



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 20, 2026 – 07:30 AM UTC

PDB ID : 9LV2 / pdb_00009lv2
Title : Crystal structure of H1 Haemagglutinin HN/18-HA2-L113S from Influenza A virus
Authors : Deng, G.; Wei, X.; Sun, H.
Deposited on : 2025-02-11
Resolution : 2.80 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
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

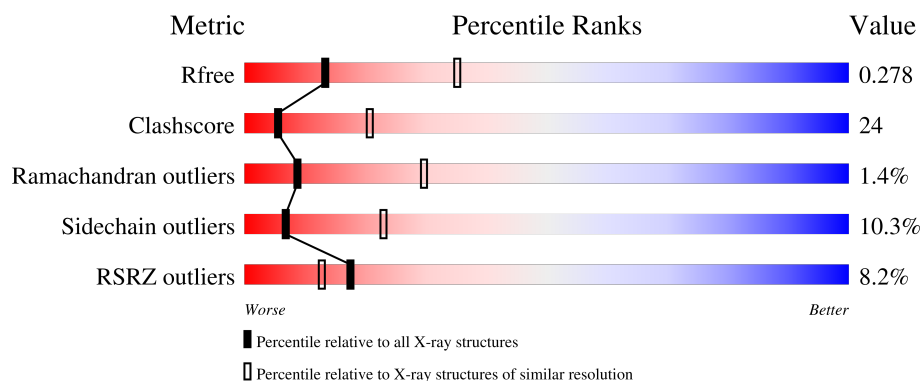
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.80 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	3866 (2.80-2.80)
Clashscore	190562	4276 (2.80-2.80)
Ramachandran outliers	187476	4196 (2.80-2.80)
Sidechain outliers	187428	4198 (2.80-2.80)
RSRZ outliers	180081	3869 (2.80-2.80)

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	321	<div> <div>5%</div> <div> <div></div> <div>61%</div> <div>33%</div> <div>6%</div> </div> </div>
1	C	321	<div> <div>5%</div> <div> <div></div> <div>64%</div> <div>32%</div> <div>.</div> </div> </div>
1	E	321	<div> <div>11%</div> <div> <div></div> <div>49%</div> <div>45%</div> <div>5%</div> <div>.</div> </div> </div>
2	B	156	<div> <div>5%</div> <div> <div></div> <div>56%</div> <div>38%</div> <div>6%</div> </div> </div>
2	D	156	<div> <div>21%</div> <div> <div></div> <div>58%</div> <div>33%</div> <div>8%</div> <div>.</div> </div> </div>

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Mol	Chain	Length	Quality of chain
2	F	156	<div><div></div><div>7%</div><div>58%</div><div>34%</div><div>8%</div></div>

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 11463 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 Hemagglutinin.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	321	Total	C	N	O	S	0	0	0
			2515	1583	441	480	11			
1	C	321	Total	C	N	O	S	0	0	0
			2515	1583	441	480	11			
1	E	321	Total	C	N	O	S	0	0	0
			2515	1583	441	480	11			

- Molecule 2 is a protein called Hemagglutinin.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	156	Total	C	N	O	S	0	0	0
			1250	785	213	245	7			
2	D	156	Total	C	N	O	S	0	0	0
			1250	785	213	245	7			
2	F	156	Total	C	N	O	S	0	0	0
			1250	785	213	245	7			

There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	113	SER	LEU	engineered mutation	UNP A0A6G5UYP3
D	113	SER	LEU	engineered mutation	UNP A0A6G5UYP3
F	113	SER	LEU	engineered mutation	UNP A0A6G5UYP3

- Molecule 3 is 2-acetamido-2-deoxy-beta-D-glucopyranose (CCD ID: NAG) (formula: C₈H₁₅NO₆).

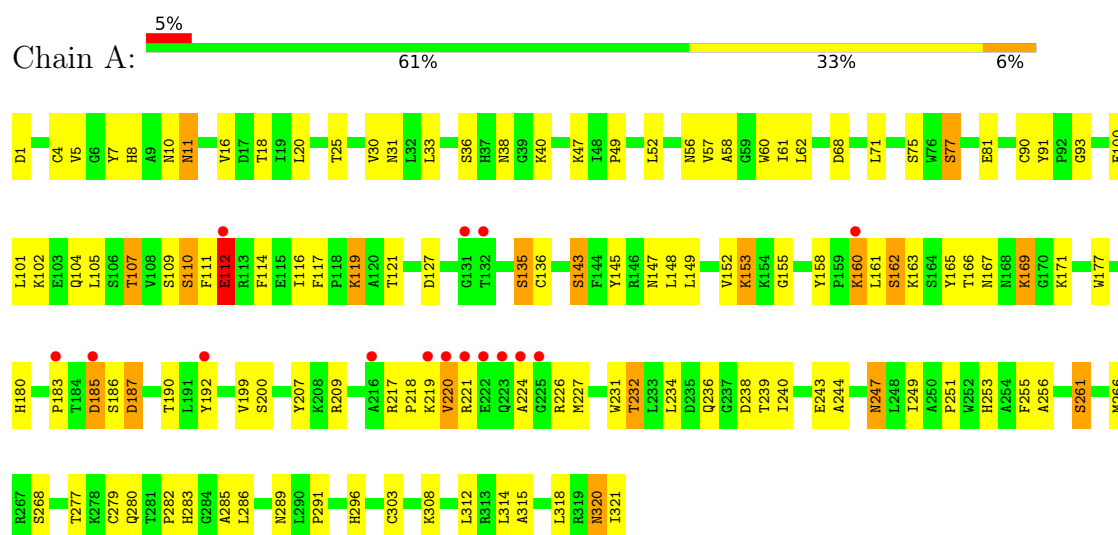


Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	A	1	Total	C	N	O	0	0
			14	8	1	5		
3	A	1	Total	C	N	O	14	0
			14	8	1	5		
3	A	1	Total	C	N	O	14	0
			14	8	1	5		
3	A	1	Total	C	N	O	14	0
			14	8	1	5		
3	C	1	Total	C	N	O	0	0
			14	8	1	5		
3	C	1	Total	C	N	O	0	0
			14	8	1	5		
3	C	1	Total	C	N	O	14	0
			14	8	1	5		
3	C	1	Total	C	N	O	14	0
			14	8	1	5		
3	E	1	Total	C	N	O	0	0
			14	8	1	5		
3	E	1	Total	C	N	O	0	0
			14	8	1	5		
3	E	1	Total	C	N	O	14	0
			14	8	1	5		
3	E	1	Total	C	N	O	14	0
			14	8	1	5		

