



Full wwPDB X-ray Structure Validation Report ⓘ

Apr 5, 2026 – 03:41 AM UTC

PDB ID : 9JCW / pdb_00009jcw
Title : Crystal structure of human MIGA1 LD targeting domain
Authors : Yang, K.L.; Zhang, L.
Deposited on : 2024-08-30
Resolution : 2.60 Å(reported)

This is a Full wwPDB X-ray Structure 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/XrayValidationReportHelp>

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:

MolProbity : 4-5-2 with Phenix2.0
Mogul : 2022.3.0, CSD as543be (2022)
Xtriage (Phenix) : 2.0
EDS : 3.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4 : 9.0.010 (Gargrove)
Density-Fitness : 1.0.12
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

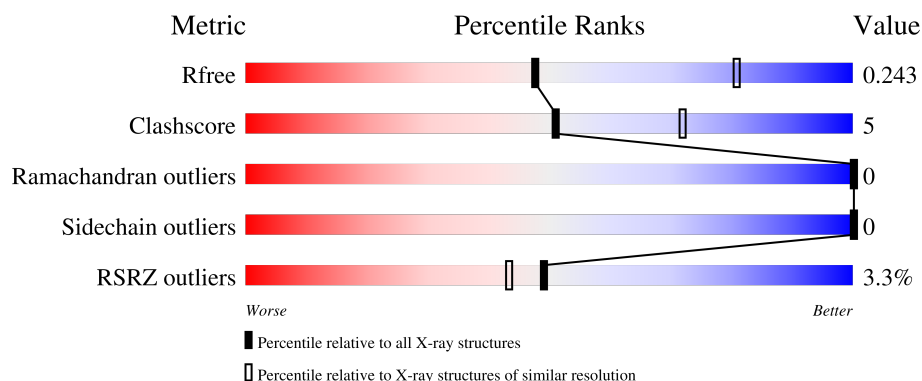
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.60 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)	Similar resolution (#Entries, resolution range(Å))
R_{free}	180053	4008 (2.60-2.60)
Clashscore	190562	4347 (2.60-2.60)
Ramachandran outliers	187476	4277 (2.60-2.60)
Sidechain outliers	187428	4277 (2.60-2.60)
RSRZ outliers	180081	4008 (2.60-2.60)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments of the lower 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 electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	258	<div> <div>91%</div> <div>9%</div> <div>•</div> </div>
1	B	258	<div> <div>86%</div> <div>13%</div> <div>•</div> </div>
1	C	258	<div> <div>87%</div> <div>12%</div> <div>•</div> </div>
1	D	258	<div> <div>7%</div> <div>84%</div> <div>10%</div> <div>5%</div> <div>•</div> </div>
1	E	258	<div> <div>90%</div> <div>10%</div> <div>•</div> </div>

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Mol	Chain	Length	Quality of chain
1	F	258	<div><div></div><div>9%</div><div></div><div>80%</div><div></div><div>19%</div><div></div></div>

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 12482 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the ZeroOcc column contains the number of atoms modelled with zero occupancy, 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.

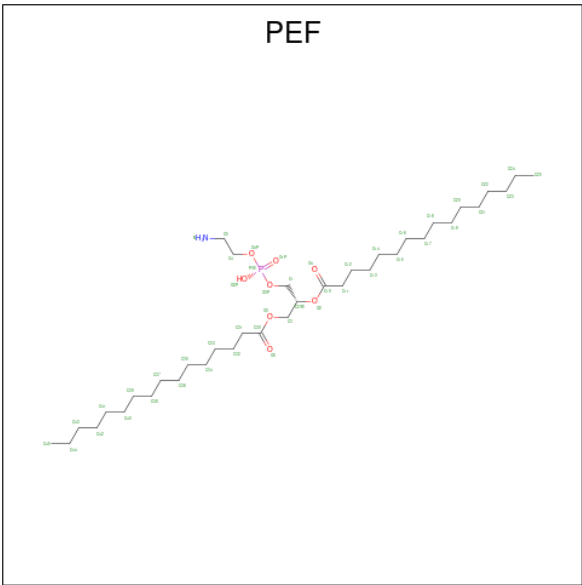
- Molecule 1 is a protein called Mitoguardin 1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	C	256	Total	C	N	O	S	0	0	0
			2079	1342	339	383	15			
1	F	255	Total	C	N	O	S	0	0	0
			1993	1283	321	375	14			
1	A	256	Total	C	N	O	S	0	0	0
			2076	1339	339	383	15			
1	E	258	Total	C	N	O	S	0	0	0
			2085	1346	341	383	15			
1	B	256	Total	C	N	O	S	0	0	0
			2079	1342	339	383	15			
1	D	245	Total	C	N	O	S	0	0	0
			1863	1192	309	349	13			

There are 6 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
C	349	MET	-	initiating methionine	UNP Q8NAN2
F	349	MET	-	initiating methionine	UNP Q8NAN2
A	349	MET	-	initiating methionine	UNP Q8NAN2
E	349	MET	-	initiating methionine	UNP Q8NAN2
B	349	MET	-	initiating methionine	UNP Q8NAN2
D	349	MET	-	initiating methionine	UNP Q8NAN2

- Molecule 2 is DI-PALMITOYL-3-SN-PHOSPHATIDYLETHANOLAMINE (CCD ID: PEF) (formula: C₃₇H₇₄NO₈P) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	C	1	Total	C	N	O	P	0	0
			47	37	1	8	1		
2	A	1	Total	C	N	O	P	0	0
			47	37	1	8	1		
2	E	1	Total	C	N	O	P	0	0
			47	37	1	8	1		
2	B	1	Total	C	N	O	P	0	0
			47	37	1	8	1		
2	D	1	Total	C	N	O	P	0	0
			47	37	1	8	1		

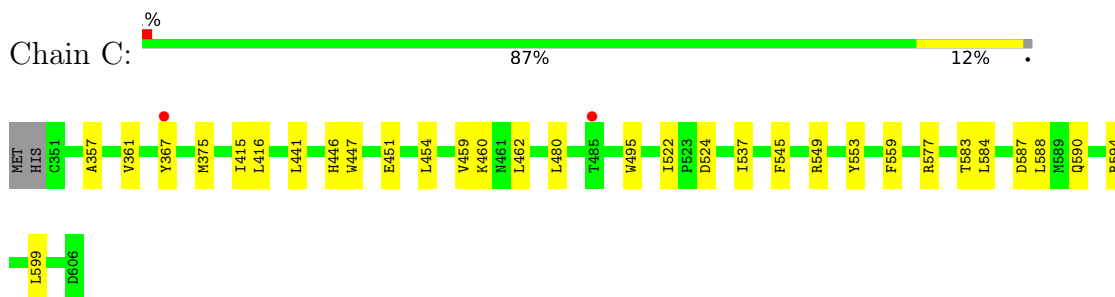
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	C	12	Total	O	0	0
			12	12		
3	F	3	Total	O	0	0
			3	3		
3	A	19	Total	O	0	0
			19	19		
3	E	22	Total	O	0	0
			22	22		
3	B	15	Total	O	0	0
			15	15		
3	D	1	Total	O	0	0
			1	1		

