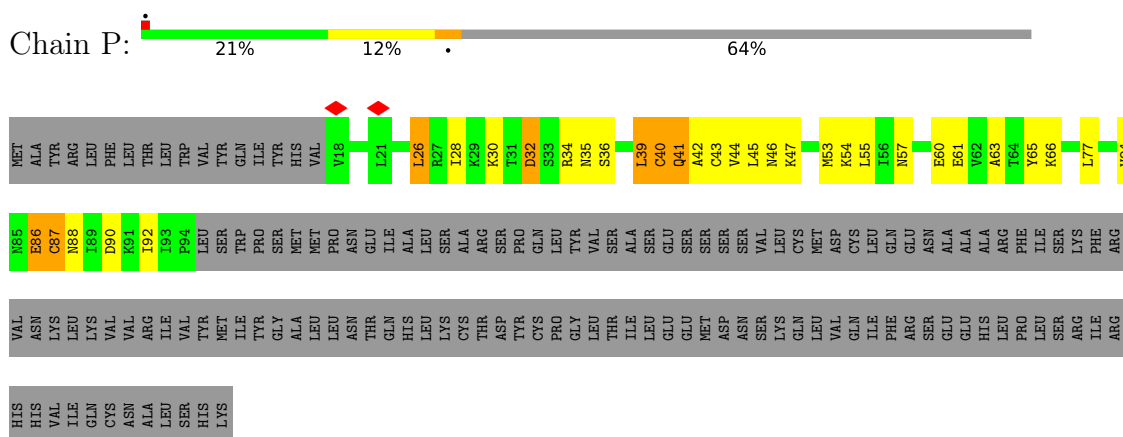
- Molecule 2 is a protein called Disease resistance protein ADR2.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	A	659	Total	C	N	O	S	0	0
			5224	3331	883	977	33		
2	B	659	Total	C	N	O	S	0	0
			5224	3331	883	977	33		
2	C	659	Total	C	N	O	S	0	0
			5224	3331	883	977	33		
2	D	659	Total	C	N	O	S	0	0
			5224	3331	883	977	33		

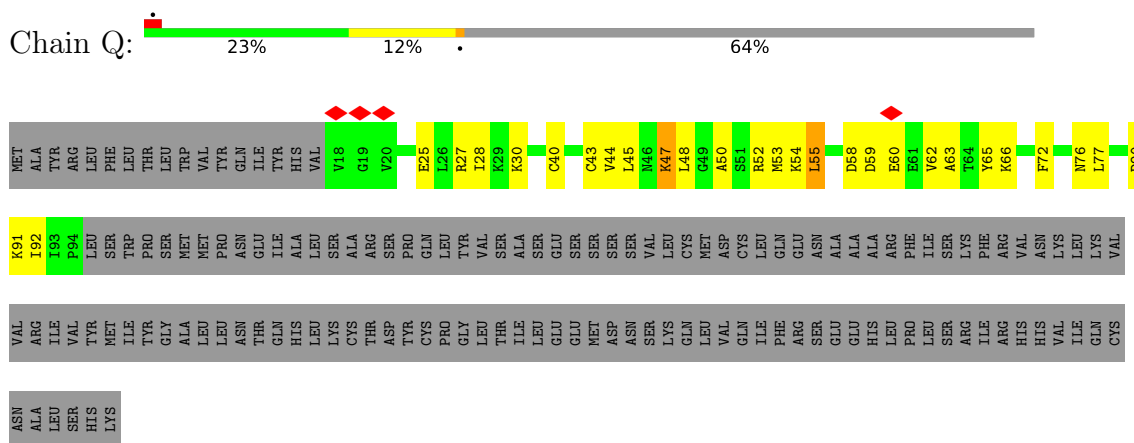
3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion in map density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red diamond above a residue indicates a poor fit to the EM map for this residue (all-atom inclusion < 40%). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

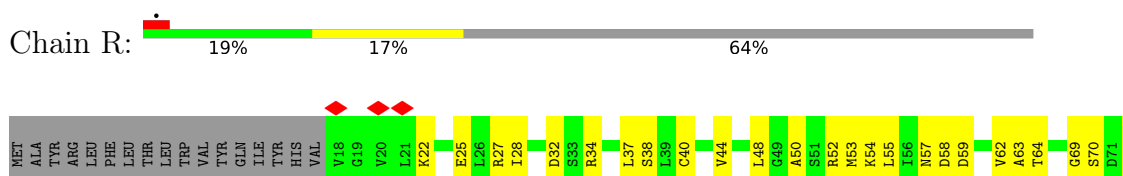
• Molecule 1: CCG40



• Molecule 1: CCG40

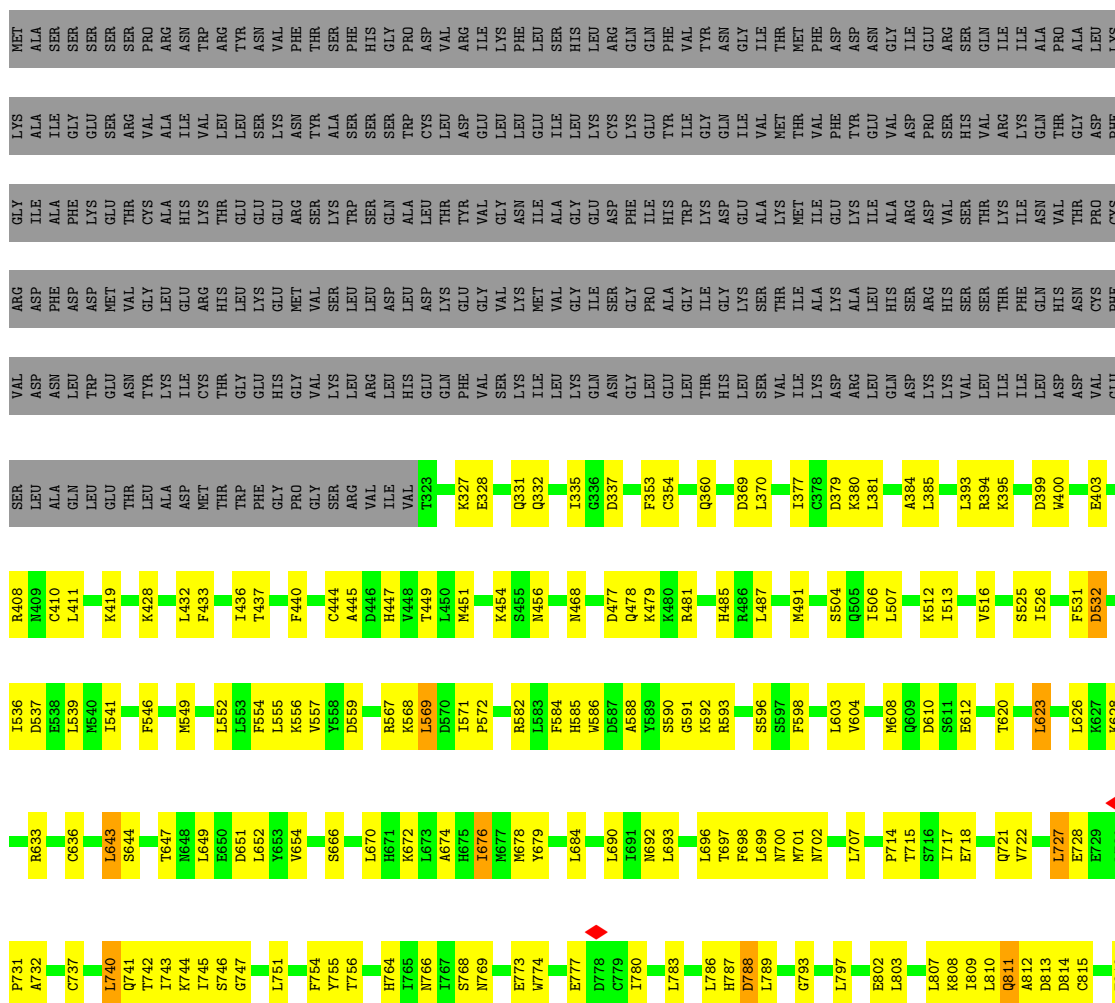


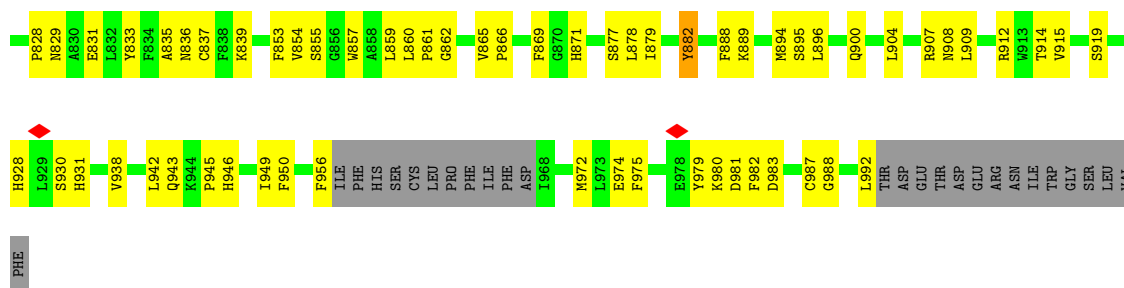
• Molecule 1: CCG40



- Molecule 2: Disease resistance protein ADR2

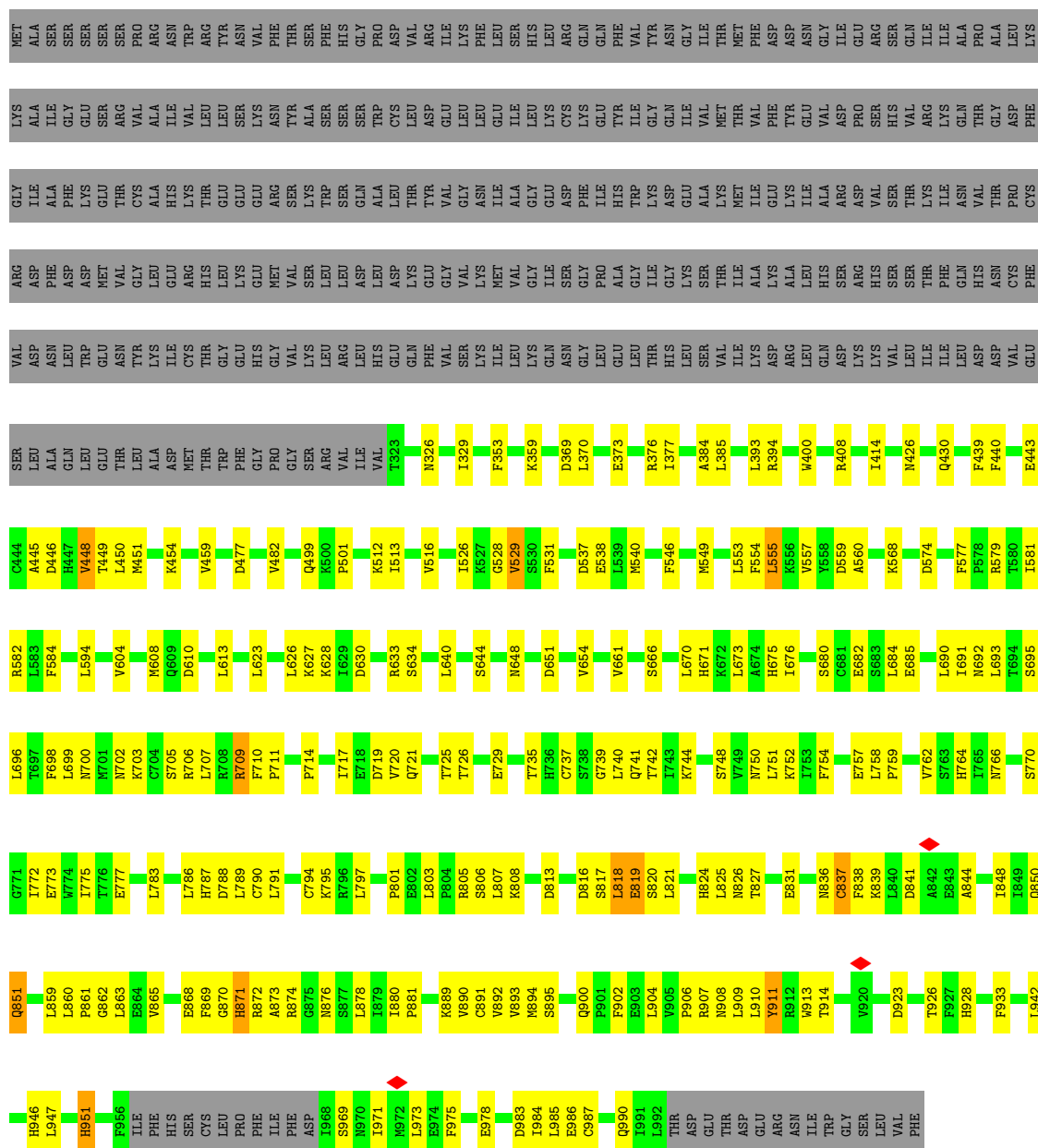
Chain B:





• Molecule 2: Disease resistance protein ADR2

Chain C: 43% 21% 35%



• Molecule 2: Disease resistance protein ADR2



MET	LYS	GLY	ARG	VAL	SER	F439	K566	A674	L751	F834	W913	THR
ALA	ILE	PHE	ASP	ASN	PHE	F440	K567	H675	K752	A835	G917	ASP
SER	GLU	LEU	ASP	TRP	GLU	E443	K568	I676	I753	N836	D923	GLU
SER	GLU	LEU	ASP	GLU	ASP	C444	D569	C681	F754	C837	I927	ARG
SER	THR	THR	MET	VAL	GLY	H447	I571	E682	Y755	F838	F927	ASN
PRO	VAL	CYS	VAL	GLY	LEU	L450	R582	S683	P756	E843	H928	ILE
ARG	ALA	ASN	THR	LEU	ASP	M451	L583	L684	P759	A844	H929	THR
ARG	VAL	THR	GLY	GLU	GLY	K454	F584	V686	V762	R845	L929	GLY
ASN	LEU	GLU	HIS	THR	TRP	K454	H585	I687	V763	R846	S930	SER
ASN	GLU	GLU	THR	GLY	PHE	K464	K586	P688	H764	I848	H931	LEU
VAL	LYS	GLU	LEU	LYS	PRO	I472	A588	S689	I765	I849	M932	VAL
PHE	TYR	ARG	VAL	VAL	GLY	Q478	S590	L690	N766	Q850	F933	PHE
THR	ALA	TRP	SER	LEU	ARG	Q499	S593	L696	I767	S851	S937	
GLY	SER	GLN	LEU	ARG	ILE	R481	L594	L699	S768	S852	V938	
GLY	SER	ALA	LEU	LEU	VAL	V482	F599	N700	S770	F853	H939	
PRO	TRP	ALA	GLU	HIS	VAL	V484	L603	M701	G771	A858	L942	
ASP	CYS	LEU	ASP	GLU	GLN	PHE	V604	N702	H784	L859	P945	
VAL	THR	THR	LYS	PHE	VAL	V485	E685	C704	N785	L860	H946	
ARG	ASP	GLY	GLY	GLY	VAL	Q499	V606	S705	L786	G862	L947	
ILE	ILE	GLU	ILE	ILE	SER	I506	E618	R708	L787	L863	F948	
LEU	CYS	LEU	GLY	GLY	LEU	L507	G621	F710	N788	L864	I949	
LEU	LYS	GLY	ILE	ILE	GLN	K512	L623	P711	C790	L865	F950	
LEU	ARG	ASP	GLY	GLY	ASN	I513	L626	T712	S792	P866	H951	
GLN	LYS	GLY	THR	GLY	LEU	V516	L629	T713	C794	E868	S952	
GLN	THR	THR	ALA	GLY	LEU	L517	L636	P714	L797	H871	F956	
VAL	LYS	ASP	ILE	ILE	THR	A520	L637	T715	V798	R874	I957	
THR	GLY	GLY	ALA	LYS	HIS	I377	L638	I716	L803	L878	ILE	
GLY	GLN	ILE	VAL	GLU	LEU	I385	T638	E717	P804	I879	PHE	
ILE	VAL	ILE	THR	ASP	SER	L385	E639	D719	R805	S883	THR	
THR	THR	THR	MET	THR	THR	S530	F531	T725	S806	R887	ASP	
MET	THR	THR	THR	ASP	ASP	F531	L643	E728	L807	K889	1968	
PHE	VAL	GLU	VAL	ARG	LYS	I536	L643	E729	K808	V890	E974	
ASP	PHE	THR	PHE	ASP	LYS	D537	S656	L730	L810	C891		
ASP	TYR	GLU	ASP	ASN	ARG	E538	L659	P731	Q811	M894	S977	
GLY	VAL	ALA	VAL	GLN	LEU	L539	V661	A732	A812	S895	E978	
ILE	ASP	ALA	ASP	ASN	GLN	K544	E662	S733	D813	L896	Y979	
ARG	PRO	ASP	ASP	LYS	ASP	A545	L663	T734	S820	N897	K980	
SER	SER	HIS	VAL	THR	LYS	L553	P664	H735	L821	E903		
GLN	VAL	THR	SER	THR	VAL	F554	S665	C737	N822	L904		
ILE	THR	ILE	THR	ILE	ILE	P556	L667	S738	L825	V905		
ILE	GLN	ILE	PHE	ILE	LEU	K556	L670	S738	P828	R907		
ASN	VAL	VAL	GLN	GLN	ASP	V557	L673	S746	N829	N908		
VAL	THR	THR	VAL	THR	ASP	W562	L673	G747	A830	L909		
THR	GLY	THR	ASP	THR	VAL	H563		S748	E831	Y911		
PRO	ASP	GLY	LEU	PRO	VAL			V749	L832	L910		
LYS	PHE				GLU			N750	Y833	R912		

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C4	Depositor
Number of particles used	34546	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION; Relion	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	50	Depositor
Minimum defocus (nm)	1600	Depositor
Maximum defocus (nm)	2700	Depositor
Magnification	105000	Depositor
Image detector	GATAN K3 BIOQUANTUM (6k x 4k)	Depositor
Maximum map value	0.059	Depositor
Minimum map value	-0.026	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.001	Depositor
Recommended contour level	0.005	Depositor
Map size (Å)	331.2, 331.2, 331.2	wwPDB
Map dimensions	400, 400, 400	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.828, 0.828, 0.828	Depositor

5 Model quality [i](#)

5.1 Standard geometry [i](#)

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	P	0.35	0/586	0.70	1/786 (0.1%)
1	Q	0.28	0/586	0.53	0/786
1	R	0.16	0/586	0.44	0/786
1	S	0.18	0/586	0.49	0/786
2	A	0.19	0/5332	0.52	2/7224 (0.0%)
2	B	0.18	0/5332	0.52	2/7224 (0.0%)
2	C	0.19	0/5332	0.51	0/7224
2	D	0.23	0/5332	0.57	4/7224 (0.1%)
All	All	0.20	0/23672	0.53	9/32040 (0.0%)

There are no bond length outliers.