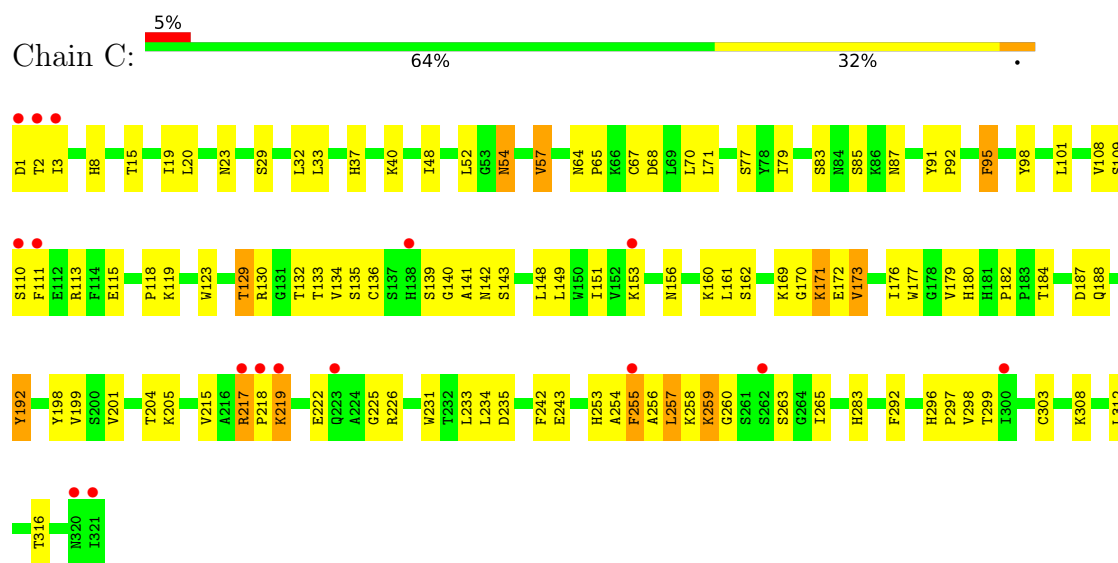
3 Residue-property plots [i](#)

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 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: Hemagglutinin

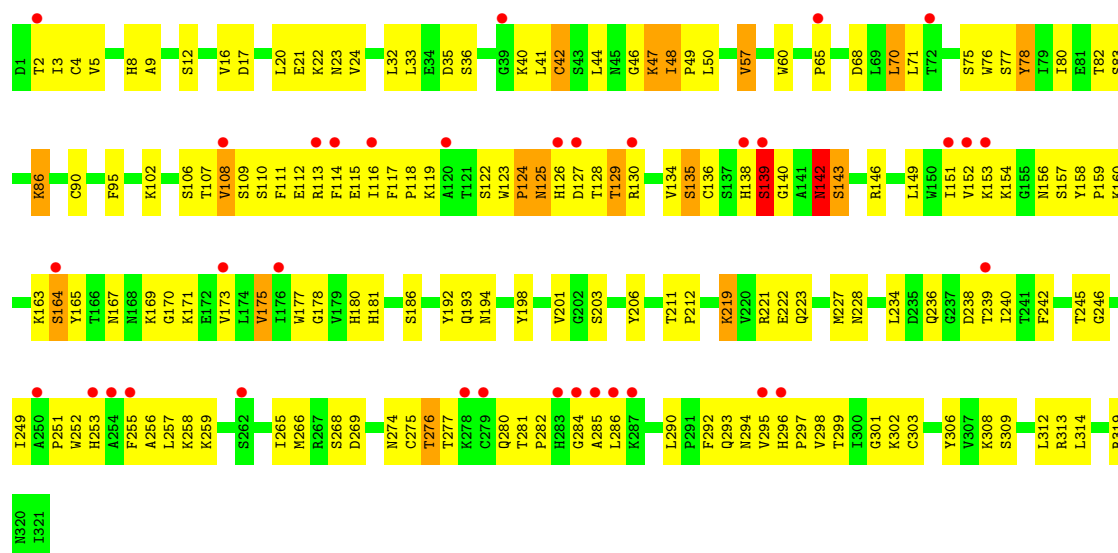


• Molecule 1: Hemagglutinin

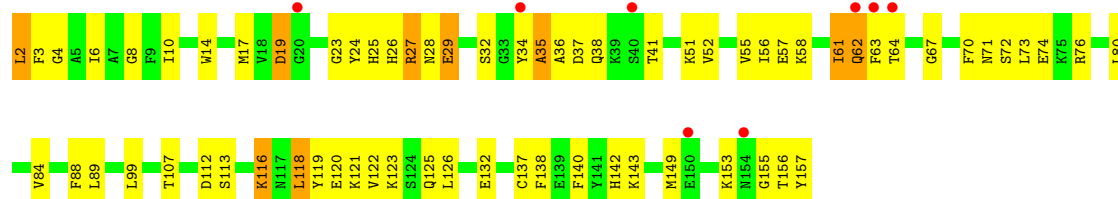


• Molecule 1: Hemagglutinin

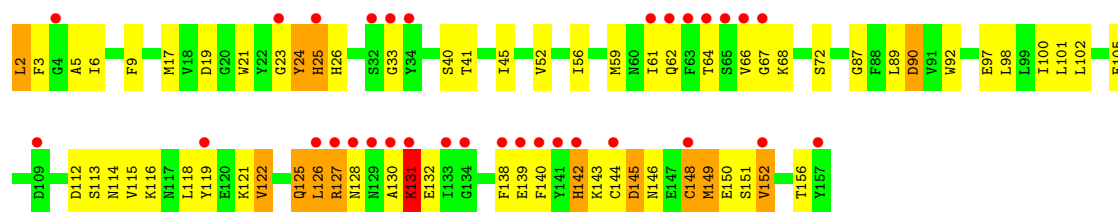




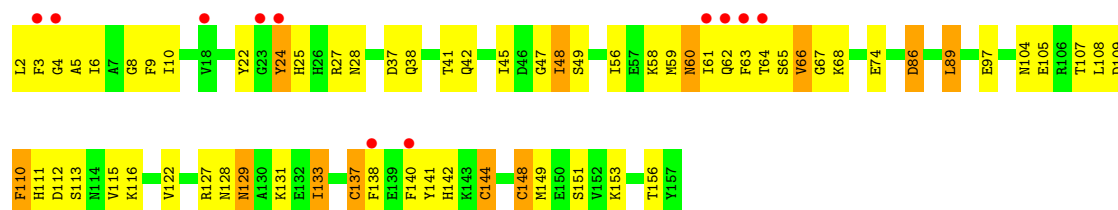
• Molecule 2: Hemagglutinin



• Molecule 2: Hemagglutinin



• Molecule 2: Hemagglutinin



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	65.09Å 249.63Å 65.51Å 90.00° 118.43° 90.00°	Depositor
Resolution (Å)	50.00 – 2.80 50.00 – 2.80	Depositor EDS
% Data completeness (in resolution range)	80.0 (50.00-2.80) 80.0 (50.00-2.80)	Depositor EDS
R_{merge}	0.28	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.47 (at 2.81Å)	Xtriage
Refinement program	REFMAC 5.8.0218	Depositor
R, R_{free}	0.243 , 0.267 0.252 , 0.278	Depositor DCC
R_{free} test set	1755 reflections (3.90%)	wwPDB-VP
Wilson B-factor (Å ²)	45.6	Xtriage
Anisotropy	0.092	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.31 , 62.2	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	0.002 for -h-l,k,h 0.002 for l,k,-h-l 0.031 for h,-k,-h-l 0.032 for -h-l,-k,l 0.032 for l,-k,h	Xtriage
F_o, F_c correlation	0.87	EDS
Total number of atoms	11463	wwPDB-VP
Average B, all atoms (Å ²)	53.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.22% 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 [i](#)

5.1 Standard geometry [i](#)

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

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	0.58	0/2577	0.73	0/3506
1	C	0.56	0/2577	0.70	0/3506
1	E	0.55	0/2577	0.76	0/3506
2	B	0.70	0/1274	0.68	0/1712
2	D	0.54	0/1274	0.67	0/1712
2	F	0.74	0/1274	0.74	0/1712
All	All	0.60	0/11553	0.72	0/15654

There are no bond length outliers.