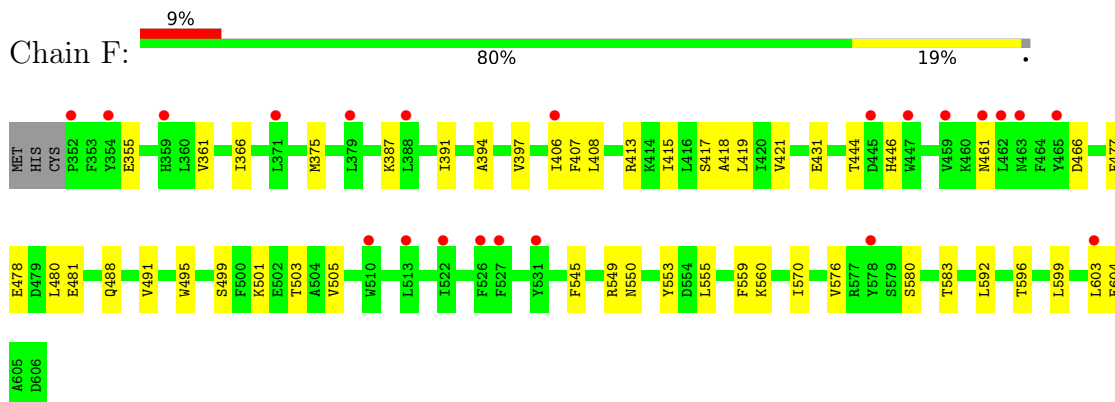
3 Residue-property plots

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 electron 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 dot above a residue indicates a poor fit to the electron density ($RSRZ > 2$). 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.

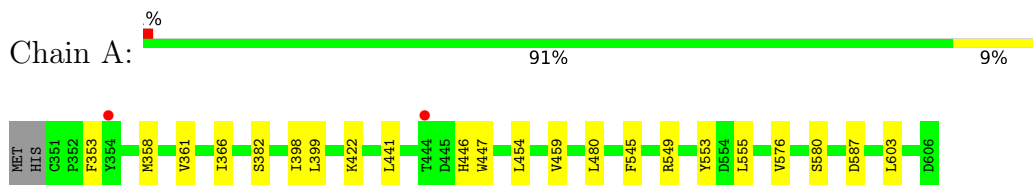
• Molecule 1: Mitoguardin 1



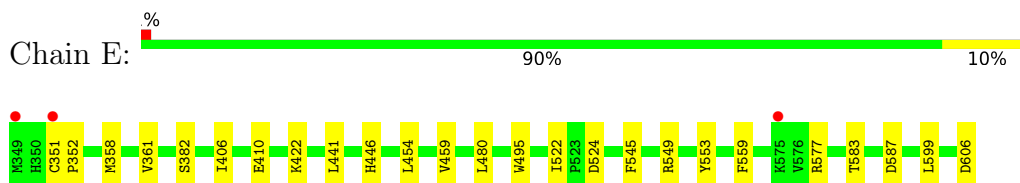
• Molecule 1: Mitoguardin 1



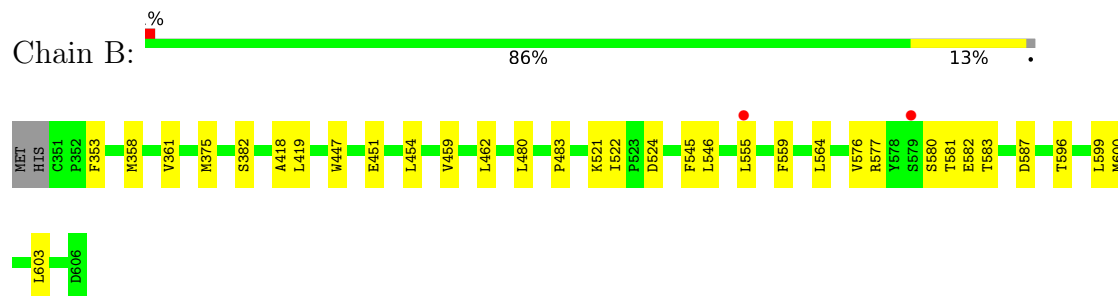
• Molecule 1: Mitoguardin 1



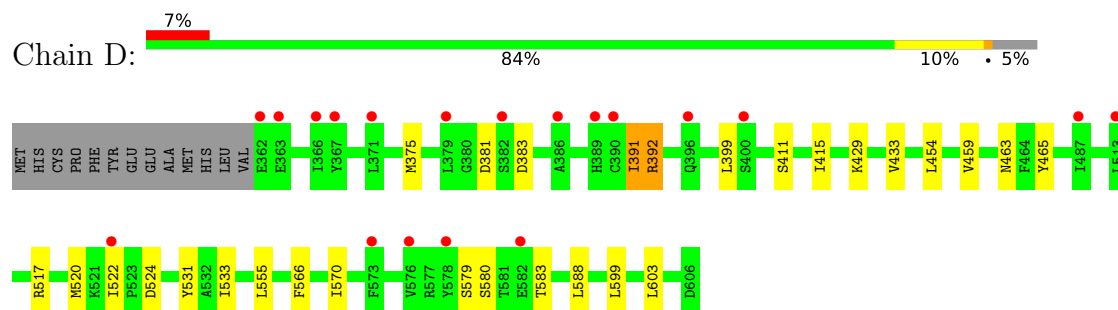
• Molecule 1: Mitoguardin 1



● Molecule 1: Mitoguardin 1



● Molecule 1: Mitoguardin 1



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	88.64Å 157.78Å 163.91Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	50.08 – 2.60 50.08 – 2.60	Depositor EDS
% Data completeness (in resolution range)	99.9 (50.08-2.60) 99.9 (50.08-2.60)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.60 (at 2.61Å)	Xtriage
Refinement program	PHENIX (1.19_4092: ???)	Depositor
R, R_{free}	0.210 , 0.244 0.209 , 0.243	Depositor DCC
R_{free} test set	3709 reflections (5.19%)	wwPDB-VP
Wilson B-factor (Å ²)	64.1	Xtriage
Anisotropy	0.057	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.31 , 52.4	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	0.005 for -h,l,k	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	12482	wwPDB-VP
Average B, all atoms (Å ²)	81.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.86% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: PEF

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	A	0.18	0/2123	0.36	0/2868
1	B	0.12	0/2126	0.32	0/2872
1	C	0.15	0/2126	0.35	0/2872
1	D	0.30	0/1900	0.53	2/2579 (0.1%)
1	E	0.12	0/2132	0.31	0/2881
1	F	0.32	0/2036	0.60	3/2759 (0.1%)
All	All	0.21	0/12443	0.42	5/16831 (0.0%)

There are no bond length outliers.