All (9) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	D	938	VAL	N-CA-C	-7.23	106.05	111.90
1	P	32	ASP	N-CA-C	-6.93	105.16	112.93
2	D	807	LEU	N-CA-C	-6.48	100.83	110.23
2	A	931	HIS	N-CA-C	-6.25	105.64	113.20
2	A	835	ALA	N-CA-C	-5.38	107.27	112.97
2	D	798	VAL	N-CA-C	-5.36	107.38	111.62
2	D	754	PHE	CA-CB-CG	5.14	118.94	113.80
2	B	854	VAL	N-CA-C	-5.09	107.46	113.42
2	B	811	GLN	N-CA-C	5.06	117.35	111.02

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen

atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	P	583	0	601	31	0
1	Q	583	0	601	19	0
1	R	583	0	601	26	0
1	S	583	0	601	34	0
2	A	5224	0	5248	171	0
2	B	5224	0	5248	173	0
2	C	5224	0	5248	155	0
2	D	5224	0	5248	195	0
All	All	23228	0	23396	783	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 17.

All (783) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:D:731:PRO:HG2	2:D:754:PHE:HB2	1.47	0.95
2:D:768:SER:HA	2:D:791:LEU:HG	1.53	0.89
2:D:714:PRO:HG2	2:D:717:ILE:HG13	1.54	0.89
2:D:507:LEU:HB3	2:D:513:ILE:HG12	1.55	0.89
2:B:678:MET:HE1	2:B:684:LEU:HD22	1.57	0.86
2:C:803:LEU:HD13	2:C:825:LEU:HD13	1.57	0.84
2:A:600:ALA:HB3	2:A:621:GLN:HE21	1.44	0.81
2:D:828:PRO:HA	2:D:853:PHE:HA	1.62	0.81
2:A:916:ILE:HD11	2:A:972:MET:HG2	1.63	0.81
2:B:888:PHE:H	2:B:992:LEU:HD11	1.44	0.80
1:R:55:LEU:HD13	2:C:906:PRO:HG2	1.63	0.80
2:B:690:LEU:HB2	2:B:693:LEU:HD11	1.64	0.80
1:P:28:ILE:HD12	1:P:30:LYS:HD3	1.64	0.80
2:D:569:LEU:HD21	2:D:586:TRP:HE1	1.45	0.80
2:A:758:LEU:HD12	2:A:759:PRO:HD2	1.62	0.80
2:B:895:SER:HB2	2:B:907:ARG:HH12	1.48	0.79
2:D:621:GLN:HE21	2:D:623:LEU:HD22	1.46	0.79
2:D:745:ILE:HB	2:D:766:ASN:HB2	1.64	0.79
1:S:45:LEU:HB2	1:S:53:MET:HG2	1.64	0.78
2:C:797:LEU:HB3	2:C:817:SER:HB3	1.64	0.77
1:Q:44:VAL:O	1:Q:48:LEU:HB3	1.85	0.76
1:P:43:CYS:HA	1:P:47:LYS:HD3	1.68	0.76
2:A:436:ILE:HD11	2:A:482:VAL:HG11	1.66	0.75