There are no bond angle outliers.

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	A	2515	0	2452	118	0
1	C	2515	0	2453	100	0
1	E	2515	0	2453	150	0
2	B	1250	0	1185	63	0
2	D	1250	0	1187	78	0
2	F	1250	0	1186	67	0
3	A	56	0	52	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	C	56	0	52	1	0
3	E	56	0	52	0	0
All	All	11463	0	11072	524	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 24.

All (524) 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:E:42:CYS:CB	1:E:275:CYS:SG	2.23	1.26
1:A:158:TYR:CE2	1:A:192:TYR:HD1	1.65	1.12
1:E:42:CYS:HB3	1:E:275:CYS:SG	1.91	1.10
2:D:126:LEU:HD22	2:D:130:ALA:CB	1.81	1.09
2:F:112:ASP:O	2:F:115:VAL:HG22	1.51	1.07
1:C:1:ASP:O	2:D:140:PHE:HB2	1.56	1.05
1:A:158:TYR:CE2	1:A:192:TYR:CD1	2.45	1.04
2:D:145:ASP:OD1	2:D:146:ASN:N	1.92	1.03
1:A:158:TYR:HE2	1:A:192:TYR:CD1	1.76	1.02
2:B:2:LEU:HD12	2:B:112:ASP:OD2	1.59	1.02
1:A:153:LYS:HB2	1:A:158:TYR:HB2	1.38	1.01
2:F:3:PHE:CE2	2:F:113:SER:HB2	1.98	0.99
1:A:303:CYS:O	2:B:61:ILE:HG12	1.63	0.96
2:D:144:CYS:SG	2:D:148:CYS:HB2	2.05	0.96
2:D:126:LEU:HD22	2:D:130:ALA:HB3	1.44	0.95
1:C:153:LYS:HD2	1:C:156:ASN:HA	1.51	0.93
1:E:124:PRO:HD2	1:E:125:ASN:OD1	1.71	0.90
2:D:2:LEU:HD22	2:D:112:ASP:OD2	1.71	0.89
1:E:153:LYS:HE3	1:E:156:ASN:HA	1.55	0.89
1:E:266:MET:HG3	1:E:282:PRO:HG3	1.55	0.88
1:C:173:VAL:HA	1:C:256:ALA:HA	1.57	0.86
2:D:144:CYS:SG	2:D:148:CYS:CB	2.64	0.86
1:E:266:MET:HE2	1:E:282:PRO:HA	1.58	0.86
1:A:158:TYR:CD2	1:A:192:TYR:HB3	2.10	0.85
2:F:65:SER:O	2:F:66:VAL:HG13	1.77	0.85
1:A:112:GLU:HB3	1:A:256:ALA:HB3	1.59	0.84
2:B:27:ARG:HG2	2:B:27:ARG:HH11	1.43	0.84
2:D:126:LEU:HD22	2:D:130:ALA:HB2	1.59	0.82
1:E:139:SER:OG	1:E:140:GLY:N	2.11	0.82
1:E:153:LYS:HB2	1:E:157:SER:O	1.79	0.82
1:A:261:SER:HB2	2:B:63:PHE:HZ	1.44	0.82