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	391	ILE	N-CA-C	-6.56	102.89	111.09
1	F	355	GLU	N-CA-C	-5.58	105.28	111.36
1	F	466	ASP	N-CA-C	-5.33	107.43	114.04
1	D	392	ARG	N-CA-C	-5.24	105.47	111.07
1	F	461	ASN	N-CA-C	5.05	116.64	108.41

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts

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	A	2076	0	2026	14	0
1	B	2079	0	2035	23	0
1	C	2079	0	2035	26	0
1	D	1863	0	1736	21	0
1	E	2085	0	2035	19	0
1	F	1993	0	1887	31	0
2	A	47	0	73	2	0
2	B	47	0	73	0	0
2	C	47	0	73	0	0
2	D	47	0	73	2	0
2	E	47	0	73	0	0
3	A	19	0	0	0	0
3	B	15	0	0	0	0
3	C	12	0	0	0	0
3	D	1	0	0	0	0
3	E	22	0	0	0	0
3	F	3	0	0	0	0
All	All	12482	0	12119	127	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 5.

All (127) 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)
1:B:522:ILE:HG22	1:B:524:ASP:H	1.53	0.73
1:F:413:ARG:HH21	1:F:431:GLU:HG2	1.55	0.72
1:C:451:GLU:CG	1:C:462:LEU:HD12	2.20	0.71
1:C:451:GLU:HG2	1:C:462:LEU:HD12	1.74	0.70
1:F:495:TRP:HA	1:D:375:MET:HE2	1.75	0.68
1:F:361:VAL:HG22	1:F:366:ILE:HG13	1.78	0.65
1:F:559:PHE:HA	1:F:599:LEU:HD21	1.79	0.62
1:B:419:LEU:HD23	1:B:555:LEU:HD23	1.83	0.61
1:E:577:ARG:HB2	1:E:583:THR:HG22	1.83	0.60
1:D:411:SER:O	1:D:415:ILE:HG13	2.02	0.60
1:B:596:THR:HG22	1:B:600:MET:HE2	1.84	0.59
1:E:522:ILE:HG22	1:E:524:ASP:H	1.67	0.59
1:C:522:ILE:HG22	1:C:524:ASP:H	1.68	0.59
1:A:358:MET:HE1	1:A:382:SER:HB3	1.83	0.59
1:E:351:CYS:HB3	1:E:352:PRO:HD3	1.84	0.59
1:C:454:LEU:HB3	1:C:459:VAL:HB	1.85	0.58
1:C:594:ARG:HG3	1:C:594:ARG:HH11	1.69	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:375:MET:HA	1:F:375:MET:HE2	1.86	0.57
1:F:570:ILE:HA	1:F:576:VAL:HG21	1.87	0.57
1:A:555:LEU:HD11	1:A:603:LEU:HD23	1.86	0.57
1:A:358:MET:HE3	1:A:361:VAL:HB	1.87	0.56
1:B:581:THR:HG23	1:B:582:GLU:OE2	2.06	0.56
1:D:399:LEU:HD13	2:D:701:PEF:H21	1.86	0.55
1:F:418:ALA:HA	1:F:421:VAL:HG22	1.88	0.55
1:C:451:GLU:HG3	1:C:462:LEU:HD12	1.88	0.54
1:D:517:ARG:HA	1:D:520:MET:HG3	1.89	0.54
1:A:398:ILE:HG22	1:A:399:LEU:HD12	1.89	0.53
1:F:478:GLU:HG3	1:E:495:TRP:CD1	2.44	0.53
1:F:592:LEU:O	1:F:596:THR:OG1	2.21	0.53
1:B:577:ARG:NE	1:B:583:THR:OG1	2.36	0.53
1:C:549:ARG:HG3	1:C:553:TYR:CE2	2.43	0.53
1:E:454:LEU:HB3	1:E:459:VAL:HB	1.90	0.52
1:C:577:ARG:HG3	1:C:587:ASP:OD2	2.09	0.52
1:E:351:CYS:HB3	1:E:352:PRO:CD	2.38	0.52
1:D:555:LEU:HD21	1:D:603:LEU:HD21	1.91	0.52
1:F:549:ARG:HG3	1:F:553:TYR:CE2	2.44	0.52
1:F:408:LEU:HD11	1:F:592:LEU:HD21	1.92	0.51
1:E:549:ARG:HG3	1:E:553:TYR:CE2	2.45	0.51
1:F:499:SER:O	1:F:503:THR:HG23	2.11	0.51
1:D:555:LEU:HD21	1:D:603:LEU:CD2	2.41	0.50
1:B:358:MET:HE1	1:B:382:SER:HB3	1.92	0.50
1:D:392:ARG:HA	1:D:463:ASN:HD21	1.76	0.50
1:F:555:LEU:HD21	1:F:603:LEU:HD12	1.92	0.50
1:B:447:TRP:CZ3	1:B:462:LEU:HD11	2.46	0.50
1:E:358:MET:HE1	1:E:382:SER:HB3	1.92	0.50
1:F:417:SER:O	1:F:421:VAL:HG13	2.12	0.49
1:A:447:TRP:CH2	2:A:701:PEF:H21	2.47	0.49
1:E:422:LYS:NZ	1:E:606:ASP:OD2	2.41	0.49
1:D:391:ILE:HG23	1:D:588:LEU:HD11	1.94	0.49
1:D:381:ASP:C	1:D:383:ASP:H	2.21	0.49
1:C:447:TRP:O	1:C:451:GLU:HG3	2.12	0.49
1:D:579:SER:OG	1:D:583:THR:HG21	2.13	0.49
1:F:488:GLN:HA	1:F:491:VAL:HG22	1.95	0.49
1:F:501:LYS:O	1:F:505:VAL:HG23	2.13	0.48
1:B:454:LEU:HB3	1:B:459:VAL:HB	1.96	0.48
1:A:441:LEU:HA	1:A:446:HIS:NE2	2.28	0.48