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:D:910:LEU:HG	2:D:978:GLU:HB2	1.66	0.75
2:B:777:GLU:HG3	2:B:802:GLU:H	1.52	0.75
2:C:737:CYS:HB2	2:C:740:LEU:HD22	1.68	0.75
2:B:628:LYS:HG3	2:B:651:ASP:HB2	1.68	0.75
1:S:85:ASN:ND2	2:D:562:TRP:O	2.20	0.74
2:A:744:LYS:HG2	2:A:766:ASN:HB3	1.69	0.74
2:D:837:CYS:SG	2:D:838:PHE:N	2.59	0.74
2:A:775:ILE:HB	2:A:801:PRO:HG2	1.67	0.73
2:A:781:LYS:HG3	2:A:804:PRO:HA	1.71	0.73
2:C:454:LYS:HZ1	2:C:553:LEU:HD21	1.52	0.73
2:D:862:GLY:HA3	2:D:947:LEU:HB2	1.71	0.73
2:C:721:GLN:HG2	2:C:744:LYS:HD2	1.71	0.73
2:C:797:LEU:CB	2:C:817:SER:HB3	2.18	0.73
2:A:880:ILE:HD11	2:A:888:PHE:HB3	1.69	0.73
2:B:742:THR:HG23	2:B:764:HIS:HD2	1.55	0.72
1:R:38:SER:HB3	2:C:904:LEU:HD13	1.72	0.72
2:B:536:ILE:HG21	2:B:539:LEU:HD22	1.72	0.71
1:P:32:ASP:HA	1:P:61:GLU:HG2	1.73	0.71
2:C:594:LEU:HB2	2:C:613:LEU:HD11	1.73	0.71
2:D:353:PHE:HB2	2:D:385:LEU:HD22	1.72	0.71
2:D:623:LEU:HD12	2:D:626:LEU:HB2	1.72	0.71
2:A:754:PHE:HD2	2:A:775:ILE:HG12	1.54	0.71
2:D:709:ARG:HH12	2:D:710:PHE:HD1	1.37	0.71
1:S:41:GLN:HE22	2:D:933:PHE:HB2	1.55	0.71
1:P:34:ARG:NH1	1:P:34:ARG:O	2.23	0.70
2:B:353:PHE:HB2	2:B:385:LEU:HD22	1.71	0.70
2:D:690:LEU:HB2	2:D:714:PRO:HB3	1.73	0.70
1:P:41:GLN:HA	1:P:44:VAL:HG12	1.74	0.69
2:C:577:PHE:O	2:C:579:ARG:NH2	2.25	0.69
2:A:803:LEU:HD12	2:A:825:LEU:HD13	1.75	0.69
2:C:700:ASN:ND2	2:C:702:ASN:OD1	2.26	0.69
2:C:353:PHE:HB2	2:C:385:LEU:HD22	1.74	0.68
1:P:42:ALA:HB2	2:A:936:ASP:HB2	1.74	0.68
2:A:353:PHE:HB2	2:A:385:LEU:HD22	1.74	0.68
2:C:870:GLY:H	2:C:990:GLN:HB2	1.59	0.68
2:D:507:LEU:HD23	2:D:513:ILE:HG23	1.75	0.68
2:A:859:LEU:HA	2:A:948:PHE:HA	1.75	0.68
2:A:552:LEU:HB3	2:A:581:ILE:HG22	1.74	0.68
2:B:904:LEU:HD23	2:B:938:VAL:HG21	1.76	0.68
2:A:681:CYS:HB2	2:A:684:LEU:HD11	1.74	0.67
2:B:593:ARG:HH22	2:B:596:SER:H	1.41	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:C:735:THR:HG23	2:C:757:GLU:HG3	1.76	0.67
2:D:569:LEU:HD21	2:D:586:TRP:NE1	2.09	0.67
2:B:721:GLN:HA	2:B:744:LYS:HB2	1.74	0.67
2:B:837:CYS:HB2	2:B:943:GLN:HE22	1.59	0.67
2:A:871:HIS:HB3	2:A:989:VAL:HB	1.77	0.66
2:B:783:LEU:HD23	2:B:786:LEU:HD13	1.77	0.66
2:B:877:SER:OG	2:B:972:MET:SD	2.53	0.66
2:D:805:ARG:HA	2:D:825:LEU:HG	1.77	0.66
1:P:36:SER:O	1:P:40:CYS:SG	2.53	0.66
2:A:859:LEU:HD21	2:A:946:HIS:HB3	1.78	0.66
2:D:933:PHE:HA	2:D:937:SER:HA	1.77	0.66
2:B:674:ALA:HA	2:B:696:LEU:HA	1.76	0.66
2:D:444:CYS:HA	2:D:481:ARG:HA	1.76	0.66
2:A:781:LYS:HZ3	2:A:824:HIS:HB3	1.60	0.66
2:D:667:ILE:HA	2:D:670:LEU:HD23	1.77	0.66
2:A:478:GLN:HB3	2:A:481:ARG:HH12	1.60	0.65
2:B:718:GLU:OE2	2:B:741:GLN:NE2	2.29	0.65
2:D:603:LEU:HD21	2:D:606:VAL:HG13	1.79	0.65
2:D:894:MET:SD	2:D:895:SER:N	2.69	0.65
2:D:709:ARG:HB3	2:D:729:GLU:C	2.22	0.65
2:B:811:GLN:OE1	2:B:931:HIS:NE2	2.28	0.65
2:D:495:VAL:HG13	2:D:499:GLN:HG3	1.79	0.65
2:B:444:CYS:HA	2:B:481:ARG:HA	1.77	0.65
2:C:450:LEU:O	2:C:582:ARG:NH2	2.27	0.65
2:A:894:MET:HG3	2:A:895:SER:H	1.62	0.65
2:C:682:GLU:O	2:C:706:ARG:NE	2.23	0.64
2:D:536:ILE:HG23	2:D:568:LYS:HE2	1.78	0.64
2:B:377:ILE:HD11	2:B:408:ARG:HG2	1.78	0.64
2:B:644:SER:HB3	2:B:666:SER:HB2	1.78	0.64
2:B:744:LYS:HG2	2:B:766:ASN:HB3	1.79	0.64
2:C:691:ILE:HD12	2:C:711:PRO:HB2	1.78	0.64
2:A:446:ASP:OD2	2:A:447:HIS:N	2.31	0.64
2:B:526:ILE:HB	2:B:549:MET:HE1	1.79	0.64
2:A:845:ARG:HG2	2:A:860:LEU:HD11	1.78	0.64
2:A:913:TRP:HD1	2:A:923:ASP:HB3	1.61	0.64
2:D:731:PRO:HG2	2:D:754:PHE:CB	2.25	0.64
1:R:80:ASP:OD2	1:R:88:ASN:ND2	2.31	0.64
2:A:785:ASN:HA	2:A:805:ARG:HH12	1.63	0.63
2:D:665:SER:HA	2:D:688:PRO:HG3	1.80	0.63
2:D:789:LEU:HB2	2:D:808:LYS:HB2	1.80	0.63
2:B:410:CYS:SG	2:B:411:LEU:N	2.72	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:837:CYS:HA	2:B:861:PRO:HB3	1.80	0.63
2:D:673:LEU:HD21	2:D:676:ILE:HD11	1.80	0.63
2:D:433:PHE:O	2:D:437:THR:HG23	1.97	0.63
2:D:682:GLU:HA	2:D:705:SER:OG	1.98	0.63
2:D:699:LEU:HG	2:D:701:MET:HE1	1.80	0.62
2:C:762:VAL:HG11	2:C:783:LEU:HB3	1.81	0.62
2:B:894:MET:HE2	2:B:909:LEU:HD22	1.80	0.62
2:D:752:LYS:HA	2:D:772:ILE:HD12	1.82	0.62
2:D:517:LEU:HD22	2:D:545:ALA:HB1	1.79	0.62
2:B:833:TYR:HB3	2:B:859:LEU:HB3	1.82	0.62
2:C:750:ASN:HB3	2:C:752:LYS:HE3	1.82	0.62
2:D:520:ALA:HB1	2:D:544:LYS:HB3	1.82	0.62
1:P:43:CYS:SG	1:P:47:LYS:NZ	2.71	0.62
2:A:907:ARG:HG3	2:A:929:LEU:HB2	1.82	0.62
2:D:930:SER:HB2	2:D:932:MET:HE1	1.80	0.62
2:A:447:HIS:O	2:A:451:MET:HG2	2.00	0.61
1:Q:52:ARG:NH2	2:B:931:HIS:O	2.32	0.61
2:A:649:LEU:HD23	2:A:670:LEU:HD13	1.82	0.61
2:A:810:LEU:O	2:A:832:LEU:HB2	2.00	0.61
2:C:837:CYS:HA	2:C:861:PRO:HB3	1.82	0.61
2:A:433:PHE:O	2:A:437:THR:HG23	1.99	0.61
2:B:812:ALA:HB1	2:B:836:ASN:HD21	1.64	0.61
2:C:685:GLU:HA	2:C:706:ARG:HB3	1.83	0.61
2:B:569:LEU:HD21	2:B:590:SER:HB2	1.82	0.61
2:B:604:VAL:HA	2:B:626:LEU:HA	1.83	0.61
2:D:593:ARG:NH1	2:D:594:LEU:O	2.34	0.61
1:P:26:LEU:HB2	1:P:92:ILE:HD11	1.83	0.60
2:B:445:ALA:O	2:B:449:THR:HG22	2.02	0.60
2:A:393:LEU:HD23	2:A:394:ARG:HB2	1.81	0.60
2:A:557:VAL:HG22	2:A:586:TRP:HA	1.81	0.60
2:C:499:GLN:HG3	2:C:501:PRO:HD2	1.83	0.60
2:C:326:ASN:HD21	2:C:329:ILE:HG13	1.65	0.60
2:C:818:LEU:O	2:C:819:GLU:C	2.43	0.60
2:D:804:PRO:HB2	2:D:807:LEU:HD12	1.82	0.60
2:B:740:LEU:HB3	2:B:743:ILE:HD11	1.84	0.60
1:S:57:ASN:OD1	1:S:64:THR:OG1	2.20	0.59
2:A:432:LEU:O	2:A:436:ILE:HG22	2.02	0.59
2:A:670:LEU:HD12	2:A:673:LEU:HD22	1.84	0.59
2:B:419:LYS:HA	2:B:491:MET:HE1	1.84	0.59
2:C:758:LEU:HD13	2:C:783:LEU:HD11	1.84	0.59
2:D:324:THR:HG22	2:D:326:ASN:H	1.65	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:P:54:LYS:HB3	1:P:66:LYS:HB2	1.84	0.59
2:D:440:PHE:HE2	2:D:451:MET:HG3	1.67	0.59
2:D:864:GLU:OE1	2:D:874:ARG:NH2	2.28	0.59
2:A:500:LYS:HA	2:A:503:LYS:HE3	1.84	0.59
2:B:889:LYS:HE3	2:B:949:ILE:HG21	1.85	0.59
2:B:894:MET:HE1	2:B:982:PHE:HB2	1.84	0.59
2:B:789:LEU:HD12	2:B:807:LEU:HD22	1.83	0.59
2:C:777:GLU:HA	2:C:801:PRO:HB3	1.83	0.59
1:Q:55:LEU:HB2	1:Q:65:TYR:CE2	2.38	0.59
2:A:569:LEU:HB3	2:A:586:TRP:HE1	1.67	0.59
2:B:432:LEU:O	2:B:436:ILE:HG22	2.03	0.59
1:Q:59:ASP:N	1:Q:62:VAL:O	2.31	0.59
2:A:923:ASP:OD1	2:A:924:GLU:N	2.35	0.59
2:D:797:LEU:HD11	2:D:821:LEU:HD13	1.83	0.58
2:D:903:GLU:O	2:D:907:ARG:NH2	2.36	0.58
1:S:82:SER:HB2	1:S:89:ILE:HG13	1.85	0.58
2:A:721:GLN:HG3	2:A:744:LYS:HD2	1.85	0.58
2:D:618:GLU:H	2:D:618:GLU:CD	2.11	0.58
2:D:883:SER:HB2	2:D:991:ILE:HD11	1.85	0.58
2:A:736:HIS:HA	2:A:759:PRO:HB3	1.85	0.58
2:B:447:HIS:O	2:B:451:MET:HG2	2.03	0.58
2:D:977:SER:HA	2:D:982:PHE:HB2	1.84	0.58
2:A:340:GLN:N	2:A:340:GLN:OE1	2.36	0.58
2:A:835:ALA:HA	2:A:946:HIS:CD2	2.39	0.58
2:A:690:LEU:HD12	2:A:693:LEU:HD13	1.85	0.58
2:B:871:HIS:HB3	2:B:879:ILE:HB	1.86	0.58
2:B:721:GLN:HB2	2:B:744:LYS:HD2	1.86	0.57
2:C:873:ALA:HB3	2:C:878:LEU:HD11	1.85	0.57
2:C:628:LYS:HD3	2:C:651:ASP:HB3	1.86	0.57
1:S:24:GLY:N	1:S:67:ILE:O	2.38	0.57
1:Q:54:LYS:O	1:Q:66:LYS:N	2.28	0.57
2:C:895:SER:HB3	2:C:983:ASP:HB2	1.85	0.57
2:A:450:LEU:O	2:A:582:ARG:NH1	2.38	0.57
2:D:809:ILE:HG13	2:D:811:GLN:HG2	1.86	0.57
2:B:369:ASP:OD2	2:B:369:ASP:N	2.37	0.57
2:C:794:CYS:SG	2:C:795:LYS:N	2.78	0.57
2:A:410:CYS:SG	2:A:411:LEU:N	2.78	0.57
2:A:661:VAL:HA	2:A:683:SER:HB3	1.87	0.57
2:B:440:PHE:CE2	2:B:451:MET:HG3	2.40	0.57
2:B:828:PRO:HA	2:B:853:PHE:HA	1.87	0.57
2:D:663:LEU:HD21	2:D:667:ILE:HG13	1.86	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:A:574:ASP:OD1	2:A:575:ILE:N	2.37	0.57
2:B:593:ARG:HH12	2:B:596:SER:HB2	1.69	0.57
2:A:454:LYS:HZ3	2:A:553:LEU:HD11	1.70	0.56
2:B:895:SER:HA	2:B:907:ARG:HH22	1.69	0.56
2:C:808:LYS:O	2:C:831:GLU:N	2.29	0.56
2:D:849:ILE:HD13	2:D:868:GLU:HG3	1.86	0.56
2:B:882:TYR:HE2	2:B:956:PHE:HB3	1.69	0.56
2:C:445:ALA:O	2:C:448:VAL:HG12	2.05	0.56
2:C:623:LEU:HD12	2:C:626:LEU:HB2	1.87	0.56
2:C:821:LEU:H	2:C:844:ALA:HB2	1.70	0.56
2:D:507:LEU:HD13	2:D:526:ILE:HG21	1.86	0.56
1:S:61:GLU:OE2	1:S:61:GLU:N	2.37	0.56
2:B:537:ASP:HB3	2:B:568:LYS:HD2	1.87	0.56
2:C:913:TRP:NE1	2:C:923:ASP:O	2.36	0.56
2:C:680:SER:HA	2:C:703:LYS:HB2	1.86	0.56
1:P:28:ILE:HG23	1:P:63:ALA:H	1.70	0.56
2:B:541:ILE:HB	2:B:572:PRO:HD3	1.87	0.56
1:R:37:LEU:HB3	2:C:904:LEU:HD11	1.87	0.56
2:A:604:VAL:O	2:A:627:LYS:N	2.38	0.56
2:A:825:LEU:HG	2:A:851:GLN:HE22	1.69	0.56
2:A:710:PHE:HD1	2:A:712:ASP:HB2	1.71	0.56
2:C:719:ASP:OD1	2:C:720:VAL:N	2.38	0.56
2:B:454:LYS:HB2	2:B:582:ARG:NH2	2.21	0.56
2:B:592:LYS:NZ	2:B:612:GLU:OE1	2.39	0.56
2:B:896:LEU:HB3	2:B:945:PRO:HG3	1.88	0.56
2:D:447:HIS:O	2:D:451:MET:HG2	2.06	0.56
1:R:57:ASN:OD1	1:R:58:ASP:N	2.39	0.55
2:C:892:VAL:HG12	2:C:893:VAL:H	1.71	0.55
1:Q:72:PHE:HB3	2:B:698:PHE:CE1	2.41	0.55
2:A:754:PHE:CD2	2:A:775:ILE:HG12	2.39	0.55
2:D:440:PHE:CE2	2:D:451:MET:HG3	2.40	0.55
2:D:450:LEU:O	2:D:582:ARG:NH2	2.36	0.55
2:D:897:ASN:ND2	2:D:983:ASP:OD2	2.40	0.55
2:D:681:CYS:O	2:D:705:SER:OG	2.24	0.55
1:S:46:ASN:OD1	1:S:47:LYS:N	2.39	0.55
2:B:742:THR:HA	2:B:764:HIS:HB3	1.88	0.55
2:D:887:ARG:HH21	2:D:992:LEU:HB3	1.71	0.55
2:C:850:GLN:NE2	2:C:868:GLU:OE1	2.28	0.55
2:C:740:LEU:HG	2:C:759:PRO:HB3	1.89	0.55
1:Q:53:MET:HA	1:Q:53:MET:HE3	1.89	0.55
2:B:742:THR:HG23	2:B:764:HIS:CD2	2.39	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:C:908:ASN:H	2:C:928:HIS:CD2	2.25	0.55
2:D:789:LEU:CB	2:D:808:LYS:HB2	2.37	0.55
2:A:508:VAL:HA	2:A:513:ILE:HD11	1.88	0.55
2:A:833:TYR:HA	2:A:859:LEU:HB3	1.88	0.55
2:B:328:GLU:HB2	2:B:468:ASN:HD22	1.71	0.55
2:C:623:LEU:HD12	2:C:626:LEU:HD12	1.89	0.55
2:D:905:VAL:HG21	2:D:980:LYS:HE3	1.87	0.55
2:D:928:HIS:NE2	2:D:930:SER:O	2.40	0.55
1:S:87:CYS:SG	1:S:88:ASN:N	2.78	0.55
2:B:788:ASP:O	2:B:789:LEU:HD23	2.07	0.55
2:D:674:ALA:HA	2:D:696:LEU:HA	1.89	0.55
2:D:908:ASN:ND2	2:D:927:PHE:O	2.34	0.55
1:R:44:VAL:HA	1:R:48:LEU:HD23	1.90	0.54
2:A:377:ILE:HD11	2:A:408:ARG:HG2	1.88	0.54
1:R:28:ILE:HD11	1:R:87:CYS:HB2	1.87	0.54
2:A:419:LYS:NZ	2:A:423:GLU:OE1	2.38	0.54
2:D:562:TRP:HZ2	2:D:567:ARG:HH21	1.53	0.54
1:P:55:LEU:H	2:A:928:HIS:CG	2.25	0.54
1:Q:43:CYS:O	1:Q:47:LYS:HG2	2.07	0.54
2:C:700:ASN:ND2	2:C:721:GLN:OE1	2.35	0.54
2:D:536:ILE:HD11	2:D:539:LEU:HB2	1.90	0.54
1:P:77:LEU:HD11	1:P:92:ILE:HG12	1.89	0.54
1:S:27:ARG:HB3	1:S:62:VAL:HG11	1.90	0.54
2:B:507:LEU:HB3	2:B:513:ILE:HG12	1.89	0.54
2:B:746:SER:HB3	2:B:768:SER:HB3	1.88	0.54
2:D:932:MET:SD	2:D:932:MET:N	2.81	0.54
2:C:892:VAL:HG11	2:C:984:ILE:HG13	1.89	0.54
2:B:808:LYS:O	2:B:831:GLU:N	2.31	0.53
2:C:816:ASP:HB2	2:C:839:LYS:HE2	1.90	0.53
2:B:860:LEU:HG	2:B:949:ILE:HD13	1.89	0.53
1:R:53:MET:SD	1:R:53:MET:N	2.82	0.53
2:A:676:ILE:HD12	2:A:678:MET:HE1	1.89	0.53
2:A:804:PRO:HD2	2:A:807:LEU:HD21	1.89	0.53
2:C:739:GLY:C	2:C:740:LEU:HD23	2.33	0.53
1:Q:54:LYS:HB3	1:Q:66:LYS:HB2	1.91	0.53
1:R:50:ALA:HB2	1:R:73:VAL:HG21	1.91	0.53
2:D:570:ASP:HA	2:D:590:SER:OG	2.08	0.53
2:C:581:ILE:HG22	2:C:581:ILE:O	2.08	0.53
2:C:690:LEU:HD11	2:C:699:LEU:HD22	1.90	0.53
2:C:889:LYS:HD2	2:C:951:HIS:CE1	2.44	0.53
2:D:512:LYS:O	2:D:516:VAL:HG13	2.09	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:D:846:ARG:NH1	2:D:847:ALA:HB2	2.24	0.53
2:A:370:LEU:HD12	2:A:400:TRP:CD1	2.43	0.53
2:D:563:HIS:HE1	2:D:566:LYS:HE2	1.73	0.53
2:D:832:LEU:HB3	2:D:860:LEU:HD21	1.90	0.53
2:B:608:MET:HA	2:B:608:MET:HE3	1.90	0.53