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:217:ARG:HB3	1:C:218:PRO:HD2	1.62	0.81
1:E:65:PRO:O	1:E:138:HIS:CD2	2.33	0.81
1:C:173:VAL:HG13	1:C:234:LEU:HB3	1.62	0.80
1:A:153:LYS:CB	1:A:158:TYR:HB2	2.11	0.80
1:E:42:CYS:CA	1:E:275:CYS:SG	2.69	0.80
1:C:1:ASP:C	2:D:140:PHE:HB2	2.07	0.79
1:C:217:ARG:CB	1:C:218:PRO:CD	2.60	0.79
2:F:42:GLN:HA	2:F:45:ILE:HD12	1.65	0.78
2:B:2:LEU:CD1	2:B:112:ASP:OD2	2.32	0.77
1:C:153:LYS:CD	1:C:156:ASN:HA	2.15	0.77
1:A:114:PHE:CE2	1:A:169:LYS:HD3	2.19	0.77
1:E:17:ASP:OD2	1:E:22:LYS:HG2	1.83	0.77
1:A:227:MET:HE3	1:A:249:ILE:HG13	1.67	0.75
1:C:217:ARG:CG	1:C:218:PRO:CD	2.65	0.75
2:B:26:HIS:HB2	2:B:149:MET:HE3	1.69	0.74
2:B:27:ARG:HG2	2:B:27:ARG:NH1	1.99	0.74
1:E:42:CYS:SG	1:E:285:ALA:HB2	2.27	0.74
1:E:123:TRP:CD2	1:E:151:ILE:HD11	2.22	0.74
2:D:119:TYR:CE1	2:D:138:PHE:HE1	2.06	0.73
2:B:27:ARG:HG3	2:B:32:SER:CB	2.19	0.73
1:A:61:ILE:O	1:A:147:ASN:ND2	2.20	0.73
1:C:217:ARG:CG	1:C:218:PRO:HD3	2.19	0.73
1:E:42:CYS:SG	1:E:285:ALA:CB	2.77	0.72
1:C:217:ARG:CB	1:C:218:PRO:HD2	2.20	0.72
1:E:82:THR:HG22	1:E:269:ASP:HA	1.70	0.72
1:C:172:GLU:HG3	1:C:257:LEU:HD12	1.72	0.71
1:E:4:CYS:SG	2:F:137:CYS:HB3	2.30	0.71
1:A:261:SER:HB2	2:B:63:PHE:CZ	2.24	0.71
1:E:112:GLU:OE2	1:E:171:LYS:NZ	2.23	0.71
1:C:205:LYS:HZ1	1:C:235:ASP:HB2	1.56	0.71
2:F:3:PHE:CZ	2:F:113:SER:HB2	2.26	0.71
1:A:207:TYR:CD1	1:C:217:ARG:HD2	2.25	0.70
1:E:76:TRP:HH2	1:E:111:PHE:CD2	2.10	0.70
2:F:45:ILE:O	2:F:49:SER:HB3	1.91	0.70
1:C:64:ASN:OD1	1:C:65:PRO:HD2	1.89	0.70
2:B:27:ARG:HG3	2:B:32:SER:OG	1.92	0.70
2:D:122:VAL:CG1	2:D:126:LEU:HD12	2.21	0.70
1:E:47:LYS:HB3	1:E:77:SER:HB3	1.74	0.70
2:D:119:TYR:CE1	2:D:138:PHE:CE1	2.80	0.70
2:B:27:ARG:HG3	2:B:32:SER:HB3	1.73	0.69
1:A:158:TYR:HD2	1:A:192:TYR:HB3	1.55	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:16:VAL:HG12	1:E:313:ARG:HG2	1.74	0.69
1:E:42:CYS:HA	1:E:275:CYS:SG	2.32	0.69
1:E:127:ASP:HB3	1:E:152:VAL:HG23	1.73	0.69
2:B:62:GLN:HG2	2:D:90:ASP:OD1	1.92	0.69
1:E:276:THR:HG23	1:E:277:THR:N	2.08	0.69
1:C:217:ARG:HB3	1:C:218:PRO:CD	2.22	0.68
2:D:122:VAL:HG12	2:D:126:LEU:HD12	1.75	0.68
1:E:48:ILE:HD13	1:E:48:ILE:N	2.07	0.68
2:F:65:SER:O	2:F:66:VAL:CG1	2.42	0.68
1:C:217:ARG:HG2	1:C:218:PRO:HD2	1.77	0.67
1:A:185:ASP:OD1	1:A:185:ASP:N	2.27	0.67
1:A:10:ASN:H	1:A:320:ASN:HD21	1.42	0.67
2:D:148:CYS:O	2:D:149:MET:C	2.37	0.67
1:E:219:LYS:NZ	1:E:222:GLU:OE2	2.20	0.67
1:C:217:ARG:HG2	1:C:218:PRO:CD	2.24	0.66
1:E:123:TRP:HE3	1:E:128:THR:HG22	1.58	0.66
1:C:54:ASN:HB2	1:C:87:ASN:HD22	1.60	0.66
1:E:180:HIS:HD2	1:E:227:MET:HG3	1.61	0.66
2:F:48:ILE:HD11	2:F:107:THR:HG23	1.78	0.66
2:D:68:LYS:HD2	2:D:68:LYS:N	2.10	0.66
1:E:142:ASN:N	1:E:142:ASN:HD22	1.94	0.66
2:F:4:GLY:O	2:F:9:PHE:CD2	2.50	0.65
2:F:41:THR:HG22	2:F:45:ILE:HD11	1.78	0.65
1:C:219:LYS:O	1:C:219:LYS:HG3	1.95	0.65
2:D:3:PHE:N	2:D:112:ASP:OD2	2.23	0.65
1:C:205:LYS:NZ	1:C:235:ASP:HB2	2.12	0.65
1:A:158:TYR:CE2	1:A:192:TYR:HB3	2.31	0.65
2:F:111:HIS:O	2:F:115:VAL:HG13	1.97	0.65
1:E:90:CYS:O	1:E:221:ARG:HD2	1.97	0.65
1:E:153:LYS:CB	1:E:157:SER:O	2.45	0.64
2:F:148:CYS:SG	2:F:149:MET:N	2.70	0.64
1:A:47:LYS:HB3	1:A:77:SER:HB3	1.80	0.64
2:D:6:ILE:HD12	2:D:112:ASP:HA	1.79	0.64
1:E:266:MET:HE2	1:E:282:PRO:CA	2.28	0.64
1:A:116:ILE:HG21	1:A:251:PRO:HB2	1.80	0.64
1:E:129:THR:HB	1:E:130:ARG:HH11	1.63	0.63
1:A:200:SER:HB3	1:A:243:GLU:HB3	1.81	0.63
2:F:28:ASN:ND2	2:F:144:CYS:O	2.32	0.63
1:E:136:CYS:HB2	1:E:143:SER:O	1.99	0.62
2:F:60:ASN:ND2	2:F:62:GLN:OE1	2.32	0.62
1:C:217:ARG:CG	1:C:218:PRO:HD2	2.29	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:F:109:ASP:O	2:F:110:PHE:C	2.42	0.62
2:D:148:CYS:O	2:D:151:SER:N	2.33	0.61
1:A:158:TYR:HD2	1:A:192:TYR:CB	2.13	0.61
1:A:314:LEU:HD23	2:B:52:VAL:HG22	1.81	0.61
1:C:148:LEU:HD21	1:C:176:ILE:HD12	1.82	0.61
1:E:227:MET:HE2	1:E:249:ILE:HG13	1.82	0.61
1:E:299:THR:HB	1:E:303:CYS:SG	2.40	0.61
2:F:65:SER:C	2:F:66:VAL:HG13	2.25	0.61
2:B:118:LEU:O	2:B:121:LYS:N	2.32	0.61
1:A:158:TYR:CD2	1:A:192:TYR:CB	2.82	0.61
1:C:91:TYR:CD1	1:C:92:PRO:HD2	2.36	0.61