1:A:454:LEU:HB3	1:A:459:VAL:HB	1.95	0.48
1:F:480:LEU:HD13	1:F:545:PHE:CD2	2.48	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:566:PHE:O	1:D:570:ILE:HG23	2.14	0.47
1:C:367:TYR:CZ	1:C:460:LYS:HD3	2.49	0.47
1:D:517:ARG:HG2	1:D:531:TYR:CD2	2.49	0.47
1:E:406:ILE:O	1:E:410:GLU:HG3	2.14	0.47
1:E:559:PHE:HA	1:E:599:LEU:HD21	1.97	0.47
1:B:521:LYS:C	1:B:522:ILE:HD13	2.39	0.47
1:B:559:PHE:HA	1:B:599:LEU:HD21	1.97	0.47
1:F:481:GLU:OE1	1:E:495:TRP:NE1	2.47	0.46
1:B:559:PHE:HD1	1:B:599:LEU:HD11	1.80	0.46
1:D:533:ILE:HG21	2:D:701:PEF:H392	1.98	0.46
1:D:579:SER:OG	1:D:580:SER:N	2.46	0.46
1:C:375:MET:HA	1:C:375:MET:HE2	1.97	0.46
1:F:413:ARG:HE	1:F:431:GLU:CG	2.28	0.46
1:F:419:LEU:HD22	1:F:555:LEU:HD11	1.98	0.46
1:C:416:LEU:HB3	1:C:537:ILE:HD13	1.97	0.46
1:B:447:TRP:O	1:B:451:GLU:HG3	2.16	0.46
1:E:559:PHE:HD1	1:E:599:LEU:HD11	1.80	0.46
1:B:580:SER:H	1:B:583:THR:HG22	1.80	0.45
1:A:576:VAL:HG22	1:A:587:ASP:HB3	1.99	0.45
1:F:477:PHE:CD1	1:F:560:LYS:HG3	2.52	0.45
1:D:599:LEU:O	1:D:603:LEU:HG	2.17	0.45
1:F:387:LYS:O	1:F:391:ILE:HG13	2.17	0.45
1:E:358:MET:HE3	1:E:361:VAL:HB	1.99	0.44
1:B:483:PRO:HG3	1:B:546:LEU:HD21	1.99	0.44
1:D:429:LYS:O	1:D:433:VAL:HG22	2.17	0.44
1:E:549:ARG:HG3	1:E:553:TYR:CD2	2.53	0.44
1:E:577:ARG:HG3	1:E:587:ASP:OD2	2.17	0.44
1:D:392:ARG:HA	1:D:463:ASN:ND2	2.33	0.44
1:F:550:ASN:H	1:F:550:ASN:HD22	1.66	0.44
1:A:353:PHE:HB2	1:A:580:SER:HA	1.99	0.43
1:C:480:LEU:HD13	1:C:545:PHE:CD2	2.53	0.43
1:E:441:LEU:HA	1:E:446:HIS:NE2	2.33	0.43
1:C:584:LEU:O	1:C:588:LEU:HD23	2.18	0.43
1:B:418:ALA:CB	1:B:603:LEU:HD22	2.48	0.43
1:C:590:GLN:O	1:C:594:ARG:HG2	2.19	0.43
1:D:465:TYR:C	1:D:465:TYR:CD1	2.97	0.43
1:C:441:LEU:HA	1:C:446:HIS:NE2	2.34	0.42
1:C:495:TRP:CZ3	1:B:375:MET:HE2	2.54	0.42
1:F:580:SER:H	1:F:583:THR:CG2	2.32	0.42
1:C:594:ARG:HD2	1:F:604:GLU:HB3	2.02	0.42
1:B:576:VAL:HG12	1:B:587:ASP:HB3	2.02	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:375:MET:HG3	1:E:495:TRP:CE3	2.55	0.42
1:F:413:ARG:HE	1:F:431:GLU:HG3	1.84	0.42
1:D:399:LEU:HD23	1:D:399:LEU:HA	1.85	0.42
1:A:361:VAL:HG22	1:A:366:ILE:HG13	2.02	0.41
1:E:480:LEU:HD13	1:E:545:PHE:CD2	2.55	0.41
1:B:577:ARG:HG3	1:B:587:ASP:OD2	2.21	0.41
1:F:415:ILE:O	1:F:419:LEU:HD23	2.20	0.41
1:A:447:TRP:HH2	2:A:701:PEF:H21	1.85	0.41
1:C:357:ALA:O	1:C:361:VAL:HG23	2.19	0.41
1:F:406:ILE:HD12	1:F:407:PHE:N	2.35	0.41
1:B:353:PHE:HB2	1:B:580:SER:HA	2.01	0.41
1:B:555:LEU:HD21	1:B:603:LEU:HD23	2.01	0.41
1:A:480:LEU:HD13	1:A:545:PHE:CD2	2.55	0.41
1:B:480:LEU:HD13	1:B:545:PHE:CD2	2.55	0.41
1:D:454:LEU:HB3	1:D:459:VAL:HB	2.02	0.41
1:D:522:ILE:HG22	1:D:524:ASP:H	1.85	0.41
1:C:577:ARG:NE	1:C:583:THR:OG1	2.43	0.41
1:A:422:LYS:HA	1:A:422:LYS:HD3	1.94	0.41
1:A:549:ARG:HG3	1:A:553:TYR:CE2	2.55	0.41
1:C:415:ILE:HD13	1:C:599:LEU:HD13	2.03	0.41
1:C:559:PHE:HD1	1:C:599:LEU:HD11	1.86	0.41
1:C:416:LEU:HB3	1:C:537:ILE:CD1	2.52	0.40
1:C:549:ARG:HG3	1:C:553:TYR:CD2	2.56	0.40
1:C:367:TYR:CE2	1:C:460:LYS:HD3	2.56	0.40
1:B:358:MET:HE3	1:B:361:VAL:HB	2.02	0.40
1:C:495:TRP:HH2	1:B:564:LEU:HD21	1.86	0.40
1:F:394:ALA:O	1:F:397:VAL:HG22	2.21	0.40
1:F:444:THR:O	1:F:446:HIS:HD2	2.04	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 X-ray entries followed by that with respect to entries of similar resolution.