2:C:559:ASP:OD1	2:C:560:ALA:N	2.42	0.53
2:C:709:ARG:NH2	2:C:726:THR:O	2.40	0.53
2:D:894:MET:HE2	2:D:894:MET:HA	1.89	0.53
2:A:678:MET:HB2	2:A:701:MET:HG3	1.90	0.53
2:A:972:MET:SD	2:A:972:MET:N	2.81	0.53
2:C:370:LEU:HD12	2:C:400:TRP:CD1	2.44	0.53
2:D:478:GLN:N	2:D:478:GLN:OE1	2.42	0.53
2:D:709:ARG:HB2	2:D:730:LEU:O	2.08	0.53
2:D:822:ASN:HB2	2:D:844:ALA:HA	1.91	0.53
2:D:701:MET:HB3	2:D:704:CYS:HB2	1.90	0.53
2:A:751:LEU:HG	2:A:752:LYS:H	1.75	0.52
2:B:697:THR:HA	2:B:717:ILE:HA	1.89	0.52
1:S:29:LYS:N	1:S:90:ASP:OD2	2.31	0.52
2:B:555:LEU:HD21	2:B:584:PHE:CD1	2.44	0.52
2:B:693:LEU:HD22	2:B:696:LEU:HD12	1.91	0.52
2:D:472:ILE:HG22	2:D:484:VAL:HG22	1.92	0.52
2:C:911:TYR:HH	2:C:913:TRP:CG	2.27	0.52
2:A:472:ILE:HG22	2:A:484:VAL:HG22	1.90	0.52
2:A:369:ASP:OD2	2:A:369:ASP:N	2.35	0.52
2:A:913:TRP:HZ2	2:A:954:LEU:HD13	1.74	0.52
2:D:670:LEU:O	2:D:693:LEU:HD23	2.10	0.52
2:C:862:GLY:O	2:C:947:LEU:N	2.43	0.52
2:A:708:ARG:HD3	2:A:709:ARG:H	1.75	0.52
2:B:512:LYS:O	2:B:516:VAL:HG13	2.10	0.52
1:R:76:ASN:HB2	1:R:78:LYS:HG2	1.90	0.52
2:D:888:PHE:CE2	2:D:952:SER:HB2	2.45	0.52
1:S:88:ASN:OD1	1:S:89:ILE:N	2.42	0.51
2:A:745:ILE:O	2:A:745:ILE:HG22	2.10	0.51
2:B:812:ALA:HB2	2:B:835:ALA:HB3	1.92	0.51
2:A:707:LEU:O	2:A:726:THR:OG1	2.24	0.51
2:C:610:ASP:OD1	2:C:633:ARG:NH1	2.44	0.51
1:Q:47:LYS:HA	2:B:679:TYR:CD2	2.45	0.51
2:A:705:SER:O	2:A:706:ARG:HD2	2.11	0.51
2:B:754:PHE:HE1	2:B:773:GLU:H	1.58	0.51
2:D:912:ARG:HB2	2:D:974:GLU:HG3	1.92	0.51
2:D:531:PHE:HE1	2:D:536:ILE:HD12	1.76	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:C:393:LEU:HG	2:C:394:ARG:HD3	1.92	0.51
2:A:495:VAL:O	2:A:499:GLN:HB2	2.11	0.50
2:A:759:PRO:HG2	2:A:762:VAL:HG23	1.93	0.50
2:D:794:CYS:HB3	2:D:813:ASP:HB3	1.92	0.50
1:Q:40:CYS:O	1:Q:44:VAL:HG12	2.11	0.50
2:B:727:LEU:HD22	2:B:751:LEU:HD22	1.93	0.50
2:C:865:VAL:HB	2:C:872:ARG:HD3	1.93	0.50
2:D:751:LEU:H	2:D:772:ILE:HG21	1.76	0.50
2:A:444:CYS:HA	2:A:481:ARG:HA	1.93	0.50
2:B:693:LEU:HD13	2:B:714:PRO:HG3	1.94	0.50
2:C:369:ASP:OD2	2:C:369:ASP:N	2.41	0.50
2:B:567:ARG:NE	2:B:568:LYS:HE3	2.27	0.50
2:A:532:ASP:HB2	2:A:558:TYR:CZ	2.46	0.50
2:B:696:LEU:HD21	2:B:699:LEU:HB2	1.92	0.50
2:D:436:ILE:HD11	2:D:482:VAL:HG21	1.94	0.50
2:C:695:SER:O	2:C:695:SER:OG	2.28	0.50
2:C:836:ASN:HB3	2:C:838:PHE:CE1	2.46	0.50
2:C:880:ILE:HD13	2:C:973:LEU:HD22	1.92	0.50
2:D:808:LYS:HA	2:D:831:GLU:O	2.12	0.50
2:A:847:ALA:O	2:A:851:GLN:NE2	2.45	0.50
2:D:623:LEU:HG	2:D:643:LEU:HD12	1.92	0.50
2:D:661:VAL:O	2:D:684:LEU:HA	2.11	0.50
2:D:749:VAL:HG23	2:D:750:ASN:OD1	2.12	0.50
1:R:28:ILE:N	1:R:63:ALA:O	2.40	0.50
2:A:696:LEU:HD22	2:A:717:ILE:HG22	1.93	0.50
2:D:731:PRO:CG	2:D:754:PHE:HB2	2.30	0.50
2:D:753:ILE:HD12	2:D:753:ILE:H	1.77	0.50
1:Q:45:LEU:HD23	1:Q:50:ALA:HB3	1.94	0.50
2:C:584:PHE:HE1	2:C:608:MET:HE1	1.77	0.50
2:C:900:GLN:OE1	2:C:907:ARG:NH1	2.45	0.50
2:D:439:PHE:CE1	2:D:530:SER:HB2	2.46	0.50
2:A:708:ARG:NH1	2:A:709:ARG:O	2.45	0.49
2:A:900:GLN:HG3	2:A:980:LYS:NZ	2.27	0.49
2:C:942:LEU:H	2:C:942:LEU:HD23	1.76	0.49
2:D:443:GLU:O	2:D:482:VAL:HG22	2.12	0.49
1:P:45:LEU:HD21	1:P:53:MET:SD	2.52	0.49
2:B:559:ASP:OD2	2:B:567:ARG:NH1	2.43	0.49
2:D:764:HIS:HA	2:D:786:LEU:HG	1.94	0.49
2:B:428:LYS:NZ	2:B:456:ASN:O	2.33	0.49
2:C:714:PRO:HD2	2:C:717:ILE:HD11	1.93	0.49
2:B:328:GLU:O	2:B:332:GLN:HG2	2.12	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:D:531:PHE:HB3	2:D:557:VAL:HG13	1.95	0.49
1:S:58:ASP:OD1	1:S:59:ASP:N	2.45	0.49
2:B:732:ALA:HA	2:B:755:TYR:CD1	2.48	0.49
2:C:984:ILE:HG23	2:C:985:LEU:H	1.77	0.49
2:B:649:LEU:HB3	2:B:670:LEU:HD21	1.95	0.49
2:B:859:LEU:HD21	2:B:946:HIS:NE2	2.27	0.49
2:D:895:SER:OG	2:D:942:LEU:O	2.27	0.49
2:A:787:HIS:HB2	2:A:808:LYS:H	1.78	0.49
2:A:359:LYS:HE2	2:A:393:LEU:HD11	1.94	0.49
2:B:571:ILE:HG21	2:B:591:GLY:N	2.28	0.49
2:B:652:LEU:HB3	2:B:676:ILE:HA	1.95	0.49
2:C:705:SER:HA	2:C:725:THR:HA	1.94	0.49
2:C:797:LEU:HB2	2:C:817:SER:HB3	1.95	0.49
2:C:910:LEU:HB2	2:C:978:GLU:HG3	1.95	0.49
2:A:878:LEU:HD13	2:A:975:PHE:HE2	1.78	0.48
2:B:803:LEU:HD23	2:B:807:LEU:HB3	1.94	0.48
1:P:55:LEU:HD13	1:P:65:TYR:CZ	2.47	0.48
2:B:546:PHE:HA	2:B:549:MET:HB3	1.94	0.48
1:P:57:ASN:OD1	2:A:979:TYR:OH	2.25	0.48
1:R:70:SER:O	1:R:73:VAL:HG12	2.12	0.48
2:C:670:LEU:HG	2:C:673:LEU:HD13	1.95	0.48
2:C:717:ILE:HG22	2:C:740:LEU:HA	1.94	0.48
2:C:787:HIS:HB2	2:C:808:LYS:HB2	1.96	0.48
1:S:31:THR:HG22	1:S:32:ASP:H	1.77	0.48
2:A:531:PHE:HB3	2:A:557:VAL:HG12	1.96	0.48
2:A:696:LEU:HD21	2:A:699:LEU:HB2	1.94	0.48
2:B:882:TYR:CE2	2:B:956:PHE:HB3	2.48	0.48
2:B:928:HIS:CE1	2:B:930:SER:H	2.30	0.48
2:C:546:PHE:HA	2:C:549:MET:HB3	1.96	0.48
2:D:432:LEU:O	2:D:436:ILE:HG22	2.13	0.48
2:D:567:ARG:C	2:D:569:LEU:H	2.20	0.48
2:D:811:GLN:HA	2:D:835:ALA:HB2	1.95	0.48
1:P:53:MET:HB2	2:A:928:HIS:HE1	1.78	0.48
2:B:532:ASP:OD1	2:B:532:ASP:N	2.35	0.48
2:C:881:PRO:HA	2:C:969:SER:HA	1.94	0.48
2:C:914:THR:HB	2:C:971:ILE:HG23	1.96	0.48
2:D:454:LYS:HD3	2:D:553:LEU:HD11	1.95	0.48
2:C:384:ALA:HA	2:C:414:ILE:HD11	1.96	0.48
2:C:783:LEU:HD12	2:C:786:LEU:HD13	1.96	0.48
2:A:562:TRP:CZ3	2:A:565:GLY:HA3	2.48	0.48
1:P:60:GLU:HG2	1:P:61:GLU:N	2.29	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:A:445:ALA:HB3	2:A:480:LYS:HG2	1.95	0.48
2:A:635:SER:O	2:A:658:THR:OG1	2.31	0.48
1:R:52:ARG:HA	1:R:52:ARG:HD3	1.70	0.48
1:S:28:ILE:HD12	1:S:90:ASP:OD2	2.14	0.48
2:B:727:LEU:HD11	2:B:747:GLY:O	2.14	0.48
2:C:707:LEU:O	2:C:726:THR:OG1	2.32	0.48
2:D:762:VAL:HG23	2:D:785:ASN:HD21	1.79	0.48
2:D:871:HIS:HB3	2:D:879:ILE:HG13	1.95	0.48
2:A:818:LEU:H	2:A:838:PHE:HD2	1.60	0.47
2:C:878:LEU:HD12	2:C:987:CYS:HB2	1.96	0.47
2:D:667:ILE:O	2:D:693:LEU:HD21	2.13	0.47
1:Q:25:GLU:HB2	1:Q:91:LYS:HE2	1.96	0.47
2:B:727:LEU:HB3	2:B:751:LEU:HD13	1.96	0.47
2:D:603:LEU:HD23	2:D:604:VAL:N	2.29	0.47
2:D:738:SER:HA	2:D:759:PRO:HD2	1.95	0.47
2:D:836:ASN:O	2:D:838:PHE:N	2.47	0.47
1:Q:30:LYS:NZ	1:Q:60:GLU:O	2.47	0.47
2:A:645:ASN:O	2:A:645:ASN:ND2	2.47	0.47
2:D:711:PRO:HB2	2:D:713:ILE:HG12	1.95	0.47
2:A:419:LYS:HG3	2:A:423:GLU:HG2	1.96	0.47
2:A:594:LEU:HD13	2:A:613:LEU:HD21	1.95	0.47
2:A:828:PRO:HG2	2:A:829:ASN:OD1	2.15	0.47
2:B:793:GLY:H	2:B:814:ASP:HB2	1.79	0.47
2:D:754:PHE:C	2:D:754:PHE:CD2	2.93	0.47
2:D:811:GLN:O	2:D:812:ALA:C	2.57	0.47
2:D:895:SER:HB3	2:D:945:PRO:HA	1.95	0.47
2:A:439:PHE:CE2	2:A:530:SER:HB2	2.50	0.47
2:A:776:THR:HG22	2:A:779:CYS:H	1.79	0.47
2:A:813:ASP:OD1	2:A:836:ASN:ND2	2.47	0.47
2:C:824:HIS:NE2	2:C:826:ASN:HB3	2.29	0.47
2:D:808:LYS:HD2	2:D:831:GLU:HB2	1.97	0.47
2:B:878:LEU:HD13	2:B:987:CYS:HB2	1.97	0.47
2:B:507:LEU:HD23	2:B:513:ILE:HG23	1.95	0.47
2:D:443:GLU:N	2:D:443:GLU:OE2	2.48	0.47
2:D:979:TYR:HB2	2:D:982:PHE:HE1	1.79	0.47
2:B:556:LYS:HG3	2:B:585:HIS:HB3	1.97	0.47
2:B:603:LEU:HD23	2:B:604:VAL:N	2.29	0.47
2:B:610:ASP:OD2	2:B:633:ARG:NH2	2.45	0.47
2:B:620:THR:O	2:B:620:THR:OG1	2.30	0.47
2:B:787:HIS:O	2:B:809:ILE:HG22	2.15	0.47
2:D:709:ARG:O	2:D:731:PRO:HA	2.15	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:S:89:ILE:HD12	1:S:89:ILE:H	1.80	0.46
2:B:504:SER:O	2:B:526:ILE:HD12	2.14	0.46
2:C:794:CYS:SG	2:C:797:LEU:HG	2.55	0.46
2:C:926:THR:HG23	2:C:926:THR:O	2.15	0.46
2:B:327:LYS:O	2:B:331:GLN:HG2	2.16	0.46
2:D:377:ILE:HD11	2:D:408:ARG:HE	1.80	0.46
1:S:41:GLN:NE2	2:D:933:PHE:HB2	2.28	0.46
2:A:984:ILE:HG22	2:A:986:GLU:H	1.80	0.46
2:B:393:LEU:HD23	2:B:394:ARG:HB2	1.96	0.46
2:B:812:ALA:HB1	2:B:836:ASN:ND2	2.30	0.46
2:B:878:LEU:HD21	2:B:988:GLY:C	2.40	0.46
2:C:772:ILE:O	2:C:797:LEU:HD23	2.16	0.46
2:C:872:ARG:NH1	2:C:874:ARG:HH11	2.14	0.46
2:D:636:CYS:HA	2:D:659:ALA:HB3	1.97	0.46
2:D:714:PRO:CG	2:D:717:ILE:HG13	2.35	0.46
1:S:55:LEU:HD22	1:S:65:TYR:HE1	1.81	0.46
2:A:644:SER:HB3	2:A:666:SER:HB2	1.96	0.46
2:A:764:HIS:HE2	2:A:766:ASN:HB2	1.79	0.46
2:B:809:ILE:O	2:B:811:GLN:HG2	2.16	0.46
2:D:809:ILE:HD12	2:D:833:TYR:HB2	1.97	0.46
2:A:912:ARG:HH21	2:A:974:GLU:HB2	1.79	0.46
2:C:608:MET:HE3	2:C:608:MET:HA	1.97	0.46
2:D:705:SER:O	2:D:725:THR:HG22	2.15	0.46
2:D:834:PHE:CD2	2:D:861:PRO:HG3	2.50	0.46
2:A:902:PHE:CD2	2:A:905:VAL:HG22	2.50	0.46
2:D:820:SER:OG	2:D:843:GLU:OE2	2.32	0.46
2:C:825:LEU:HG	2:C:851:GLN:NE2	2.31	0.46
2:D:745:ILE:HG22	2:D:746:SER:N	2.31	0.46
2:A:445:ALA:O	2:A:449:THR:HG22	2.15	0.46
2:B:381:LEU:HD23	2:B:487:LEU:HD12	1.98	0.46
2:C:685:GLU:OE2	2:C:706:ARG:NH1	2.43	0.46
2:C:904:LEU:HA	2:C:933:PHE:CE1	2.51	0.46
2:D:709:ARG:HB3	2:D:729:GLU:CB	2.46	0.46
2:A:526:ILE:HG13	2:A:549:MET:HE1	1.98	0.46
2:C:661:VAL:O	2:C:684:LEU:HA	2.15	0.46
2:D:808:LYS:HB3	2:D:808:LYS:HE2	1.54	0.46
2:D:858:ALA:HB1	2:D:860:LEU:HD21	1.98	0.46
2:A:464:LYS:HE2	2:A:464:LYS:HB3	1.83	0.46
2:C:975:PHE:HB3	2:C:984:ILE:HG12	1.97	0.46
2:D:845:ARG:HE	2:D:866:PRO:HA	1.81	0.46
1:R:25:GLU:HB3	1:R:93:ILE:HG13	1.98	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:R:27:ARG:HA	1:R:64:THR:HA	1.98	0.45
2:A:916:ILE:HD12	2:A:971:ILE:HG23	1.98	0.45
2:D:438:VAL:HG21	2:D:506:ILE:HD13	1.97	0.45
2:D:563:HIS:CE1	2:D:566:LYS:HE2	2.50	0.45
2:D:710:PHE:HB3	2:D:712:ASP:OD1	2.17	0.45
2:B:525:SER:C	2:B:526:ILE:HD13	2.41	0.45
2:C:640:LEU:HD12	2:C:640:LEU:HA	1.86	0.45
2:C:848:ILE:O	2:C:860:LEU:HD21	2.15	0.45
2:D:439:PHE:HE1	2:D:530:SER:HB2	1.81	0.45
2:D:845:ARG:HH21	2:D:866:PRO:HA	1.81	0.45
1:S:55:LEU:HD21	2:D:906:PRO:HG3	1.99	0.45
2:A:805:ARG:NH2	2:A:806:SER:HB3	2.31	0.45
2:B:552:LEU:HD21	2:B:555:LEU:HB3	1.99	0.45
2:B:900:GLN:HG3	2:B:980:LYS:HD3	1.98	0.45
2:C:538:GLU:H	2:C:568:LYS:HB3	1.81	0.45
2:A:592:LYS:O	2:A:593:ARG:HG2	2.16	0.45
2:A:608:MET:HE3	2:A:608:MET:HA	1.99	0.45
2:A:736:HIS:HB2	2:A:759:PRO:HA	1.99	0.45
2:B:478:GLN:HB3	2:B:481:ARG:HD3	1.98	0.45
2:C:449:THR:HA	2:C:459:VAL:HG11	1.99	0.45
2:C:751:LEU:O	2:C:772:ILE:HA	2.16	0.45
2:C:869:PHE:CZ	2:C:891:CYS:HB2	2.51	0.45
2:A:747:GLY:N	2:A:770:SER:OG	2.49	0.45
2:A:913:TRP:CZ2	2:A:954:LEU:HD13	2.52	0.45
2:B:395:LYS:NZ	2:B:403:GLU:OE2	2.45	0.45
2:C:373:GLU:HG2	2:C:376:ARG:HH21	1.81	0.45
2:C:690:LEU:HB2	2:C:693:LEU:HD11	1.98	0.45
1:S:54:LYS:HB2	1:S:66:LYS:HB2	1.98	0.45
2:A:426:ASN:O	2:A:430:GLN:HG3	2.15	0.45
2:A:730:LEU:N	2:A:731:PRO:HD3	2.32	0.45
2:D:891:CYS:HA	2:D:948:PHE:O	2.16	0.45
2:A:621:GLN:NE2	2:A:623:LEU:HB3	2.31	0.45
2:C:513:ILE:HB	2:C:531:PHE:CE1	2.50	0.45
2:D:693:LEU:HD12	2:D:693:LEU:H	1.82	0.45
2:A:696:LEU:HD11	2:A:699:LEU:HD22	1.99	0.45
2:B:780:ILE:HA	2:B:783:LEU:HD13	1.99	0.45
2:B:819:GLU:HB3	2:B:839:LYS:HE2	1.99	0.45
2:B:857:TRP:HB2	2:B:950:PHE:HA	1.98	0.45
2:B:907:ARG:HH21	2:B:982:PHE:HA	1.81	0.45
2:C:604:VAL:O	2:C:627:LYS:N	2.48	0.45
2:D:913:TRP:NE1	2:D:923:ASP:OD1	2.50	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:D:793:GLY:HA2	2:D:812:ALA:O	2.16	0.45
2:D:859:LEU:O	2:D:860:LEU:HD23	2.17	0.45
1:Q:27:ARG:HG3	1:Q:90:ASP:HB3	1.98	0.45
1:Q:47:LYS:HE2	2:B:679:TYR:CE1	2.52	0.44
1:S:23:SER:HB2	1:S:66:LYS:HD2	1.98	0.44
2:B:571:ILE:HG13	2:B:572:PRO:HD2	1.99	0.44
2:B:754:PHE:HB2	2:B:774:TRP:CE3	2.52	0.44
2:B:894:MET:HE3	2:B:894:MET:HB3	1.74	0.44
2:C:676:ILE:HD12	2:C:696:LEU:HD12	2.00	0.44
2:A:691:ILE:C	2:A:714:PRO:HB3	2.43	0.44
2:A:752:LYS:O	2:A:773:GLU:N	2.48	0.44
2:A:771:GLY:HA3	2:A:796:ARG:CZ	2.47	0.44
2:B:835:ALA:C	2:B:837:CYS:H	2.25	0.44