1:E:76:TRP:CH2	1:E:111:PHE:CD2	2.89	0.61
1:A:114:PHE:CE2	1:A:169:LYS:CD	2.84	0.60
1:A:318:LEU:HD12	2:B:6:ILE:HD13	1.82	0.60
1:E:193:GLN:HG3	1:E:194:ASN:ND2	2.16	0.60
2:F:115:VAL:HG23	2:F:116:LYS:N	2.16	0.60
2:B:27:ARG:CG	2:B:32:SER:OG	2.49	0.60
1:E:76:TRP:CH2	1:E:111:PHE:HD2	2.20	0.59
1:C:54:ASN:OD1	1:C:54:ASN:N	2.29	0.59
1:E:123:TRP:CE3	1:E:151:ILE:HD11	2.36	0.59
2:D:140:PHE:HE2	2:D:149:MET:HE1	1.66	0.59
1:E:68:ASP:OD2	1:E:146:ARG:NE	2.36	0.59
1:A:186:SER:O	1:A:190:THR:HG23	2.02	0.59
1:C:67:CYS:HB3	1:C:70:LEU:HD12	1.85	0.59
2:F:5:ALA:O	2:F:8:GLY:N	2.35	0.59
1:C:110:SER:OG	1:C:258:LYS:HB3	2.03	0.59
1:C:54:ASN:HB2	1:C:87:ASN:ND2	2.18	0.59
2:B:24:TYR:CE1	2:B:37:ASP:HB2	2.38	0.58
1:A:227:MET:CE	1:A:249:ILE:HG13	2.33	0.58
1:E:268:SER:HB3	1:E:282:PRO:HB3	1.85	0.58
2:F:133:ILE:HD12	2:F:137:CYS:O	2.04	0.58
1:A:38:ASN:HD21	1:A:285:ALA:HB3	1.69	0.58
1:C:160:LYS:HZ3	1:C:243:GLU:HG3	1.68	0.58
2:D:127:ARG:HG3	2:D:127:ARG:NH1	2.18	0.58
1:E:164:SER:HA	1:E:240:ILE:O	2.03	0.58
2:F:127:ARG:HD3	2:F:127:ARG:C	2.29	0.58
2:D:25:HIS:ND1	2:D:33:GLY:O	2.36	0.58
2:D:127:ARG:HG3	2:D:127:ARG:HH11	1.68	0.58
1:C:113:ARG:HG3	1:C:255:PHE:CE1	2.39	0.58
1:E:4:CYS:SG	2:F:137:CYS:CB	2.92	0.58
1:E:301:GLY:H	2:F:63:PHE:HE1	1.50	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:2:LEU:O	2:F:113:SER:OG	2.22	0.57
1:A:158:TYR:HD2	1:A:192:TYR:CA	2.16	0.57
2:B:58:LYS:HD2	2:D:97:GLU:HB3	1.86	0.57
1:C:109:SER:HB3	1:C:260:GLY:HA3	1.85	0.57
1:E:292:PHE:CE1	2:F:59:MET:HE3	2.40	0.57
1:E:123:TRP:HZ3	1:E:149:LEU:HD23	1.70	0.57
1:E:126:HIS:CE1	1:E:159:PRO:HD2	2.40	0.57
1:E:286:LEU:HD11	1:E:295:VAL:HG21	1.86	0.57
2:D:145:ASP:CG	2:D:146:ASN:N	2.63	0.56
2:B:29:GLU:HA	2:B:29:GLU:OE1	2.04	0.56
2:B:56:ILE:HD12	2:B:57:GLU:N	2.19	0.56
1:E:77:SER:HG	1:E:78:TYR:HD1	1.53	0.56
2:B:25:HIS:HB2	2:B:34:TYR:CD1	2.41	0.56
1:C:77:SER:O	1:C:263:SER:HA	2.05	0.56
1:E:24:VAL:HG11	2:F:108:LEU:HD11	1.87	0.56
1:A:266:MET:HE2	1:A:282:PRO:HG3	1.87	0.56
1:A:183:PRO:HG3	1:A:224:ALA:HB3	1.88	0.55
2:B:34:TYR:O	2:B:35:ALA:HB2	2.06	0.55
1:A:158:TYR:HD2	1:A:192:TYR:HA	1.71	0.55
1:C:32:LEU:HD12	2:D:100:ILE:HD11	1.88	0.55
1:C:299:THR:HB	1:C:303:CYS:SG	2.46	0.55
2:D:142:HIS:ND1	2:D:143:LYS:O	2.39	0.55
1:A:207:TYR:CE1	1:C:217:ARG:HD2	2.42	0.55
1:E:115:GLU:CD	1:E:118:PRO:HA	2.32	0.55
1:E:266:MET:CG	1:E:282:PRO:HG3	2.32	0.55
1:E:108:VAL:HG21	1:E:257:LEU:HD22	1.87	0.55
1:E:111:PHE:HE1	1:E:255:PHE:CB	2.20	0.55
1:E:153:LYS:CE	1:E:156:ASN:HA	2.31	0.55
1:A:33:LEU:HB2	1:A:312:LEU:HB2	1.89	0.55
1:A:180:HIS:HB3	1:A:247:ASN:HB3	1.89	0.55
2:F:115:VAL:CG2	2:F:116:LYS:N	2.70	0.55
1:A:117:PHE:CE1	1:A:165:TYR:HB2	2.42	0.54
1:C:3:ILE:HA	2:D:26:HIS:HB3	1.89	0.54
1:A:52:LEU:HD11	1:A:57:VAL:HG12	1.89	0.54
1:A:93:GLY:HA3	1:A:227:MET:O	2.06	0.54
2:D:119:TYR:CZ	2:D:138:PHE:HE1	2.24	0.54
1:A:136:CYS:HB2	1:A:143:SER:O	2.08	0.54
2:D:98:LEU:HD12	2:D:102:LEU:HD11	1.89	0.54
1:E:40:LYS:O	1:E:284:GLY:HA2	2.08	0.54
1:E:165:TYR:HB3	1:E:240:ILE:HG22	1.89	0.54
1:A:291:PRO:HG3	2:B:56:ILE:HG22	1.89	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:D:5:ALA:HB3	2:D:112:ASP:OD1	2.07	0.54
2:B:118:LEU:O	2:B:119:TYR:C	2.51	0.53
2:B:17:MET:SD	2:B:23:GLY:HA3	2.47	0.53
2:B:51:LYS:NZ	2:B:107:THR:OG1	2.37	0.53
1:E:119:LYS:HD3	1:E:149:LEU:HD21	1.90	0.53
1:C:8:HIS:HB2	2:D:21:TRP:HA	1.90	0.53
2:D:142:HIS:CE1	2:D:143:LYS:O	2.62	0.53
1:A:11:ASN:H	1:A:11:ASN:ND2	2.06	0.53
1:C:48:ILE:HD12	1:C:48:ILE:H	1.74	0.53
2:D:145:ASP:O	2:D:149:MET:SD	2.67	0.53
1:E:41:LEU:HD23	1:E:80:ILE:HG12	1.89	0.53
1:C:161:LEU:O	1:C:243:GLU:HA	2.09	0.53
1:E:135:SER:HB3	1:E:221:ARG:HB3	1.89	0.53
1:A:75:SER:HB2	1:A:110:SER:HB3	1.91	0.53
1:A:234:LEU:HD22	1:A:240:ILE:HB	1.91	0.53
2:B:126:LEU:HD21	2:B:140:PHE:CE1	2.44	0.53
1:A:33:LEU:HD13	1:A:312:LEU:HD12	1.90	0.52
2:B:23:GLY:HA3	2:B:36:ALA:HA	1.89	0.52
1:E:115:GLU:HA	1:E:253:HIS:CD2	2.44	0.52
1:A:147:ASN:HA	1:A:253:HIS:HB2	1.91	0.52
1:E:125:ASN:OD1	1:E:125:ASN:N	2.25	0.52
1:C:68:ASP:HA	1:C:71:LEU:HD23	1.91	0.52