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	A	254/258 (98%)	250 (98%)	4 (2%)	0	100	100
1	B	254/258 (98%)	250 (98%)	4 (2%)	0	100	100
1	C	254/258 (98%)	249 (98%)	5 (2%)	0	100	100
1	D	243/258 (94%)	237 (98%)	6 (2%)	0	100	100
1	E	256/258 (99%)	249 (97%)	7 (3%)	0	100	100
1	F	253/258 (98%)	245 (97%)	8 (3%)	0	100	100
All	All	1514/1548 (98%)	1480 (98%)	34 (2%)	0	100	100

There are no Ramachandran outliers to report.

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 X-ray entries followed by that with respect to entries of similar resolution.

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	A	226/233 (97%)	226 (100%)	0	100	100
1	B	227/233 (97%)	227 (100%)	0	100	100
1	C	227/233 (97%)	227 (100%)	0	100	100
1	D	189/233 (81%)	189 (100%)	0	100	100
1	E	226/233 (97%)	226 (100%)	0	100	100
1	F	209/233 (90%)	209 (100%)	0	100	100
All	All	1304/1398 (93%)	1304 (100%)	0	100	100

There are no protein residues with a non-rotameric sidechain to report.

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (13) such sidechains are listed below:

Mol	Chain	Res	Type
1	C	389	HIS
1	C	393	GLN
1	F	515	GLN
1	A	389	HIS
1	A	393	GLN

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Mol	Chain	Res	Type
1	E	393	GLN
1	E	443	GLN
1	E	461	ASN
1	E	561	ASN
1	B	396	GLN
1	B	443	GLN
1	B	590	GLN
1	D	561	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](#)

5 ligands are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. 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 $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
2	PEF	A	701	-	46,46,46	0.30	0	49,51,51	0.37	0
2	PEF	B	701	-	46,46,46	0.29	0	49,51,51	0.39	0
2	PEF	E	701	-	46,46,46	1.07	3 (6%)	49,51,51	0.94	2 (4%)
2	PEF	C	701	-	46,46,46	0.30	0	49,51,51	0.31	0
2	PEF	D	701	-	46,46,46	1.03	4 (8%)	49,51,51	1.03	4 (8%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	PEF	A	701	-	-	28/50/50/50	-
2	PEF	B	701	-	-	25/50/50/50	-
2	PEF	E	701	-	-	17/50/50/50	-
2	PEF	C	701	-	-	25/50/50/50	-
2	PEF	D	701	-	-	25/50/50/50	-

All (7) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	D	701	PEF	O2-C2	-3.08	1.39	1.46
2	E	701	PEF	O3-C30	3.01	1.42	1.33
2	D	701	PEF	O3-C30	2.96	1.42	1.33
2	E	701	PEF	O2-C10	2.92	1.42	1.34
2	E	701	PEF	O2-C2	-2.60	1.40	1.46
2	D	701	PEF	O2-C10	2.52	1.41	1.34
2	D	701	PEF	O3-C3	-2.04	1.40	1.45

All (6) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	D	701	PEF	O2-C10-C11	4.33	120.84	111.48
2	E	701	PEF	O2-C10-C11	4.31	120.80	111.48
2	D	701	PEF	C2-O2-C10	-3.21	110.10	117.80
2	E	701	PEF	O3-C30-C31	2.72	120.12	111.83
2	D	701	PEF	O3-C30-C31	2.44	119.29	111.83
2	D	701	PEF	O2-C10-O4	-2.10	118.79	123.70

There are no chirality outliers.

All (120) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	C	701	PEF	O4P-C4-C5-N
2	C	701	PEF	C1-O3P-P-O1P
2	C	701	PEF	C1-O3P-P-O4P
2	C	701	PEF	C4-O4P-P-O1P
2	A	701	PEF	O4P-C4-C5-N

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Mol	Chain	Res	Type	Atoms
2	A	701	PEF	C11-C10-O2-C2
2	A	701	PEF	C1-O3P-P-O1P
2	A	701	PEF	C1-O3P-P-O2P
2	A	701	PEF	C4-O4P-P-O3P
2	E	701	PEF	O4P-C4-C5-N
2	E	701	PEF	C1-O3P-P-O1P
2	B	701	PEF	O4P-C4-C5-N
2	B	701	PEF	C11-C10-O2-C2
2	B	701	PEF	C31-C30-O3-C3
2	B	701	PEF	O5-C30-O3-C3
2	B	701	PEF	C1-O3P-P-O2P
2	D	701	PEF	O4P-C4-C5-N
2	D	701	PEF	C1-O3P-P-O1P
2	D	701	PEF	C1-O3P-P-O2P
2	D	701	PEF	C1-O3P-P-O4P
2	B	701	PEF	O4-C10-O2-C2
2	E	701	PEF	C31-C30-O3-C3
2	D	701	PEF	C41-C42-C43-C44
2	A	701	PEF	O4-C10-O2-C2
2	D	701	PEF	C14-C15-C16-C17
2	E	701	PEF	O5-C30-O3-C3
2	B	701	PEF	C21-C22-C23-C24
2	E	701	PEF	C30-C31-C32-C33
2	C	701	PEF	C10-C11-C12-C13
2	C	701	PEF	C30-C31-C32-C33
2	C	701	PEF	C11-C10-O2-C2
2	C	701	PEF	O4-C10-O2-C2
2	C	701	PEF	C18-C19-C20-C21
2	B	701	PEF	C35-C36-C37-C38
2	A	701	PEF	C37-C38-C39-C40
2	B	701	PEF	C36-C37-C38-C39
2	E	701	PEF	C19-C20-C21-C22
2	D	701	PEF	C21-C22-C23-C24
2	C	701	PEF	C17-C18-C19-C20
2	A	701	PEF	C16-C17-C18-C19
2	A	701	PEF	C34-C35-C36-C37
2	A	701	PEF	C41-C42-C43-C44
2	D	701	PEF	C19-C20-C21-C22
2	D	701	PEF	C20-C21-C22-C23
2	A	701	PEF	C39-C40-C41-C42
2	C	701	PEF	C22-C23-C24-C25
2	A	701	PEF	C33-C34-C35-C36

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Mol	Chain	Res	Type	Atoms
2	A	701	PEF	C38-C39-C40-C41
2	A	701	PEF	C32-C33-C34-C35
2	A	701	PEF	C36-C37-C38-C39
2	E	701	PEF	C34-C35-C36-C37
2	D	701	PEF	C12-C13-C14-C15
2	A	701	PEF	C31-C30-O3-C3
2	B	701	PEF	C15-C16-C17-C18
2	E	701	PEF	C17-C18-C19-C20
2	E	701	PEF	C41-C42-C43-C44
2	D	701	PEF	C35-C36-C37-C38
2	D	701	PEF	C11-C10-O2-C2
2	A	701	PEF	C21-C22-C23-C24
2	D	701	PEF	C30-C31-C32-C33
2	C	701	PEF	C20-C21-C22-C23
2	D	701	PEF	C11-C12-C13-C14
2	C	701	PEF	C13-C14-C15-C16
2	A	701	PEF	C10-C11-C12-C13
2	A	701	PEF	O2-C2-C3-O3
2	E	701	PEF	C36-C37-C38-C39
2	C	701	PEF	C33-C34-C35-C36
2	C	701	PEF	C35-C36-C37-C38
2	C	701	PEF	C40-C41-C42-C43
2	A	701	PEF	O5-C30-O3-C3
2	C	701	PEF	O3P-C1-C2-C3
2	B	701	PEF	O3P-C1-C2-C3
2	D	701	PEF	O4-C10-O2-C2
2	B	701	PEF	C20-C21-C22-C23
2	A	701	PEF	C1-C2-C3-O3
2	A	701	PEF	C17-C18-C19-C20
2	E	701	PEF	C10-C11-C12-C13
2	B	701	PEF	C33-C34-C35-C36
2	A	701	PEF	C35-C36-C37-C38
2	B	701	PEF	O2-C2-C3-O3
2	B	701	PEF	C11-C12-C13-C14
2	D	701	PEF	C22-C23-C24-C25
2	B	701	PEF	C16-C17-C18-C19
2	B	701	PEF	C41-C42-C43-C44
2	C	701	PEF	C2-C1-O3P-P
2	B	701	PEF	C34-C35-C36-C37
2	C	701	PEF	C41-C42-C43-C44
2	E	701	PEF	C42-C43-C44-C45
2	D	701	PEF	C37-C38-C39-C40