1:Q:47:LYS:HE2	1:Q:47:LYS:HB3	1.85	0.44
1:S:55:LEU:HD13	1:S:65:TYR:CE1	2.52	0.44
2:A:641:PRO:HG2	2:A:643:LEU:HD21	2.00	0.44
2:B:810:LEU:C	2:B:811:GLN:HG2	2.41	0.44
2:C:529:VAL:HG13	2:C:555:LEU:HA	1.99	0.44
2:C:709:ARG:HD2	2:C:729:GLU:HB3	1.97	0.44
2:D:439:PHE:HB2	2:D:440:PHE:CD1	2.53	0.44
2:D:748:SER:O	2:D:751:LEU:HD22	2.18	0.44
2:D:874:ARG:HA	2:D:874:ARG:HD3	1.81	0.44
1:S:27:ARG:HH12	1:S:93:ILE:HD11	1.81	0.44
2:A:764:HIS:HA	2:A:788:ASP:HB3	1.99	0.44
2:D:704:CYS:O	2:D:705:SER:OG	2.31	0.44
2:D:784:HIS:HD2	2:D:785:ASN:ND2	2.15	0.44
2:D:888:PHE:HE2	2:D:952:SER:HB2	1.82	0.44
1:Q:77:LEU:HD22	1:Q:92:ILE:O	2.17	0.44
2:A:673:LEU:HB3	2:A:693:LEU:HD11	1.98	0.44
2:B:399:ASP:N	2:B:399:ASP:OD1	2.51	0.44
2:B:915:VAL:HG22	2:B:919:SER:HA	1.99	0.44
2:C:439:PHE:HB2	2:C:440:PHE:CD1	2.52	0.44
2:C:443:GLU:OE1	2:C:443:GLU:N	2.51	0.44
2:D:464:LYS:HB3	2:D:464:LYS:HE2	1.74	0.44
2:D:728:GLU:HG2	2:D:750:ASN:HB2	1.98	0.44
2:A:600:ALA:HB3	2:A:621:GLN:NE2	2.23	0.44
2:B:862:GLY:O	2:B:946:HIS:HA	2.18	0.44
2:C:813:ASP:OD1	2:C:813:ASP:N	2.50	0.44
2:D:686:VAL:CG2	2:D:710:PHE:HB2	2.47	0.44
1:R:32:ASP:OD1	1:R:32:ASP:N	2.40	0.44
1:S:43:CYS:SG	1:S:47:LYS:HE3	2.58	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:S:51:SER:HB2	2:D:788:ASP:OD2	2.18	0.44
2:A:724:GLY:HA2	2:A:747:GLY:HA3	2.00	0.44
2:C:644:SER:HB3	2:C:666:SER:HB2	2.00	0.44
2:A:370:LEU:HD12	2:A:400:TRP:HD1	1.83	0.44
2:A:895:SER:OG	2:A:945:PRO:HA	2.18	0.44
2:B:692:ASN:OD1	2:B:692:ASN:N	2.50	0.44
2:B:833:TYR:CB	2:B:859:LEU:HB3	2.47	0.44
2:B:972:MET:HE2	2:B:972:MET:HA	2.00	0.44
2:D:889:LYS:HD3	2:D:950:PHE:O	2.17	0.44
1:R:59:ASP:HB3	1:R:62:VAL:O	2.18	0.43
1:S:29:LYS:O	1:S:29:LYS:HG3	2.18	0.43
1:S:91:LYS:HA	1:S:91:LYS:HD3	1.67	0.43
2:B:727:LEU:HB2	2:B:751:LEU:HA	2.00	0.43
2:C:894:MET:SD	2:C:895:SER:N	2.91	0.43
2:D:681:CYS:O	2:D:681:CYS:SG	2.76	0.43
2:A:658:THR:O	2:A:682:GLU:HB3	2.17	0.43
2:B:797:LEU:HD13	2:B:813:ASP:OD2	2.18	0.43
2:D:715:THR:HA	2:D:737:CYS:HB3	2.00	0.43
2:D:878:LEU:HD13	2:D:988:GLY:HA2	2.00	0.43
2:C:670:LEU:HD12	2:C:671:HIS:N	2.33	0.43
2:C:735:THR:HG21	2:C:758:LEU:C	2.43	0.43
2:C:754:PHE:CE2	2:C:775:ILE:HG23	2.53	0.43
2:D:809:ILE:CG1	2:D:811:GLN:HG2	2.49	0.43
1:P:53:MET:HB2	2:A:928:HIS:CE1	2.53	0.43
2:B:582:ARG:HB3	2:B:604:VAL:HG12	2.00	0.43
2:B:731:PRO:HG2	2:B:754:PHE:HA	2.00	0.43
2:C:869:PHE:CE2	2:C:889:LYS:HB2	2.53	0.43
1:P:41:GLN:CA	1:P:44:VAL:HG12	2.46	0.43
2:A:327:LYS:O	2:A:331:GLN:HG2	2.19	0.43
2:D:894:MET:N	2:D:946:HIS:O	2.52	0.43
2:A:549:MET:HE2	2:A:552:LEU:HD13	2.00	0.43
2:A:729:GLU:OE1	2:A:751:LEU:HB3	2.19	0.43
2:A:878:LEU:HD11	2:A:989:VAL:HG22	1.99	0.43
2:C:540:MET:SD	2:C:540:MET:N	2.92	0.43
2:C:818:LEU:O	2:C:820:SER:N	2.52	0.43
2:C:876:ASN:C	2:C:876:ASN:OD1	2.61	0.43
2:D:327:LYS:O	2:D:331:GLN:HG2	2.18	0.43
2:D:451:MET:HG2	2:D:451:MET:H	1.64	0.43
2:D:792:SER:HA	2:D:811:GLN:HB2	2.00	0.43
2:B:702:ASN:HB2	2:B:721:GLN:OE1	2.17	0.43
2:C:537:ASP:OD1	2:C:538:GLU:N	2.52	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:C:651:ASP:OD1	2:C:675:HIS:HB2	2.19	0.43
2:C:670:LEU:HD12	2:C:671:HIS:H	1.83	0.43
2:C:748:SER:HB2	2:C:770:SER:HB3	2.01	0.43
2:D:728:GLU:O	2:D:753:ILE:HD13	2.18	0.43
2:A:328:GLU:HB2	2:A:468:ASN:HD22	1.83	0.43
2:A:603:LEU:HD23	2:A:604:VAL:N	2.33	0.43
2:A:693:LEU:HD22	2:A:696:LEU:HB2	2.00	0.43
2:C:451:MET:H	2:C:451:MET:HG2	1.56	0.43
2:D:419:LYS:O	2:D:423:GLU:HG2	2.19	0.43
1:P:39:LEU:HD13	1:P:39:LEU:HA	1.67	0.43
1:Q:58:ASP:HA	1:Q:63:ALA:HA	2.01	0.43
2:A:526:ILE:CG1	2:A:549:MET:HE1	2.49	0.43
2:B:647:THR:O	2:B:672:LYS:HB2	2.18	0.43
2:B:786:LEU:HD21	2:B:789:LEU:HG	2.00	0.43
2:D:555:LEU:HD21	2:D:584:PHE:CD2	2.53	0.43
2:D:686:VAL:HG22	2:D:710:PHE:HB2	2.01	0.43
2:D:709:ARG:H	2:D:709:ARG:HG3	1.51	0.43
2:A:439:PHE:HB2	2:A:440:PHE:CD1	2.54	0.42
2:C:670:LEU:HG	2:C:673:LEU:CD1	2.48	0.42
2:D:373:GLU:O	2:D:377:ILE:HG12	2.19	0.42
2:D:618:GLU:OE2	2:D:618:GLU:N	2.42	0.42
2:D:714:PRO:HG2	2:D:717:ILE:CG1	2.36	0.42
2:D:917:GLY:HA3	2:D:968:ILE:HD11	2.00	0.42
2:A:681:CYS:CB	2:A:684:LEU:HD11	2.48	0.42
2:A:804:PRO:HD2	2:A:807:LEU:HD11	2.01	0.42
2:B:354:CYS:HB3	2:B:360:GLN:O	2.19	0.42
2:C:377:ILE:HD11	2:C:408:ARG:CZ	2.50	0.42
2:D:399:ASP:N	2:D:399:ASP:OD1	2.51	0.42
2:D:537:ASP:OD1	2:D:537:ASP:N	2.51	0.42
1:P:42:ALA:O	1:P:46:ASN:N	2.45	0.42
2:B:444:CYS:SG	2:B:479:LYS:HD3	2.60	0.42
2:B:715:THR:HA	2:B:737:CYS:SG	2.59	0.42
2:B:908:ASN:OD1	2:B:928:HIS:HB2	2.20	0.42
2:C:675:HIS:CD2	2:C:698:PHE:HE1	2.37	0.42
2:C:744:LYS:HA	2:C:766:ASN:O	2.19	0.42
2:A:584:PHE:HE2	2:A:608:MET:HE1	1.84	0.42
2:A:912:ARG:HD2	2:A:913:TRP:H	1.84	0.42
2:B:531:PHE:HB3	2:B:557:VAL:HG12	2.01	0.42
2:B:912:ARG:HB3	2:B:975:PHE:HA	2.01	0.42
2:C:526:ILE:HG13	2:C:549:MET:HE1	2.02	0.42
2:C:574:ASP:N	2:C:574:ASP:OD1	2.51	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:C:719:ASP:HA	2:C:741:GLN:O	2.20	0.42
2:C:789:LEU:HB3	2:C:791:LEU:HD13	2.00	0.42
2:D:684:LEU:HD21	2:D:687:ILE:HG23	2.00	0.42
2:D:749:VAL:HA	2:D:770:SER:HA	2.02	0.42
2:D:793:GLY:N	2:D:812:ALA:HB3	2.35	0.42
2:B:384:ALA:HB2	2:B:487:LEU:HD11	2.01	0.42
2:B:569:LEU:HD12	2:B:588:ALA:HB1	2.01	0.42
2:C:528:GLY:HA2	2:C:553:LEU:O	2.19	0.42
2:C:859:LEU:HD21	2:C:946:HIS:CE1	2.53	0.42
1:P:32:ASP:OD1	1:P:32:ASP:O	2.36	0.42
1:R:70:SER:HB2	1:R:72:PHE:CE2	2.54	0.42
2:A:444:CYS:O	2:A:448:VAL:HG23	2.18	0.42
2:A:837:CYS:HA	2:A:861:PRO:HB3	2.02	0.42
2:B:433:PHE:O	2:B:437:THR:HG22	2.18	0.42
2:C:764:HIS:CD2	2:C:788:ASP:HB3	2.55	0.42
2:D:871:HIS:O	2:D:878:LEU:HD12	2.19	0.42
1:P:39:LEU:HG	1:P:86:GLU:HB2	2.02	0.42
1:P:87:CYS:SG	1:P:88:ASN:N	2.92	0.42
2:A:631:LEU:HD13	2:A:637:LEU:HD21	2.00	0.42
2:B:328:GLU:HB2	2:B:468:ASN:ND2	2.34	0.42
2:B:697:THR:O	2:B:718:GLU:N	2.45	0.42
2:B:866:PRO:HD2	2:B:869:PHE:CE2	2.55	0.42
1:R:27:ARG:HD2	1:R:91:LYS:HB2	2.02	0.42
2:A:563:HIS:CG	2:A:564:THR:H	2.38	0.42
2:B:745:ILE:HG22	2:B:745:ILE:O	2.20	0.42
2:C:630:ASP:C	2:C:630:ASP:OD1	2.62	0.42
2:C:820:SER:HG	2:C:841:ASP:HB2	1.85	0.42
2:C:871:HIS:NE2	2:C:878:LEU:HD13	2.35	0.42
2:C:872:ARG:HH12	2:C:874:ARG:HG2	1.85	0.42
2:D:789:LEU:HD13	2:D:808:LYS:H	1.84	0.42
2:A:332:GLN:OE1	2:D:395:LYS:NZ	2.52	0.42
2:A:556:LYS:HA	2:A:585:HIS:O	2.20	0.42
2:C:359:LYS:HE3	2:C:359:LYS:HB3	1.82	0.42
2:C:744:LYS:HG2	2:C:766:ASN:HB3	2.02	0.42
2:A:841:ASP:OD1	2:A:843:GLU:N	2.52	0.42
2:A:904:LEU:H	2:A:904:LEU:HD23	1.84	0.42
2:B:567:ARG:HE	2:B:568:LYS:HE3	1.85	0.42
2:B:728:GLU:CD	2:B:728:GLU:H	2.28	0.42
2:B:914:THR:HB	2:B:974:GLU:HB2	2.02	0.42
2:C:698:PHE:HB2	2:C:719:ASP:HB3	2.02	0.42
2:D:708:ARG:HH21	2:D:709:ARG:HH11	1.67	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:D:769:ASN:O	2:D:769:ASN:ND2	2.53	0.42
2:D:979:TYR:C	2:D:980:LYS:HG3	2.45	0.42
1:P:39:LEU:O	1:P:42:ALA:HB3	2.19	0.41
2:A:347:SER:O	2:A:351:THR:HG23	2.21	0.41
2:A:377:ILE:CD1	2:A:408:ARG:HG2	2.50	0.41
2:A:754:PHE:CD1	2:A:755:TYR:N	2.88	0.41
2:B:623:LEU:HD11	2:B:643:LEU:HD12	2.02	0.41
2:B:793:GLY:N	2:B:814:ASP:HB2	2.33	0.41
2:B:836:ASN:H	2:B:942:LEU:HD22	1.84	0.41
2:B:896:LEU:N	2:B:983:ASP:OD1	2.52	0.41
2:C:512:LYS:O	2:C:516:VAL:HG13	2.20	0.41
2:C:721:GLN:HE21	2:C:744:LYS:HE3	1.84	0.41
2:C:807:LEU:HB3	2:C:827:THR:HG21	2.02	0.41
2:C:892:VAL:HG13	2:C:986:GLU:O	2.20	0.41
2:D:709:ARG:NH1	2:D:710:PHE:HD1	2.11	0.41
1:S:51:SER:OG	1:S:52:ARG:N	2.53	0.41
2:A:811:GLN:HB2	2:A:833:TYR:CD2	2.55	0.41
2:B:370:LEU:HD12	2:B:400:TRP:CD1	2.55	0.41
2:B:690:LEU:HB2	2:B:693:LEU:HD21	2.02	0.41
2:B:700:ASN:HB2	2:B:721:GLN:OE1	2.19	0.41
2:B:789:LEU:HG	2:B:807:LEU:HD13	2.02	0.41
2:D:708:ARG:HE	2:D:709:ARG:HG3	1.85	0.41
1:R:27:ARG:HH11	1:R:91:LYS:HB2	1.84	0.41
1:R:80:ASP:OD2	1:R:82:SER:OG	2.38	0.41
1:S:52:ARG:NH1	1:S:52:ARG:HB2	2.35	0.41
2:B:684:LEU:HD23	2:B:707:LEU:HD21	2.01	0.41
2:C:719:ASP:OD1	2:C:719:ASP:C	2.64	0.41
2:C:872:ARG:HH22	2:C:874:ARG:HG2	1.84	0.41
1:P:42:ALA:HB2	2:A:936:ASP:CB	2.44	0.41
1:P:66:LYS:HB3	1:P:66:LYS:HE3	1.77	0.41
1:P:90:ASP:OD1	1:P:90:ASP:N	2.41	0.41
2:A:440:PHE:HZ	2:A:554:PHE:CE1	2.38	0.41
2:A:859:LEU:HG	2:A:947:LEU:O	2.20	0.41
2:B:335:ILE:HG22	2:B:337:ASP:H	1.85	0.41
2:B:829:ASN:OD1	2:B:855:SER:OG	2.39	0.41
2:D:638:THR:HG22	2:D:639:GLU:HG2	2.02	0.41
2:A:443:GLU:OE1	2:A:443:GLU:N	2.54	0.41
2:B:697:THR:C	2:B:698:PHE:HD2	2.29	0.41
2:D:700:ASN:CG	2:D:702:ASN:HD22	2.27	0.41
2:D:786:LEU:O	2:D:829:ASN:ND2	2.29	0.41
1:P:35:ASN:HB2	1:P:39:LEU:HD23	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:R:80:ASP:OD1	1:R:80:ASP:N	2.52	0.41
2:A:880:ILE:O	2:A:970:ASN:N	2.54	0.41
2:A:894:MET:HG3	2:A:982:PHE:HB3	2.02	0.41
2:C:627:LYS:HE3	2:C:627:LYS:HB2	1.89	0.41
2:C:648:ASN:OD1	2:C:648:ASN:N	2.49	0.41
2:A:440:PHE:CD1	2:A:440:PHE:N	2.88	0.41
2:A:440:PHE:HE2	2:A:451:MET:HG3	1.85	0.41
2:B:377:ILE:HD12	2:B:408:ARG:HA	2.03	0.41
2:B:539:LEU:HD12	2:B:539:LEU:HA	1.82	0.41
2:B:557:VAL:HG22	2:B:586:TRP:HA	2.03	0.41
2:B:907:ARG:HG2	2:B:930:SER:OG	2.21	0.41
2:C:426:ASN:O	2:C:430:GLN:HG3	2.20	0.41
1:S:52:ARG:HB2	1:S:52:ARG:HH11	1.85	0.41
2:B:549:MET:HG2	2:B:552:LEU:HD12	2.03	0.41
2:D:825:LEU:HD22	2:D:851:GLN:HG2	2.02	0.41
2:A:621:GLN:OE1	2:A:621:GLN:N	2.54	0.41
2:A:683:SER:OG	2:A:685:GLU:HG3	2.20	0.41
2:A:709:ARG:NE	2:A:728:GLU:OE1	2.49	0.41
2:A:913:TRP:HH2	2:A:954:LEU:HD22	1.86	0.41
2:B:979:TYR:O	2:B:981:ASP:N	2.54	0.41
2:C:692:ASN:O	2:C:692:ASN:CG	2.63	0.41
2:D:752:LYS:CA	2:D:772:ILE:HD12	2.50	0.41
2:D:789:LEU:HB3	2:D:809:ILE:HG22	2.02	0.41
1:P:53:MET:SD	1:P:53:MET:N	2.95	0.41
1:R:40:CYS:HB2	1:R:87:CYS:HB3	1.71	0.41
1:S:43:CYS:O	1:S:47:LYS:HB2	2.21	0.41
2:A:381:LEU:HB2	2:A:485:HIS:CE1	2.56	0.41
2:A:712:ASP:CG	2:A:713:ILE:H	2.29	0.41
2:A:837:CYS:SG	2:A:944:LYS:HE3	2.61	0.41
2:B:769:ASN:ND2	2:B:793:GLY:O	2.53	0.41
2:C:758:LEU:HD23	2:C:758:LEU:HA	1.93	0.41
2:D:369:ASP:OD2	2:D:369:ASP:N	2.45	0.41
2:D:764:HIS:CD2	2:D:788:ASP:HB3	2.55	0.41
2:D:793:GLY:H	2:D:812:ALA:HB3	1.85	0.41
1:R:34:ARG:O	2:C:904:LEU:HD21	2.20	0.40
1:S:53:MET:HB2	2:D:931:HIS:HE1	1.86	0.40
2:A:454:LYS:NZ	2:A:553:LEU:HD11	2.35	0.40
2:A:709:ARG:NE	2:A:728:GLU:HB3	2.36	0.40
1:R:81:CYS:SG	1:R:86:GLU:HB3	2.61	0.40
1:S:51:SER:OG	1:S:68:THR:HG23	2.22	0.40
2:B:628:LYS:HB2	2:B:628:LYS:HE3	1.93	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:701:MET:HE2	2:B:722:VAL:HG22	2.02	0.40
2:D:711:PRO:HG3	2:D:756:THR:HG21	2.02	0.40
2:D:745:ILE:HD12	2:D:745:ILE:N	2.36	0.40
2:D:849:ILE:HD12	2:D:849:ILE:H	1.86	0.40
2:B:379:ASP:HB3	2:B:485:HIS:CE1	2.56	0.40
2:B:440:PHE:CD1	2:B:440:PHE:N	2.89	0.40
2:B:754:PHE:HB2	2:B:774:TRP:CZ3	2.56	0.40
2:C:894:MET:N	2:C:946:HIS:O	2.54	0.40
2:A:471:LEU:HD23	2:A:471:LEU:HA	1.88	0.40
2:A:593:ARG:NH1	2:A:594:LEU:O	2.54	0.40
2:B:756:THR:HG1	2:B:774:TRP:HH2	1.70	0.40
2:C:439:PHE:HB2	2:C:440:PHE:CE1	2.55	0.40
2:D:451:MET:SD	2:D:604:VAL:HG11	2.62	0.40
2:D:803:LEU:O	2:D:805:ARG:N	2.54	0.40
1:R:22:LYS:HB3	1:R:69:GLY:O	2.21	0.40
1:S:52:ARG:O	1:S:68:THR:HG22	2.21	0.40
2:A:754:PHE:CD1	2:A:754:PHE:C	3.00	0.40
2:A:779:CYS:O	2:A:780:ILE:HD13	2.21	0.40
2:B:636:CYS:O	2:B:636:CYS:SG	2.80	0.40
2:C:773:GLU:O	2:C:797:LEU:HA	2.21	0.40
2:C:805:ARG:HG2	2:C:806:SER:N	2.36	0.40
2:D:569:LEU:HD22	2:D:588:ALA:O	2.21	0.40