1:E:75:SER:HA	1:E:109:SER:O	2.10	0.52
2:F:27:ARG:HD2	2:F:27:ARG:O	2.08	0.52
2:B:76:ARG:HH12	2:F:74:GLU:CD	2.18	0.52
1:E:146:ARG:HH11	1:E:146:ARG:HG2	1.74	0.52
1:A:112:GLU:OE1	1:A:112:GLU:HA	2.10	0.52
2:F:131:LYS:HB2	2:F:141:TYR:CZ	2.44	0.52
2:B:62:GLN:HE21	2:B:62:GLN:HA	1.75	0.51
2:B:4:GLY:O	2:B:8:GLY:HA3	2.10	0.51
2:D:126:LEU:HD13	2:D:138:PHE:CD2	2.45	0.51
1:A:247:ASN:N	1:A:247:ASN:OD1	2.43	0.51
2:F:129:ASN:OD1	2:F:129:ASN:N	2.44	0.51
1:A:16:VAL:HG11	1:A:315:ALA:HB2	1.92	0.51
2:F:3:PHE:HD2	2:F:112:ASP:HB3	1.74	0.51
1:A:177:TRP:HZ3	1:A:232:THR:HG22	1.75	0.51
2:B:71:ASN:OD1	2:B:74:GLU:HG3	2.11	0.51
2:D:122:VAL:CG1	2:D:126:LEU:CD1	2.89	0.51
2:D:131:LYS:HG3	2:D:132:GLU:N	2.26	0.51
2:F:24:TYR:OH	2:F:37:ASP:OD2	2.24	0.51
1:A:177:TRP:CZ3	1:A:232:THR:HG22	2.46	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:209:ARG:HD2	1:C:215:VAL:HG21	1.91	0.51
2:D:41:THR:O	2:D:45:ILE:HG13	2.10	0.51
1:C:20:LEU:HD12	2:D:105:GLU:OE2	2.11	0.51
1:E:42:CYS:SG	1:E:285:ALA:HB3	2.50	0.51
1:E:50:LEU:O	1:E:80:ILE:HD12	2.11	0.51
2:D:148:CYS:O	2:D:150:GLU:N	2.44	0.51
1:A:47:LYS:O	1:A:77:SER:OG	2.27	0.50
1:C:123:TRP:CE2	1:C:151:ILE:HD11	2.46	0.50
2:D:118:LEU:O	2:D:121:LYS:N	2.44	0.50
1:E:83:SER:HB2	1:E:269:ASP:OD2	2.11	0.50
1:A:100:GLU:O	1:A:104:GLN:HG2	2.11	0.50
1:C:136:CYS:HB2	1:C:143:SER:O	2.11	0.50
2:D:122:VAL:HG13	2:D:126:LEU:HD12	1.91	0.50
1:A:207:TYR:OH	1:A:209:ARG:HG3	2.11	0.50
1:E:65:PRO:HB3	1:E:146:ARG:NH2	2.27	0.50
1:A:220:VAL:HG22	1:A:221:ARG:HG2	1.92	0.50
2:D:125:GLN:HE21	2:D:152:VAL:HG13	1.76	0.50
1:E:123:TRP:CZ3	1:E:149:LEU:HD23	2.47	0.50
2:F:4:GLY:O	2:F:9:PHE:HD2	1.94	0.50
1:A:161:LEU:HD23	1:A:162:SER:N	2.27	0.49
1:A:283:HIS:NE2	1:A:296:HIS:HD2	2.10	0.49
1:E:5:VAL:O	2:F:10:ILE:HD13	2.12	0.49
1:E:65:PRO:HA	1:E:68:ASP:OD1	2.12	0.49
1:E:123:TRP:O	1:E:128:THR:HG23	2.12	0.49
1:C:119:LYS:HG3	1:C:149:LEU:HD21	1.94	0.49
1:C:1:ASP:C	1:C:2:THR:HG23	2.37	0.49
2:D:3:PHE:O	2:D:116:LYS:HD3	2.12	0.49
1:A:112:GLU:CB	1:A:256:ALA:HB3	2.35	0.49
1:E:127:ASP:OD2	1:E:130:ARG:HG2	2.11	0.49
1:E:153:LYS:HB2	1:E:157:SER:C	2.37	0.49
2:D:113:SER:OG	2:F:2:LEU:O	2.25	0.49
2:F:5:ALA:CB	2:F:115:VAL:CG2	2.91	0.49
1:C:259:LYS:O	1:C:260:GLY:C	2.54	0.49
2:D:3:PHE:HB2	2:D:112:ASP:CG	2.37	0.49
2:D:62:GLN:NE2	2:F:86:ASP:OD2	2.46	0.49
1:E:117:PHE:CE1	1:E:163:LYS:HE3	2.47	0.49
1:A:119:LYS:HD2	1:A:149:LEU:HD13	1.94	0.49
1:C:225:GLY:O	1:C:226:ARG:HD2	2.13	0.49
2:B:26:HIS:C	2:B:26:HIS:CD2	2.91	0.49
1:E:2:THR:CG2	2:F:27:ARG:HB3	2.42	0.49
1:E:169:LYS:HE2	1:E:169:LYS:HB3	1.56	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:116:LYS:HG3	2:B:116:LYS:O	2.12	0.49
1:E:167:ASN:HD21	1:E:169:LYS:HB2	1.77	0.49
1:E:303:CYS:O	2:F:61:ILE:HB	2.12	0.49
1:A:56:ASN:OD1	1:A:58:ALA:HB3	2.13	0.49
1:C:139:SER:C	1:C:141:ALA:H	2.20	0.49
1:E:86:LYS:NZ	1:E:86:LYS:HB2	2.28	0.49
2:B:27:ARG:NH1	2:B:27:ARG:CG	2.72	0.48
1:E:276:THR:CG2	1:E:277:THR:N	2.71	0.48
1:C:64:ASN:OD1	1:C:65:PRO:CD	2.61	0.48
2:D:126:LEU:HD13	2:D:138:PHE:HD2	1.78	0.48
1:E:170:GLY:H	1:E:236:GLN:HE21	1.61	0.48
1:E:266:MET:HE1	1:E:280:GLN:HG3	1.94	0.48
2:D:59:MET:HE1	2:D:92:TRP:CZ3	2.48	0.48
1:E:32:LEU:HA	1:E:290:LEU:HD22	1.95	0.48
1:E:242:PHE:CZ	1:E:251:PRO:HG3	2.49	0.48
2:F:142:HIS:CD2	2:F:142:HIS:H	2.30	0.48
2:F:151:SER:HB2	2:F:156:THR:O	2.13	0.48
2:D:122:VAL:HG13	2:D:126:LEU:CD1	2.43	0.48
1:C:1:ASP:C	1:C:2:THR:CG2	2.87	0.48
1:C:188:GLN:NE2	1:C:192:TYR:HD2	2.12	0.48
2:D:3:PHE:HB2	2:D:112:ASP:HB3	1.95	0.48
1:E:297:PRO:HG3	1:E:306:TYR:CE2	2.49	0.48
1:E:8:HIS:ND1	1:E:9:ALA:N	2.62	0.48
1:E:181:HIS:CE1	1:E:212:PRO:HA	2.49	0.48
2:D:130:ALA:O	2:D:131:LYS:C	2.57	0.48
1:E:130:ARG:HD2	1:E:130:ARG:N	2.29	0.48
1:A:167:ASN:HB3	1:A:236:GLN:HA	1.96	0.47
1:C:15:THR:OG1	1:C:23:ASN:HA	2.14	0.47
1:C:101:LEU:HB2	1:C:231:TRP:CE2	2.49	0.47
1:E:57:VAL:HG13	1:E:102:LYS:HZ3	1.77	0.47
1:E:57:VAL:HG13	1:E:102:LYS:NZ	2.30	0.47
1:E:129:THR:C	1:E:130:ARG:HD2	2.39	0.47
1:A:57:VAL:HA	1:A:60:TRP:HE3	1.79	0.47
1:E:47:LYS:HD2	1:E:47:LYS:HA	1.53	0.47
1:C:254:ALA:C	1:C:255:PHE:CG	2.92	0.47