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Mol	Chain	Res	Type	Atoms
2	C	701	PEF	O3P-C1-C2-O2
2	B	701	PEF	O3P-C1-C2-O2
2	A	701	PEF	C12-C13-C14-C15
2	E	701	PEF	C16-C17-C18-C19
2	E	701	PEF	O2-C2-C3-O3
2	D	701	PEF	C40-C41-C42-C43
2	D	701	PEF	C31-C32-C33-C34
2	B	701	PEF	C10-C11-C12-C13
2	D	701	PEF	C18-C19-C20-C21
2	C	701	PEF	C14-C15-C16-C17
2	A	701	PEF	C22-C23-C24-C25
2	D	701	PEF	C10-C11-C12-C13
2	A	701	PEF	C11-C12-C13-C14
2	B	701	PEF	C1-C2-C3-O3
2	C	701	PEF	C1-O3P-P-O2P
2	A	701	PEF	C1-O3P-P-O4P
2	A	701	PEF	C4-O4P-P-O1P
2	B	701	PEF	C1-O3P-P-O1P
2	B	701	PEF	C1-O3P-P-O4P
2	C	701	PEF	C15-C16-C17-C18
2	E	701	PEF	C18-C19-C20-C21
2	C	701	PEF	C32-C33-C34-C35
2	E	701	PEF	C1-C2-C3-O3
2	B	701	PEF	C22-C23-C24-C25
2	D	701	PEF	O3-C30-C31-C32
2	D	701	PEF	C13-C14-C15-C16
2	B	701	PEF	C40-C41-C42-C43
2	C	701	PEF	C36-C37-C38-C39
2	D	701	PEF	C17-C18-C19-C20
2	D	701	PEF	C42-C43-C44-C45
2	E	701	PEF	C11-C12-C13-C14

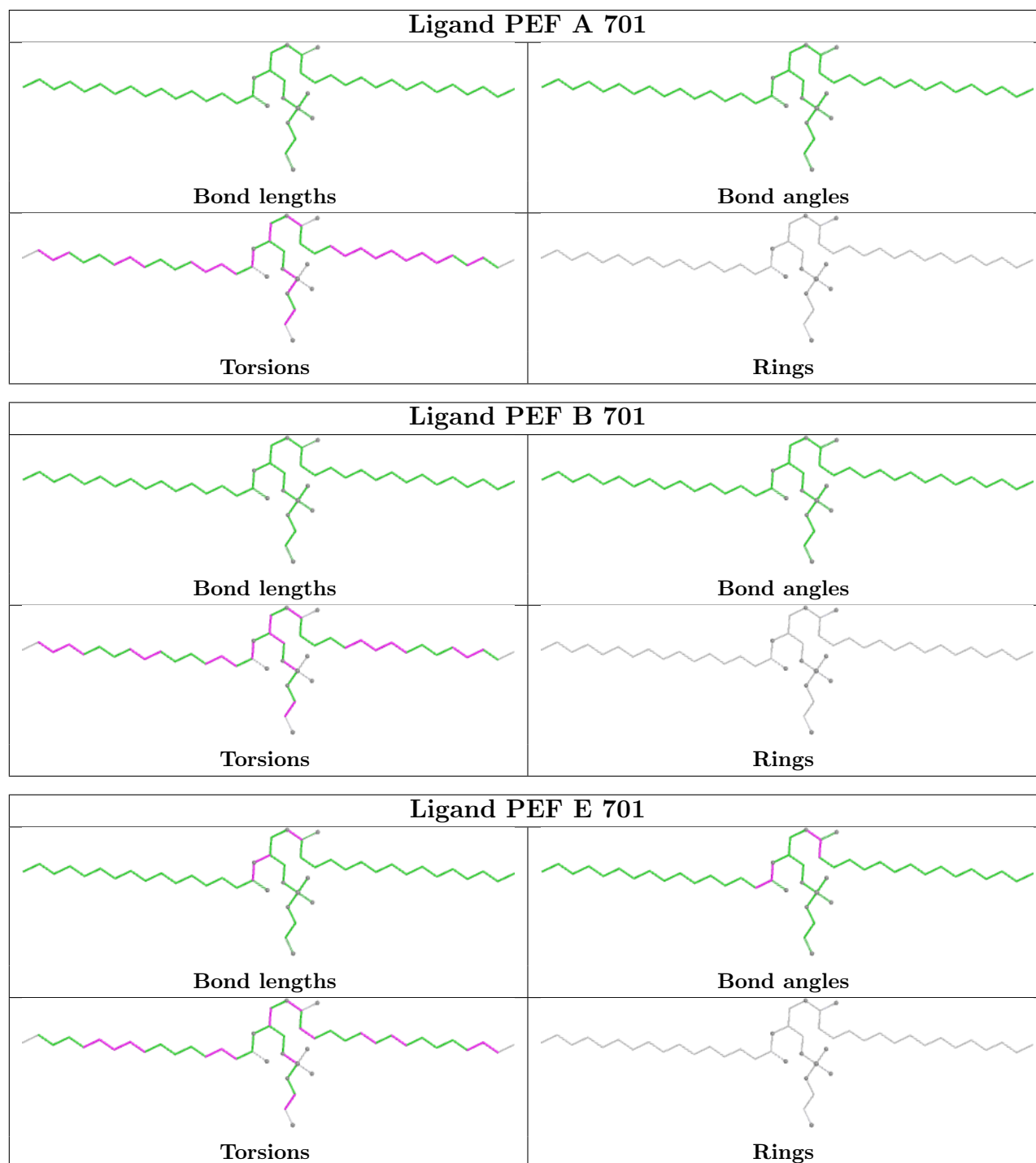
There are no ring outliers.