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all PDB entries followed by that with respect to all EM entries.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	P	75/216 (35%)	67 (89%)	8 (11%)	0	100	100
1	Q	75/216 (35%)	66 (88%)	9 (12%)	0	100	100
1	R	75/216 (35%)	66 (88%)	9 (12%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	S	75/216 (35%)	66 (88%)	8 (11%)	1 (1%)	9	41
2	A	655/1007 (65%)	580 (88%)	72 (11%)	3 (0%)	24	60
2	B	655/1007 (65%)	578 (88%)	77 (12%)	0	100	100
2	C	655/1007 (65%)	573 (88%)	77 (12%)	5 (1%)	16	52
2	D	655/1007 (65%)	573 (88%)	79 (12%)	3 (0%)	24	60
All	All	2920/4892 (60%)	2569 (88%)	339 (12%)	12 (0%)	31	65

All (12) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	C	819	GLU
2	D	837	CYS
2	C	851	GLN
2	C	890	VAL
1	S	87	CYS
2	A	593	ARG
2	C	790	CYS
2	D	812	ALA
2	A	938	VAL
2	C	837	CYS
2	D	593	ARG
2	A	711	PRO

5.3.2 Protein sidechains ⓘ

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all PDB entries followed by that with respect to all EM entries.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	P	68/196 (35%)	61 (90%)	7 (10%)	7	25
1	Q	68/196 (35%)	64 (94%)	4 (6%)	18	42
1	R	68/196 (35%)	66 (97%)	2 (3%)	37	58
1	S	68/196 (35%)	67 (98%)	1 (2%)	57	70
2	A	597/907 (66%)	582 (98%)	15 (2%)	42	62

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
2	B	597/907 (66%)	580 (97%)	17 (3%)	38	60
2	C	597/907 (66%)	577 (97%)	20 (3%)	32	55
2	D	597/907 (66%)	575 (96%)	22 (4%)	30	52
All	All	2660/4412 (60%)	2572 (97%)	88 (3%)	34	56

All (88) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	P	26	LEU
1	P	39	LEU
1	P	40	CYS
1	P	41	GLN
1	P	84	VAL
1	P	86	GLU
1	P	87	CYS
1	Q	28	ILE
1	Q	47	LYS
1	Q	55	LEU
1	Q	76	ASN
1	R	54	LYS
1	R	92	ILE
1	S	31	THR
2	A	537	ASP
2	A	571	ILE
2	A	581	ILE
2	A	620	THR
2	A	721	GLN
2	A	730	LEU
2	A	762	VAL
2	A	780	ILE
2	A	805	ARG
2	A	832	LEU
2	A	833	TYR
2	A	838	PHE
2	A	898	HIS
2	A	931	HIS
2	A	943	GLN
2	B	380	LYS
2	B	477	ASP
2	B	506	ILE
2	B	532	ASP

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Mol	Chain	Res	Type
2	B	554	PHE
2	B	569	LEU
2	B	598	PHE
2	B	623	LEU
2	B	643	LEU
2	B	654	VAL
2	B	676	ILE
2	B	727	LEU
2	B	740	LEU
2	B	788	ASP
2	B	815	CYS
2	B	865	VAL
2	B	882	TYR
2	C	446	ASP
2	C	448	VAL
2	C	477	ASP
2	C	482	VAL
2	C	529	VAL
2	C	554	PHE
2	C	555	LEU
2	C	557	VAL
2	C	634	SER
2	C	654	VAL
2	C	709	ARG
2	C	710	PHE
2	C	742	THR
2	C	818	LEU
2	C	863	LEU
2	C	871	HIS
2	C	902	PHE
2	C	909	LEU
2	C	911	TYR
2	C	951	HIS
2	D	329	ILE
2	D	412	ASP
2	D	495	VAL
2	D	513	ILE
2	D	517	LEU
2	D	554	PHE
2	D	570	ASP
2	D	571	ILE
2	D	599	PHE

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Mol	Chain	Res	Type
2	D	629	ILE
2	D	639	GLU
2	D	656	SER
2	D	709	ARG
2	D	719	ASP
2	D	752	LYS
2	D	753	ILE
2	D	754	PHE
2	D	806	SER
2	D	807	LEU
2	D	808	LYS
2	D	809	ILE
2	D	832	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (29) such sidechains are listed below:

Mol	Chain	Res	Type
1	Q	41	GLN
1	R	46	ASN
2	A	485	HIS
2	A	645	ASN
2	A	692	ASN
2	A	824	HIS
2	A	897	ASN
2	A	900	GLN
2	A	934	ASN
2	B	468	ASN
2	B	607	ASN
2	B	614	GLN
2	B	824	HIS
2	B	836	ASN
2	C	473	HIS
2	C	478	GLN
2	C	551	ASN
2	C	625	ASN
2	C	785	ASN
2	D	447	HIS
2	D	602	ASN
2	D	614	GLN
2	D	621	GLN
2	D	769	ASN
2	D	784	HIS

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Mol	Chain	Res	Type
2	D	811	GLN
2	D	824	HIS
2	D	931	HIS
2	D	934	ASN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains [i](#)

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

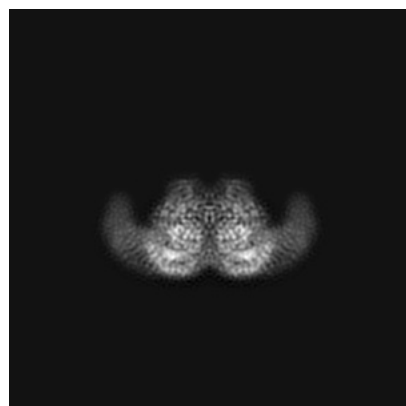
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-53346. These allow visual inspection of the internal detail of the map and identification of artifacts.

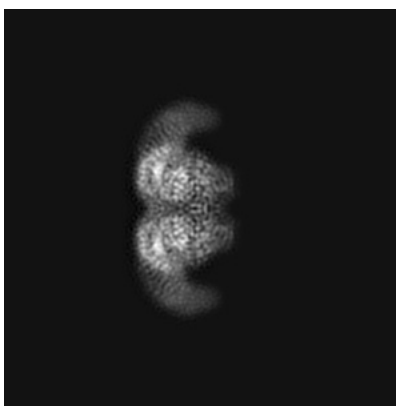
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

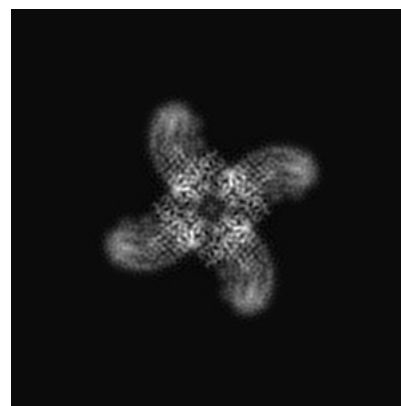
6.1.1 Primary map



X

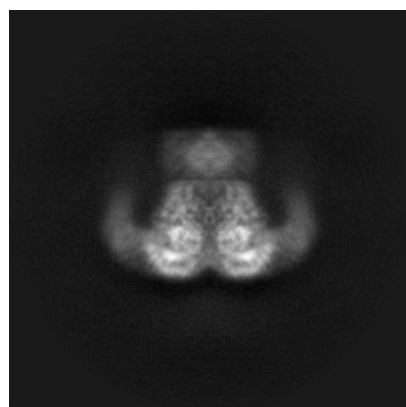


Y

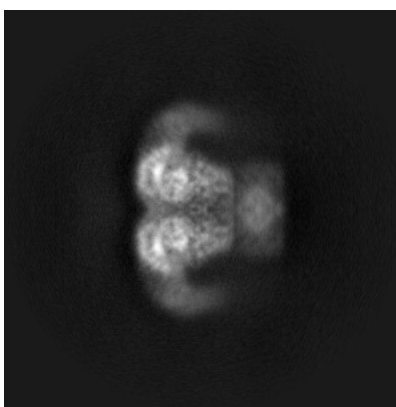


Z

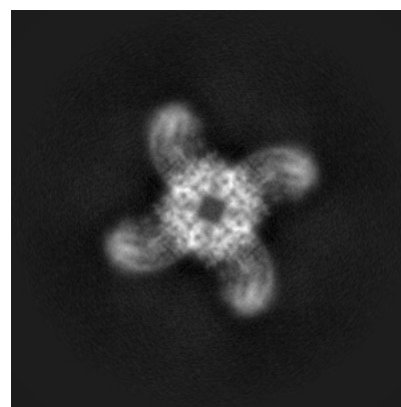
6.1.2 Raw map



X



Y



Z

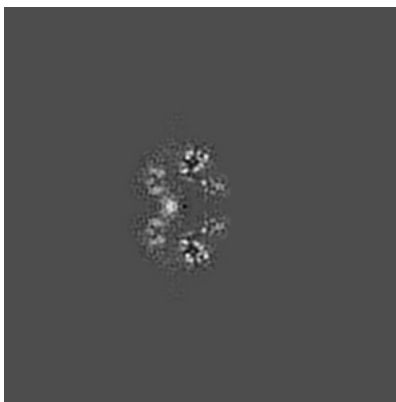
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

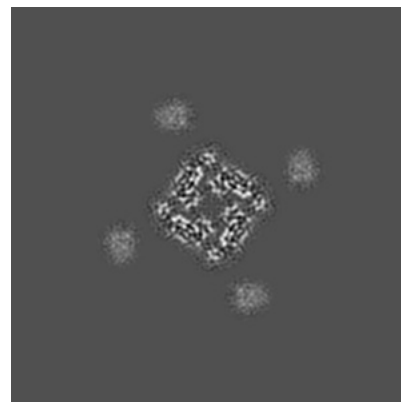
6.2.1 Primary map



X Index: 200

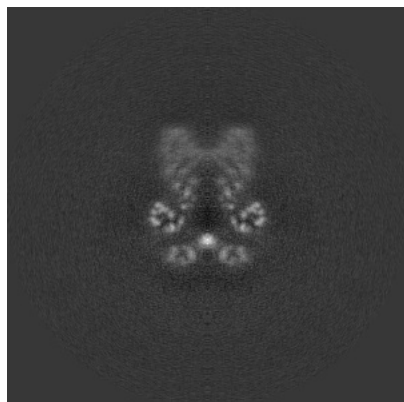


Y Index: 200

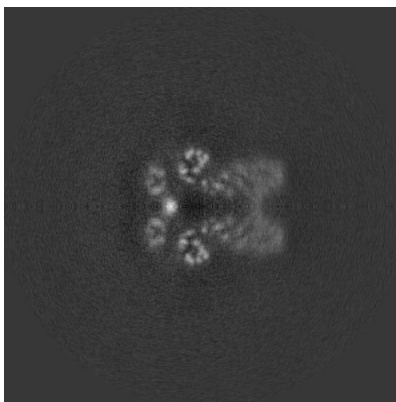


Z Index: 200

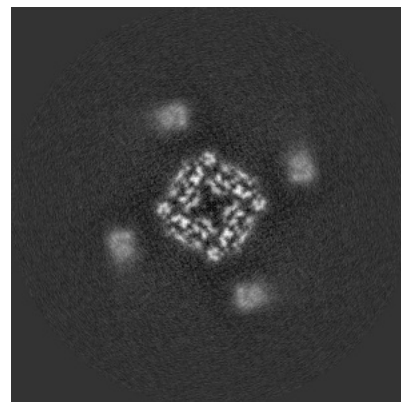
6.2.2 Raw map



X Index: 200



Y Index: 200

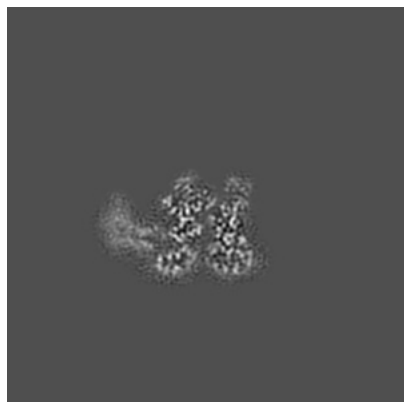


Z Index: 200

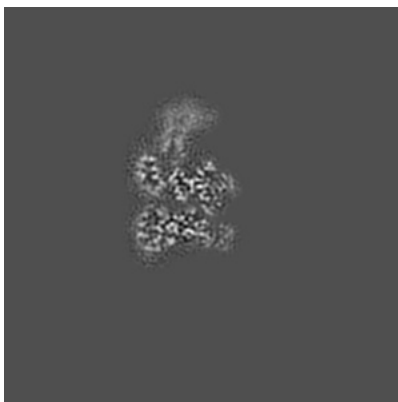
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

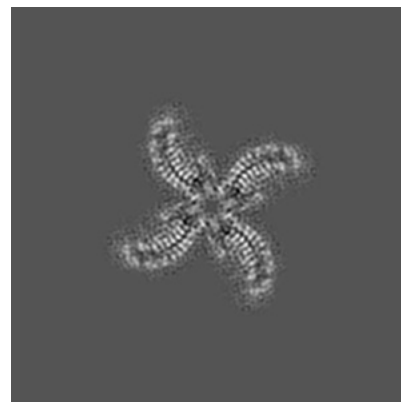
6.3.1 Primary map



X Index: 225

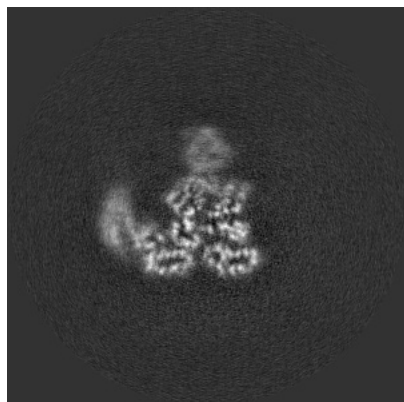


Y Index: 225

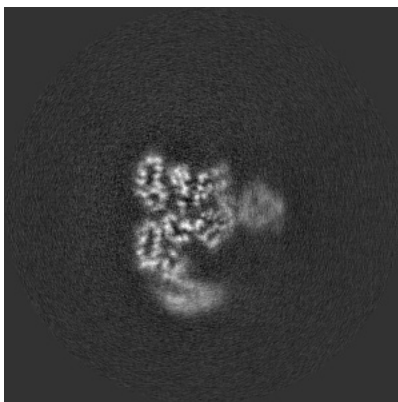


Z Index: 152

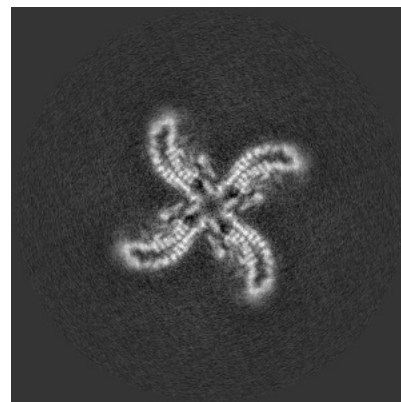
6.3.2 Raw map



X Index: 232



Y Index: 168

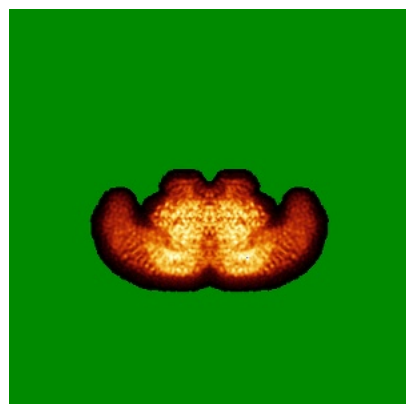


Z Index: 153

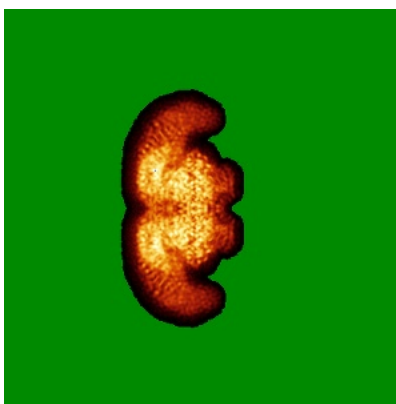
The images above show the largest variance slices of the map in three orthogonal directions.