2:D:142:HIS:ND1	2:D:142:HIS:C	2.72	0.47
1:E:41:LEU:HD21	1:E:268:SER:OG	2.14	0.47
1:A:101:LEU:HB2	1:A:231:TRP:CE2	2.49	0.47
1:C:123:TRP:CD2	1:C:151:ILE:HD11	2.49	0.47
2:D:125:GLN:O	2:D:125:GLN:HG3	2.12	0.47
2:F:48:ILE:CD1	2:F:107:THR:HG23	2.44	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:F:109:ASP:O	2:F:110:PHE:O	2.32	0.47
1:A:91:TYR:CE1	1:A:227:MET:HG3	2.49	0.47
1:A:165:TYR:O	1:A:239:THR:HG23	2.14	0.47
2:B:142:HIS:ND1	2:B:143:LYS:O	2.35	0.47
1:E:116:ILE:HG13	1:E:165:TYR:CD2	2.50	0.47
1:E:119:LYS:HE2	1:E:252:TRP:CZ2	2.49	0.47
1:A:61:ILE:HD11	1:A:105:LEU:HD11	1.97	0.46
3:C:402:NAG:O7	3:C:402:NAG:O3	2.23	0.46
2:D:125:GLN:HE21	2:D:152:VAL:CG1	2.28	0.46
1:E:238:ASP:OD1	1:E:239:THR:N	2.42	0.46
1:E:46:GLY:O	1:E:48:ILE:HD13	2.14	0.46
2:F:5:ALA:O	2:F:6:ILE:C	2.58	0.46
2:F:9:PHE:CE1	2:F:10:ILE:HG13	2.50	0.46
1:A:147:ASN:ND2	1:A:255:PHE:HZ	2.13	0.46
1:C:255:PHE:N	1:C:255:PHE:CD2	2.83	0.46
1:A:167:ASN:ND2	1:A:171:LYS:O	2.48	0.46
1:C:108:VAL:HG12	1:C:110:SER:O	2.15	0.46
1:A:20:LEU:O	2:F:47:GLY:HA2	2.16	0.46
1:A:90:CYS:HB2	1:A:135:SER:O	2.16	0.46
1:A:277:THR:HG23	1:A:279:CYS:H	1.80	0.46
1:C:52:LEU:HD11	1:C:57:VAL:HG12	1.98	0.46
1:C:160:LYS:HE2	1:C:198:TYR:OH	2.15	0.46
1:C:303:CYS:O	2:D:61:ILE:HG12	2.15	0.46
1:A:11:ASN:H	1:A:11:ASN:HD22	1.63	0.46
2:B:38:GLN:HA	2:B:41:THR:HB	1.97	0.46
2:D:151:SER:OG	2:D:156:THR:OG1	2.33	0.46
2:B:26:HIS:CD2	2:B:26:HIS:O	2.69	0.46
2:B:55:VAL:HG22	2:B:99:LEU:HD21	1.96	0.46
1:C:169:LYS:C	1:C:171:LYS:H	2.24	0.46
1:E:167:ASN:HB2	1:E:234:LEU:HD23	1.98	0.46
1:C:95:PHE:HB3	1:C:98:TYR:HB2	1.98	0.46
2:B:122:VAL:HG13	2:B:138:PHE:CE2	2.50	0.46
1:C:2:THR:O	2:D:26:HIS:HB2	2.16	0.46
2:D:126:LEU:CD2	2:D:130:ALA:HB2	2.38	0.46
1:E:60:TRP:CZ2	1:E:111:PHE:HE2	2.34	0.46
2:F:5:ALA:CB	2:F:115:VAL:HG21	2.45	0.46
1:A:153:LYS:HE2	1:A:190:THR:O	2.16	0.45
1:A:166:THR:HG23	1:A:239:THR:OG1	2.16	0.45
1:A:187:ASP:OD1	1:A:187:ASP:N	2.48	0.45
1:A:218:PRO:O	1:A:226:ARG:NH2	2.35	0.45
2:D:131:LYS:HE2	2:D:131:LYS:HB2	1.51	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:107:THR:HG23	1:E:259:LYS:HD2	1.98	0.45
1:A:114:PHE:CD1	1:A:114:PHE:C	2.95	0.45
1:C:132:THR:HG22	1:C:142:ASN:HB3	1.98	0.45
2:D:144:CYS:SG	2:D:149:MET:SD	3.15	0.45
1:E:135:SER:CB	1:E:221:ARG:HB3	2.46	0.45
1:A:163:LYS:HA	1:A:163:LYS:HD2	1.62	0.45
1:C:29:SER:HA	1:C:316:THR:H	1.82	0.45
1:C:292:PHE:HZ	2:D:59:MET:HE3	1.81	0.45
1:A:217:ARG:NH2	1:E:203:SER:O	2.49	0.45
1:A:283:HIS:CD2	1:A:296:HIS:HD2	2.35	0.45
1:C:296:HIS:ND1	1:C:298:VAL:HG22	2.32	0.45
2:D:130:ALA:O	2:D:131:LYS:O	2.34	0.45
1:C:133:THR:OG1	1:C:134:VAL:N	2.49	0.45
1:C:254:ALA:C	1:C:255:PHE:CD2	2.94	0.45
1:A:127:ASP:HB3	1:A:152:VAL:HG23	1.97	0.45
1:A:57:VAL:HG21	1:A:102:LYS:HG2	1.97	0.45
1:A:62:LEU:O	1:A:145:TYR:HB3	2.17	0.45
1:A:266:MET:HE2	1:A:282:PRO:CD	2.47	0.45
1:C:54:ASN:C	1:C:85:SER:HA	2.42	0.45
1:E:4:CYS:N	2:F:25:HIS:O	2.47	0.44
1:E:222:GLU:O	1:E:223:GLN:HG2	2.17	0.44
1:A:199:VAL:HG13	1:A:244:ALA:HB2	1.99	0.44
1:C:115:GLU:OE1	1:C:118:PRO:HA	2.16	0.44
2:F:129:ASN:O	2:F:141:TYR:HB2	2.17	0.44
2:F:149:MET:O	2:F:153:LYS:HG3	2.16	0.44
2:D:52:VAL:O	2:D:56:ILE:HG12	2.18	0.44
2:F:45:ILE:O	2:F:49:SER:CB	2.63	0.44
2:F:61:ILE:HD12	2:F:63:PHE:H	1.82	0.44
1:A:7:TYR:CZ	2:B:6:ILE:HG23	2.52	0.44
1:C:217:ARG:HG3	1:C:218:PRO:HD3	1.97	0.44
2:D:3:PHE:HB2	2:D:112:ASP:CB	2.48	0.44
1:E:123:TRP:CG	1:E:151:ILE:HD11	2.52	0.44
1:A:38:ASN:ND2	1:A:285:ALA:HB3	2.30	0.44
1:E:20:LEU:HD12	2:F:105:GLU:OE2	2.17	0.44
1:A:158:TYR:CD2	1:A:192:TYR:HA	2.49	0.44
1:A:234:LEU:CD1	1:A:238:ASP:HB3	2.47	0.44
1:A:47:LYS:NZ	1:A:75:SER:OG	2.38	0.44
1:C:37:HIS:CE1	1:C:283:HIS:HB3	2.53	0.44
1:E:240:ILE:HD13	1:E:242:PHE:HE1	1.82	0.44
2:F:122:VAL:HG12	2:F:138:PHE:CE1	2.53	0.44
2:B:63:PHE:CD1	2:B:63:PHE:O	2.71	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:207:TYR:CE1	1:C:217:ARG:CD	3.01	0.44
2:B:62:GLN:HA	2:B:62:GLN:NE2	2.33	0.44
2:B:73:LEU:HA	2:B:73:LEU:HD23	1.61	0.44
2:B:132:GLU:HB2	2:F:127:ARG:NH2	2.32	0.44
1:E:44:LEU:O	1:E:47:LYS:HB2	2.17	0.44