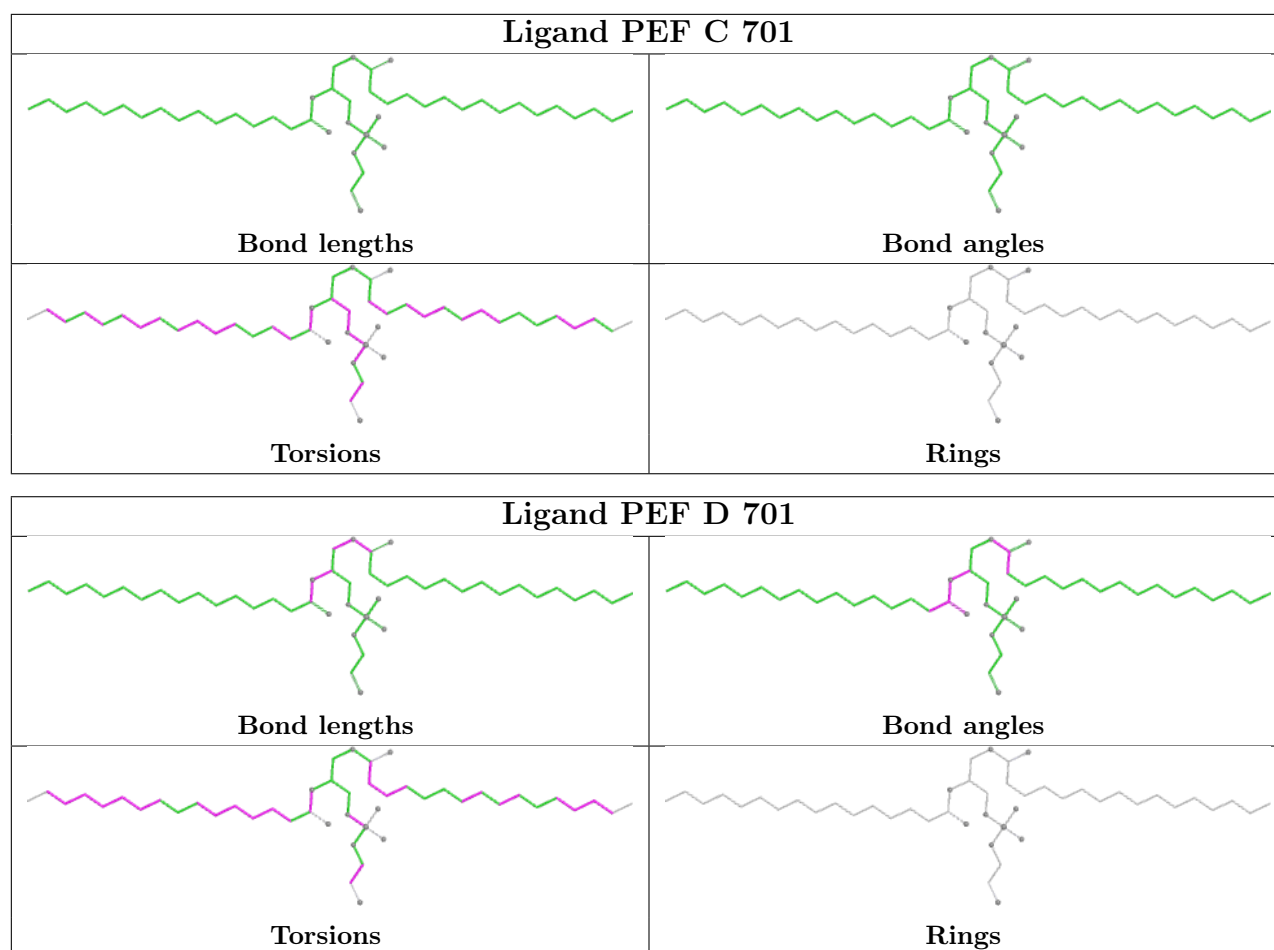
2 monomers are involved in 4 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	701	PEF	2	0
2	D	701	PEF	2	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will

also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.





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 Fit of model and data

6.1 Protein, DNA and RNA chains

In the following table, the column labelled ‘#RSRZ > 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95th percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q < 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	A	256/258 (99%)	-0.09	2 (0%) 82 80	44, 67, 100, 113	0
1	B	256/258 (99%)	0.03	2 (0%) 82 80	44, 72, 108, 133	0
1	C	256/258 (99%)	-0.09	2 (0%) 82 80	49, 68, 95, 115	0
1	D	245/258 (94%)	0.66	19 (7%) 19 15	57, 99, 137, 166	0
1	E	258/258 (100%)	-0.10	3 (1%) 76 73	45, 67, 99, 123	0
1	F	255/258 (98%)	0.75	22 (8%) 16 12	67, 106, 152, 177	0
All	All	1526/1548 (98%)	0.19	50 (3%) 49 43	44, 76, 129, 177	0

All (50) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	578	TYR	6.1
1	F	445	ASP	5.8
1	D	362	GLU	4.9
1	F	447	TRP	4.7
1	E	349	MET	4.5
1	F	354	TYR	4.3
1	D	389	HIS	3.8
1	F	352	PRO	3.6
1	D	379	LEU	3.6
1	D	390	CYS	3.6
1	D	367	TYR	3.4
1	F	465	TYR	3.1
1	F	359	HIS	3.0
1	E	351	CYS	3.0
1	D	363	GLU	2.9
1	D	573	PHE	2.9
1	F	522	ILE	2.9
1	F	462	LEU	2.9
1	F	513	LEU	2.9

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Mol	Chain	Res	Type	RSRZ
1	D	576	VAL	2.8
1	D	396	GLN	2.8
1	D	513	LEU	2.8
1	F	510	TRP	2.8
1	A	444	THR	2.7
1	D	382	SER	2.6
1	D	400	SER	2.5
1	D	487	ILE	2.5
1	A	354	TYR	2.5
1	E	575	LYS	2.4
1	F	526	PHE	2.3
1	D	371	LEU	2.3
1	D	582	GLU	2.3
1	F	531	TYR	2.2
1	B	555	LEU	2.2
1	D	366	ILE	2.2
1	D	386	ALA	2.2
1	F	463	ASN	2.2
1	F	371	LEU	2.2
1	C	485	THR	2.1
1	F	388	LEU	2.1
1	D	522	ILE	2.1
1	F	527	PHE	2.1
1	F	379	LEU	2.1
1	F	603	LEU	2.1
1	C	367	TYR	2.1
1	B	579	SER	2.1
1	F	406	ILE	2.1
1	F	578	TYR	2.1
1	F	459	VAL	2.1
1	F	461	ASN	2.0

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

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

6.3 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

6.4 Ligands ⓘ

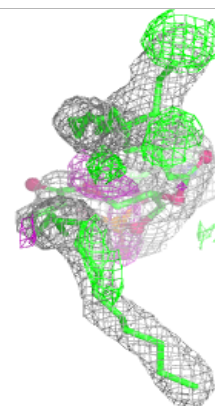
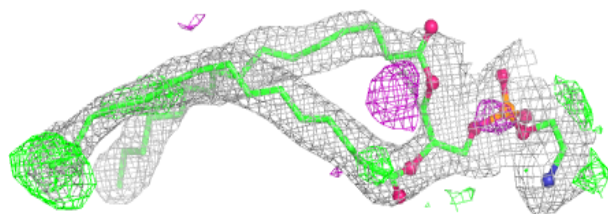
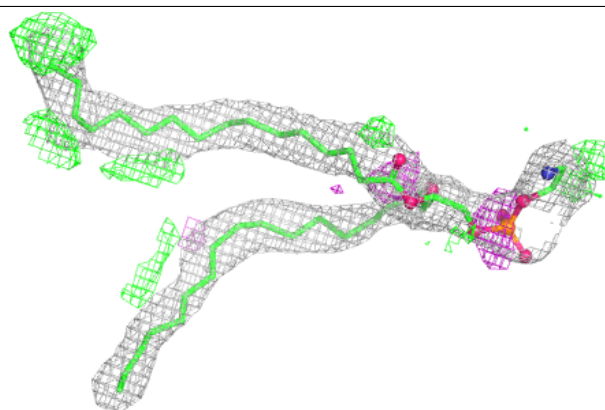
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
2	PEF	B	701	47/47	0.83	0.22	47,77,111,134	0
2	PEF	A	701	47/47	0.85	0.21	53,77,114,132	0
2	PEF	D	701	47/47	0.85	0.23	70,97,151,168	0
2	PEF	C	701	47/47	0.86	0.20	45,75,123,132	0
2	PEF	E	701	47/47	0.86	0.20	51,72,100,128	0

The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation to approximate a three-dimensional view.