6.4 Orthogonal standard-deviation projections (False-color) [i](#)

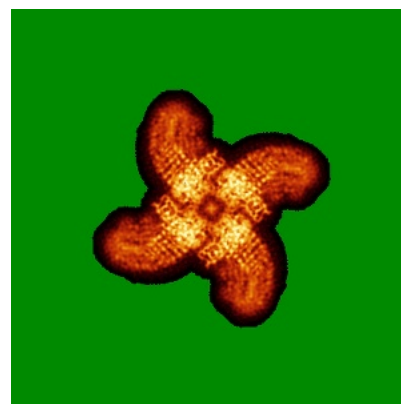
6.4.1 Primary map



X

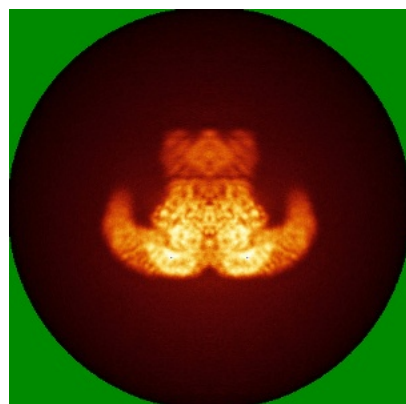


Y

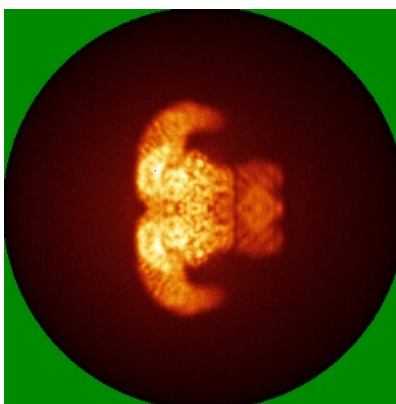


Z

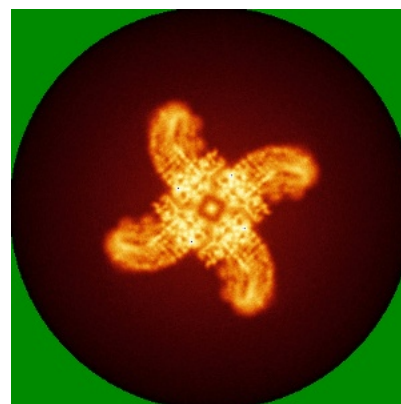
6.4.2 Raw map



X



Y

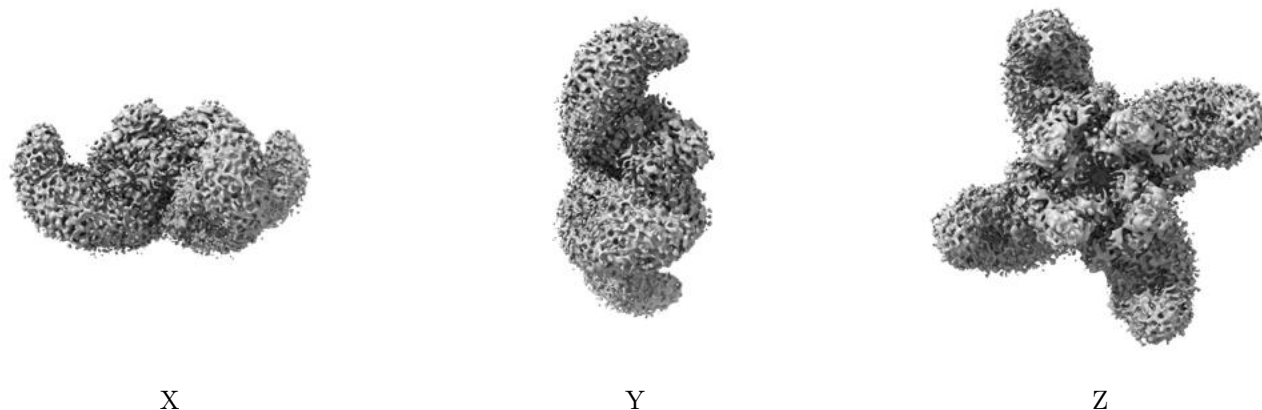


Z

The images above show the map standard deviation projections with false color in three orthogonal directions. Minimum values are shown in green, max in blue, and dark to light orange shades represent small to large values respectively.

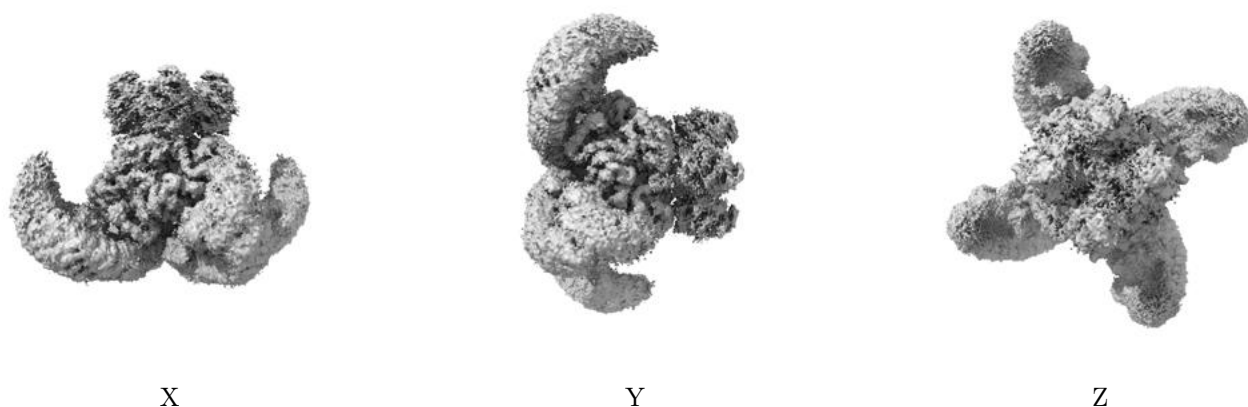
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.005. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.5.2 Raw map



These images show the 3D surface of the raw map. The raw map's contour level was selected so that its surface encloses the same volume as the primary map does at its recommended contour level.

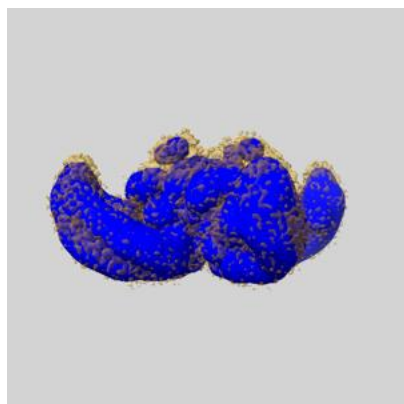
6.6 Mask visualisation [i](#)

This section shows the 3D surface view of the primary map at 50% transparency overlaid with the specified mask at 0% transparency

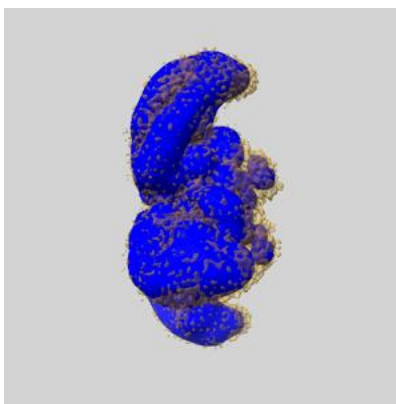
A mask typically either:

- Encompasses the whole structure
- Separates out a domain, a functional unit, a monomer or an area of interest from a larger structure

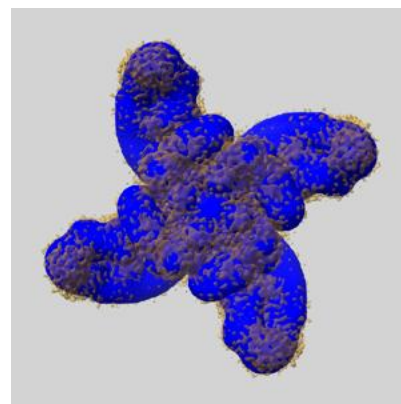
6.6.1 emd_53346_msk_1.map [i](#)



X



Y

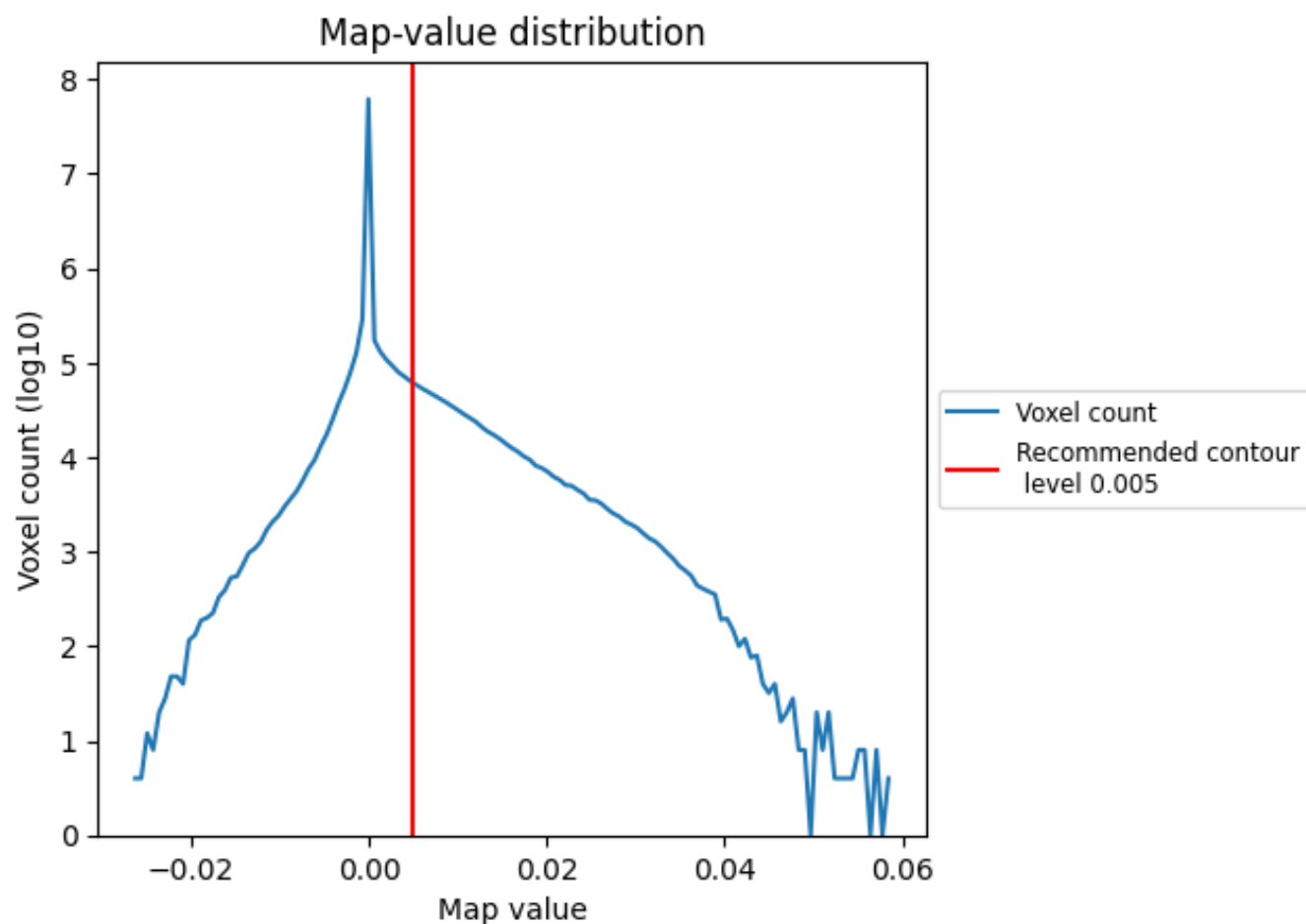


Z

7 Map analysis [i](#)

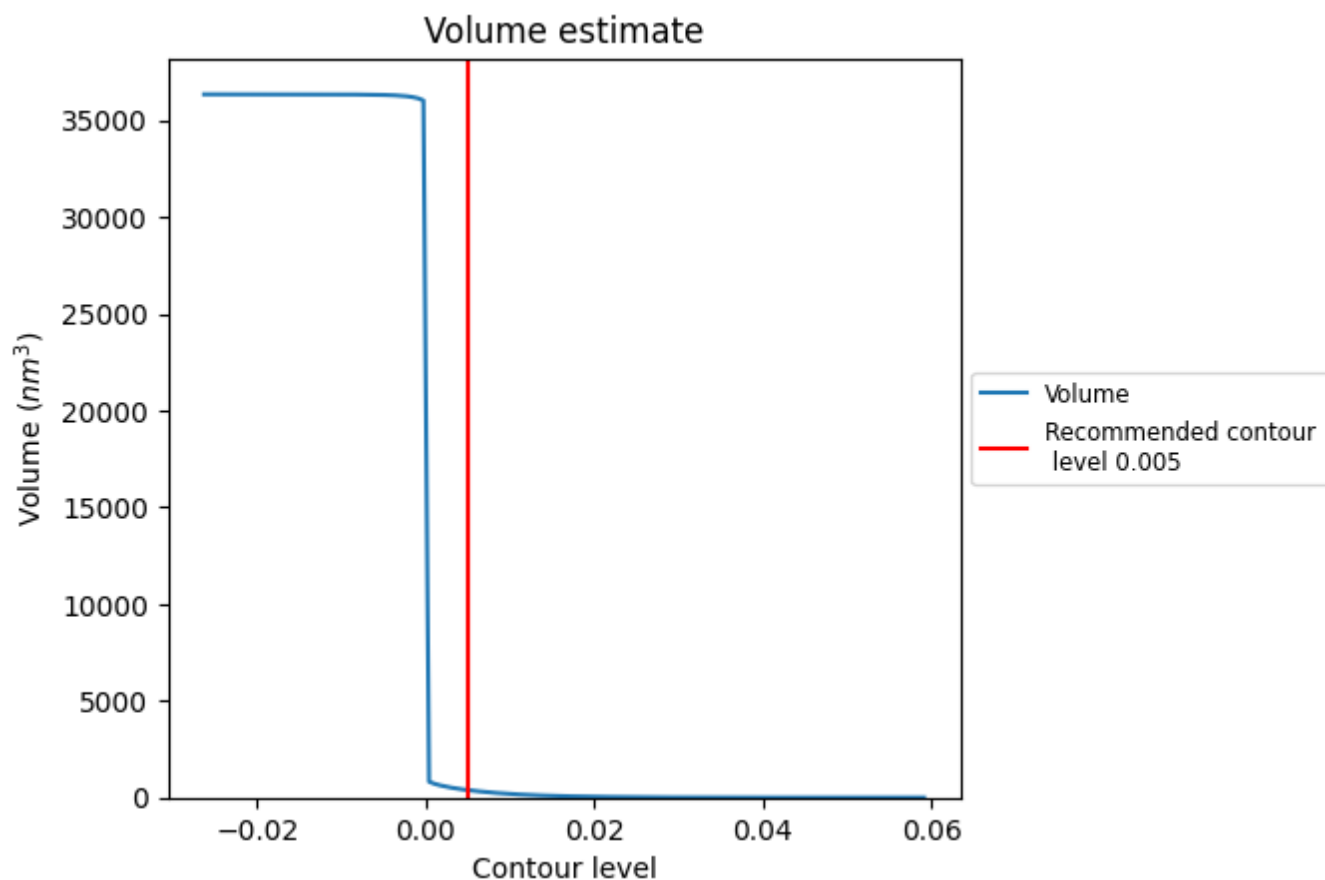
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



The map-value distribution is plotted in 128 intervals along the x-axis. The y-axis is logarithmic. A spike in this graph at zero usually indicates that the volume has been masked.

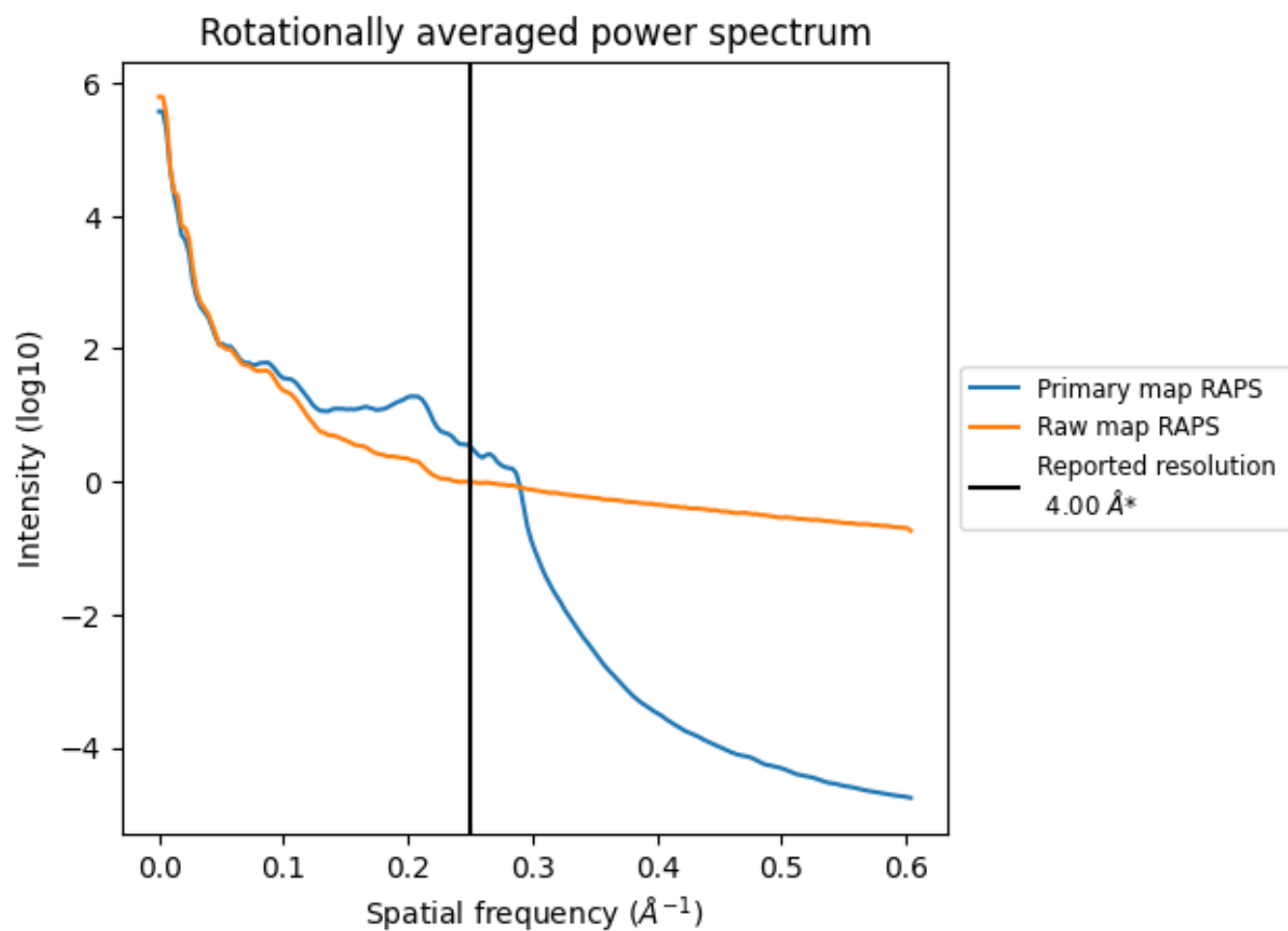
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 386 nm^3 ; this corresponds to an approximate mass of 348 kDa.

The volume estimate graph shows how the enclosed volume varies with the contour level. The recommended contour level is shown as a vertical line and the intersection between the line and the curve gives the volume of the enclosed surface at the given level.

7.3 Rotationally averaged power spectrum ⓘ

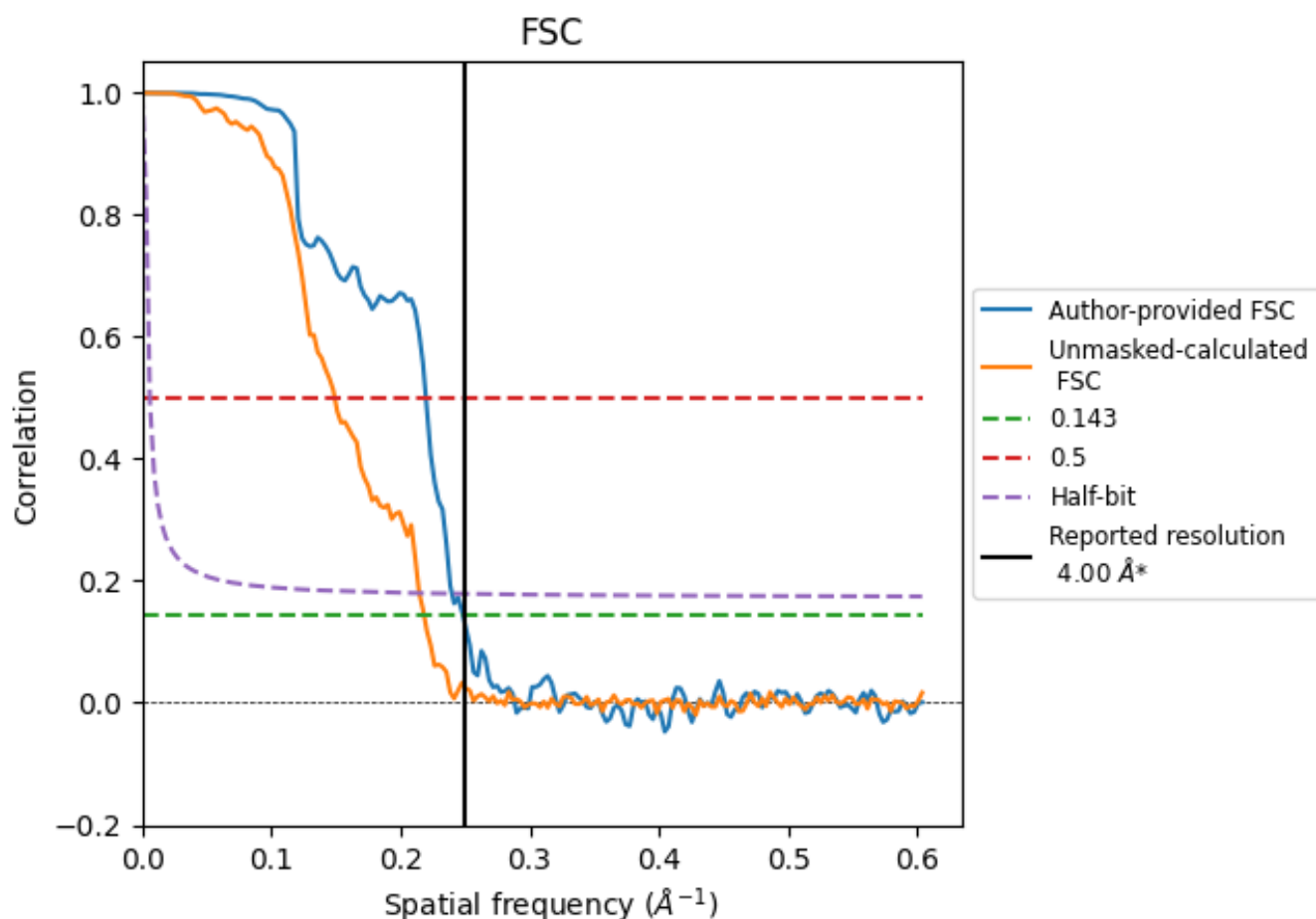


*Reported resolution corresponds to spatial frequency of 0.250 \AA^{-1}

8 Fourier-Shell correlation [i](#)

Fourier-Shell Correlation (FSC) is the most commonly used method to estimate the resolution of single-particle and subtomogram-averaged maps. The shape of the curve depends on the imposed symmetry, mask and whether or not the two 3D reconstructions used were processed from a common reference. The reported resolution is shown as a black line. A curve is displayed for the half-bit criterion in addition to lines showing the 0.143 gold standard cut-off and 0.5 cut-off.

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.250 \AA^{-1}

8.2 Resolution estimates [i](#)

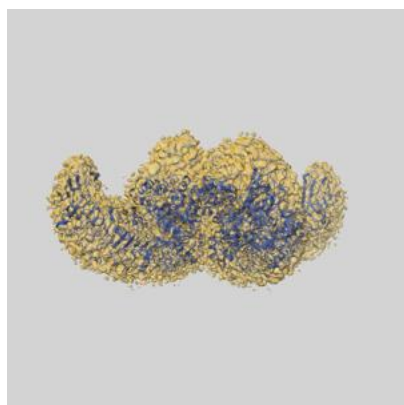
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	4.00	-	-
Author-provided FSC curve	4.03	4.55	4.17
Unmasked-calculated*	4.58	6.71	4.66

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 4.58 differs from the reported value 4.0 by more than 10 %

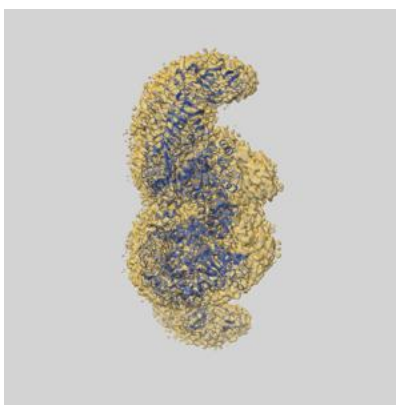
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-53346 and PDB model 9QT4. Per-residue inclusion information can be found in section [3](#) on page [5](#).

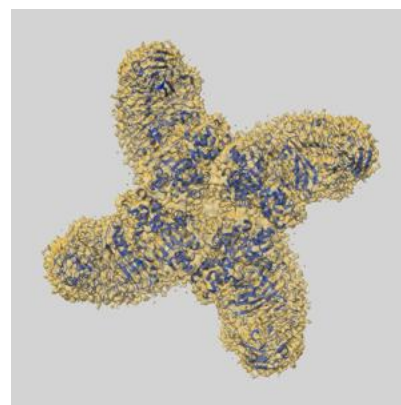
9.1 Map-model overlay [i](#)



X



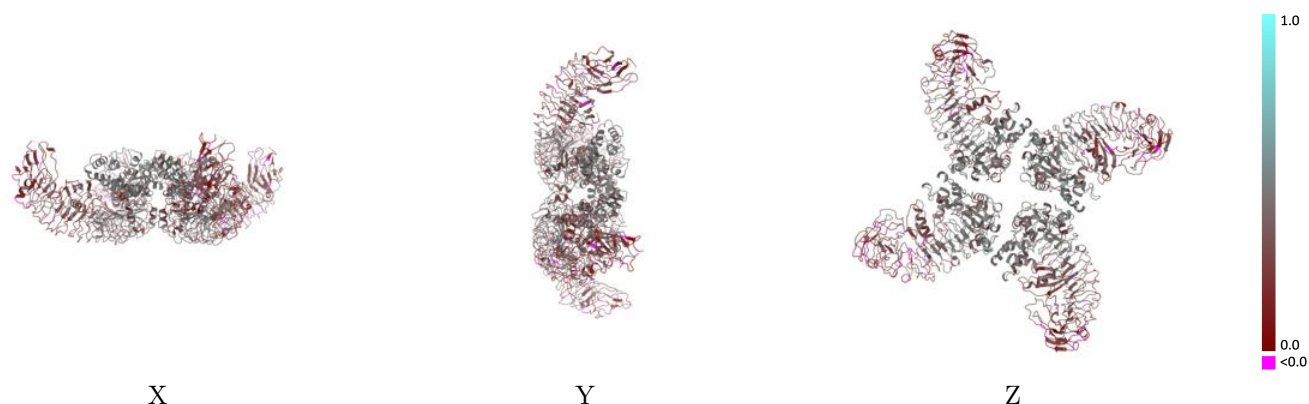
Y



Z

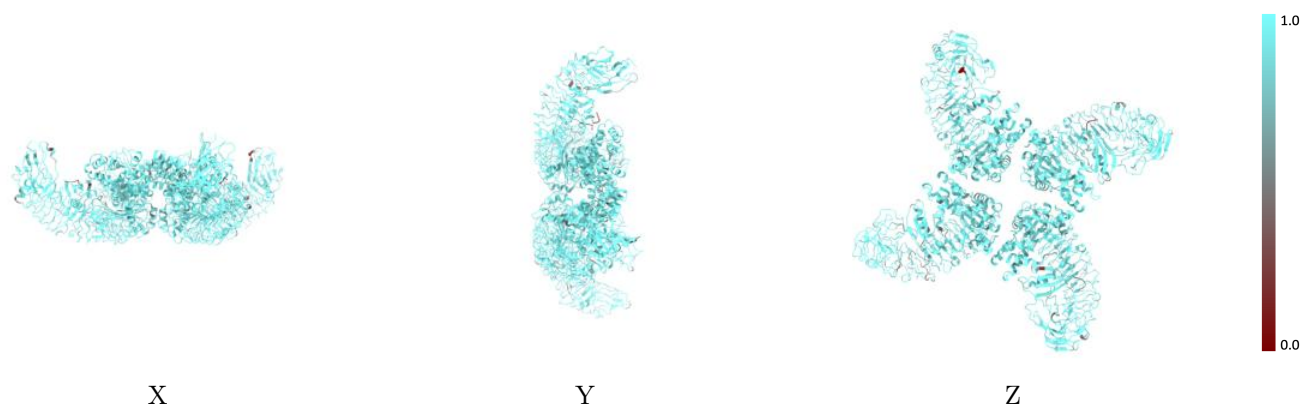
The images above show the 3D surface view of the map at the recommended contour level 0.005 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

9.2 Q-score mapped to coordinate model [i](#)



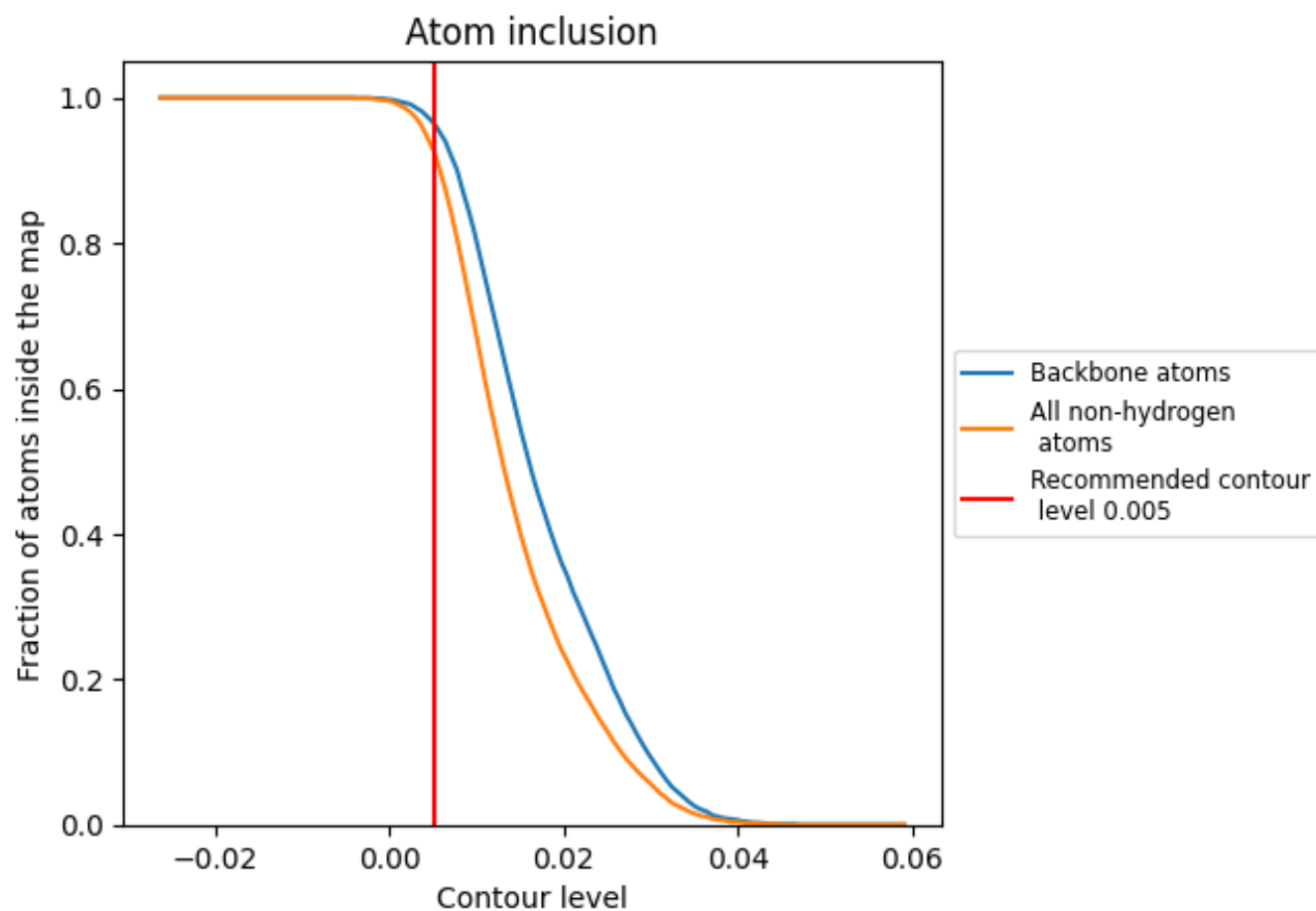
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions at which atoms can be resolved. Low Q-score values may therefore be expected for many entries.

9.3 Atom inclusion mapped to coordinate model [i](#)



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.005).

9.4 Atom inclusion [i](#)



At the recommended contour level, 97% of all backbone atoms, 93% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary ⓘ

The table lists the average atom inclusion at the recommended contour level (0.005) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	<div><div></div>0.9290</div>	<div><div></div>0.3400</div>
A	<div><div></div>0.9380</div>	<div><div></div>0.3480</div>
B	<div><div></div>0.9360</div>	<div><div></div>0.3540</div>
C	<div><div></div>0.9390</div>	<div><div></div>0.3480</div>
D	<div><div></div>0.9240</div>	<div><div></div>0.3310</div>
P	<div><div></div>0.8800</div>	<div><div></div>0.2910</div>
Q	<div><div></div>0.8590</div>	<div><div></div>0.2850</div>
R	<div><div></div>0.8720</div>	<div><div></div>0.2970</div>
S	<div><div></div>0.9010</div>	<div><div></div>0.2980</div>

1.0

0.0

<0.0