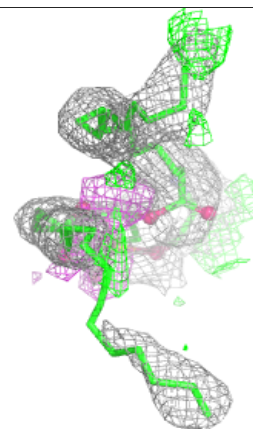
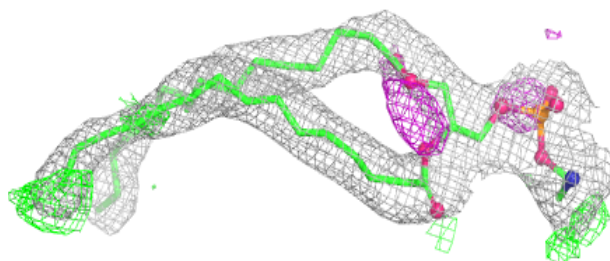
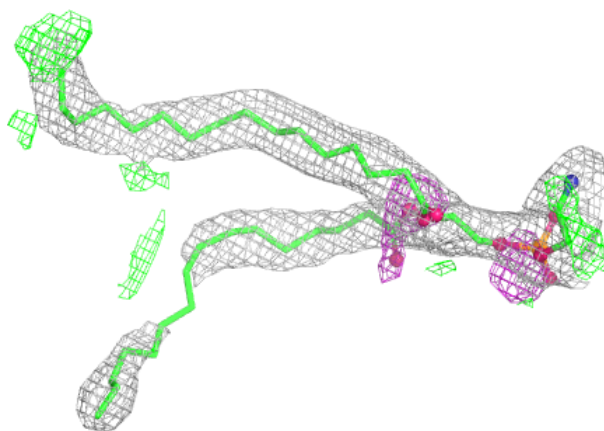
Electron density around PEF B 701:

2mF_o-DF_c (at 0.7 rmsd) in gray
mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

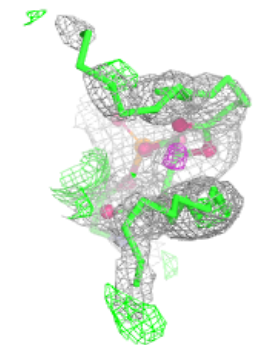
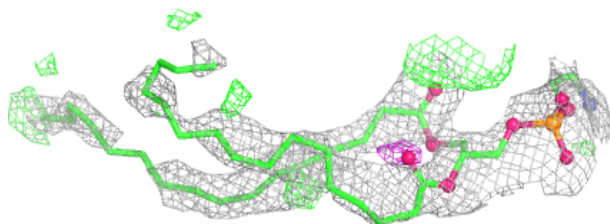
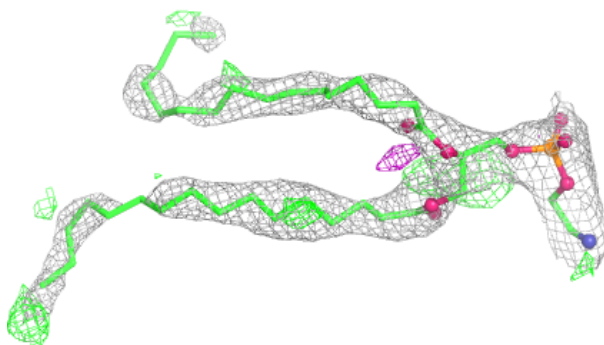


Electron density around PEF A 701:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

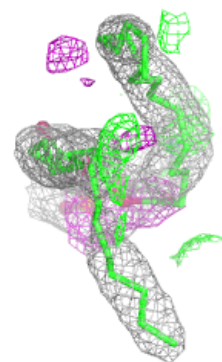
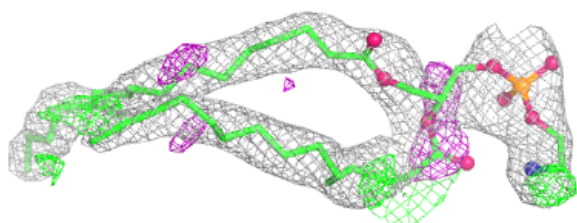
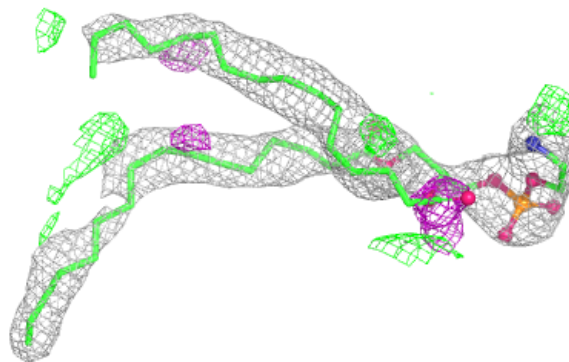
**Electron density around PEF D 701:**

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

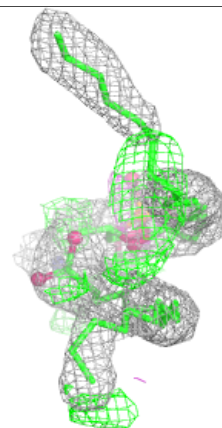
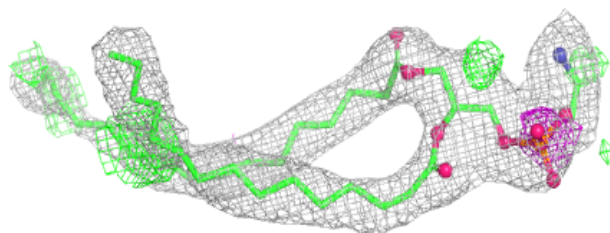
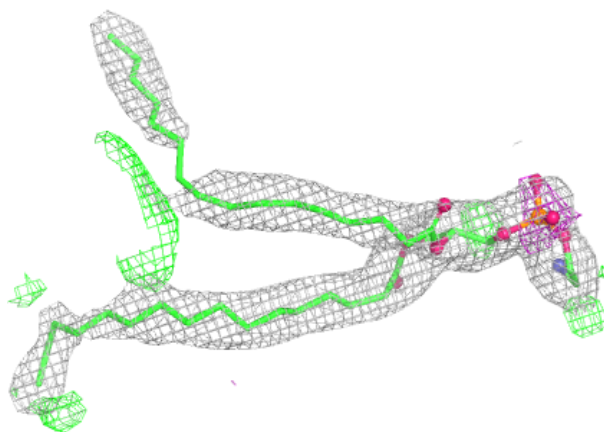


Electron density around PEF C 701:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

**Electron density around PEF E 701:**

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



6.5 Other polymers [i](#)

There are no such residues in this entry.