1:E:173:VAL:HG13	1:E:255:PHE:O	2.18	0.44
1:A:40:LYS:O	1:A:280:GLN:NE2	2.47	0.43
1:E:21:GLU:CD	1:E:319:ARG:HH22	2.22	0.43
1:A:52:LEU:HD12	1:A:81:GLU:HG2	2.00	0.43
1:A:107:THR:O	1:A:107:THR:OG1	2.35	0.43
2:D:89:LEU:HD12	2:D:89:LEU:HA	1.84	0.43
1:E:17:ASP:CG	1:E:22:LYS:HG2	2.42	0.43
2:B:27:ARG:HA	2:B:32:SER:OG	2.18	0.43
1:E:119:LYS:HD3	1:E:149:LEU:CD2	2.48	0.43
1:C:115:GLU:HG3	1:C:253:HIS:NE2	2.33	0.43
1:E:71:LEU:O	1:E:71:LEU:HD23	2.17	0.43
1:E:119:LYS:O	1:E:128:THR:HG21	2.19	0.43
1:A:31:ASN:ND2	1:A:33:LEU:O	2.51	0.43
1:A:308:LYS:HE3	2:B:89:LEU:HD21	2.01	0.43
2:D:17:MET:HE1	2:D:23:GLY:N	2.33	0.43
1:E:124:PRO:HD2	1:E:125:ASN:H	1.84	0.43
1:E:308:LYS:HD2	2:F:89:LEU:HD13	2.00	0.43
1:E:309:SER:OG	2:F:97:GLU:OE2	2.34	0.43
1:E:312:LEU:HD23	1:E:312:LEU:HA	1.87	0.43
1:A:5:VAL:HG11	2:B:122:VAL:HG11	2.01	0.43
1:C:64:ASN:HA	1:C:65:PRO:HD3	1.93	0.43
1:C:171:LYS:HB3	1:C:257:LEU:O	2.19	0.43
1:C:179:VAL:HG22	1:C:199:VAL:HG21	2.01	0.43
1:E:111:PHE:CE1	1:E:255:PHE:CB	3.00	0.43
2:D:9:PHE:HE2	2:D:116:LYS:HE3	1.83	0.43
2:B:80:LEU:O	2:B:84:VAL:HG23	2.19	0.43
1:A:62:LEU:HB3	1:A:145:TYR:CD1	2.54	0.43
1:A:91:TYR:CD1	1:A:227:MET:HG3	2.53	0.43
1:E:113:ARG:HG3	1:E:114:PHE:N	2.33	0.43
2:B:119:TYR:O	2:B:122:VAL:HG12	2.19	0.43
1:E:60:TRP:CZ2	1:E:111:PHE:CE2	3.06	0.43
2:D:118:LEU:O	2:D:119:TYR:C	2.62	0.42
2:F:63:PHE:CG	2:F:63:PHE:O	2.71	0.42
2:B:62:GLN:HB3	2:B:63:PHE:H	1.50	0.42
1:C:108:VAL:CG1	1:C:110:SER:O	2.66	0.42
2:F:127:ARG:HD3	2:F:127:ARG:O	2.19	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:207:TYR:CD1	1:C:217:ARG:CD	2.98	0.42
1:A:234:LEU:HD12	1:A:238:ASP:HB3	1.99	0.42
1:E:2:THR:HG23	2:F:27:ARG:HB3	2.00	0.42
1:E:234:LEU:HD11	1:E:238:ASP:HB3	2.00	0.42
1:A:153:LYS:NZ	1:A:155:GLY:O	2.43	0.42
1:E:33:LEU:HD11	1:E:294:ASN:HB3	2.02	0.42
1:E:177:TRP:CE2	1:E:201:VAL:HG21	2.54	0.42
1:A:4:CYS:HA	2:B:137:CYS:HA	2.02	0.42
1:C:180:HIS:ND1	1:C:182:PRO:HG3	2.35	0.42
1:E:175:VAL:HG21	1:E:240:ILE:CD1	2.50	0.42
2:B:51:LYS:HG3	1:C:19:ILE:HD11	2.02	0.42
1:C:2:THR:O	2:D:26:HIS:CB	2.67	0.42
2:D:97:GLU:O	2:D:101:LEU:HD13	2.19	0.42
1:E:198:TYR:HA	1:E:212:PRO:HD2	2.01	0.42
1:E:203:SER:N	1:E:206:TYR:O	2.53	0.42
2:F:58:LYS:HA	2:F:58:LYS:HD3	1.66	0.42
1:A:47:LYS:HB3	1:A:77:SER:CB	2.49	0.42
1:C:57:VAL:HG22	1:C:98:TYR:OH	2.19	0.42
1:C:296:HIS:ND1	1:C:297:PRO:HD2	2.33	0.42
1:E:49:PRO:HB2	1:E:80:ILE:HD11	2.02	0.42
2:B:123:LYS:HB2	2:B:138:PHE:HZ	1.85	0.42
1:E:115:GLU:CA	1:E:253:HIS:CD2	3.03	0.42
1:E:314:LEU:HD12	2:F:104:ASN:OD1	2.20	0.42
2:F:38:GLN:O	2:F:42:GLN:HB2	2.20	0.42
1:A:148:LEU:HD23	1:A:148:LEU:HA	1.89	0.42
1:A:268:SER:HB2	1:A:282:PRO:HB3	2.02	0.42
1:C:129:THR:C	1:C:130:ARG:HG2	2.44	0.42
2:D:24:TYR:CD1	2:D:24:TYR:N	2.88	0.42
1:E:123:TRP:HB3	1:E:126:HIS:HB2	2.00	0.42
2:F:5:ALA:HB3	2:F:112:ASP:OD1	2.19	0.42
1:A:285:ALA:O	1:A:286:LEU:HD23	2.19	0.41
2:B:14:TRP:CE3	2:B:17:MET:HE2	2.55	0.41
1:E:106:SER:HB3	1:E:265:ILE:HG13	2.02	0.41
1:A:145:TYR:HB2	1:A:148:LEU:HB2	2.03	0.41
1:A:277:THR:HG21	1:A:280:GLN:HG2	2.00	0.41
1:A:266:MET:HE2	1:A:282:PRO:CG	2.49	0.41
2:B:149:MET:O	2:B:153:LYS:HG3	2.20	0.41
1:C:160:LYS:HZ2	1:C:160:LYS:HG2	1.69	0.41
1:C:233:LEU:CD2	1:C:257:LEU:HD11	2.50	0.41
1:E:123:TRP:HB2	1:E:128:THR:CG2	2.50	0.41
1:E:193:GLN:HG3	1:E:194:ASN:N	2.36	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:293:GLN:NE2	1:E:306:TYR:HB2	2.34	0.41
1:A:25:THR:HG22	1:A:320:ASN:HB2	2.02	0.41
1:A:68:ASP:O	1:A:71:LEU:HB2	2.19	0.41
1:A:158:TYR:CE2	1:A:192:TYR:CB	3.03	0.41
2:B:125:GLN:HE22	2:B:155:GLY:HA2	1.86	0.41
2:D:67:GLY:C	2:D:68:LYS:HD2	2.46	0.41
2:D:131:LYS:CG	2:D:132:GLU:N	2.83	0.41
1:A:38:ASN:O	1:A:40:LYS:HG2	2.21	0.41
2:D:127:ARG:HB3	2:D:128:ASN:H	1.46	0.41
1:E:122:SER:C	1:E:124:PRO:HD3	2.45	0.41
1:E:153:LYS:HD2	1:E:193:GLN:H	1.85	0.41
1:E:171:LYS:HE3	1:E:256:ALA:HB1	2.02	0.41
2:B:2:LEU:HD12	2:B:3:PHE:H	1.86	0.41
2:B:29:GLU:OE1	2:B:29:GLU:CA	2.68	0.41
1:C:184:THR:OG1	1:C:187:ASP:OD1	2.39	0.41
1:E:142:ASN:N	1:E:142:ASN:ND2	2.65	0.41
1:E:167:ASN:ND2	1:E:169:LYS:H	2.18	0.41
1:A:209:ARG:HH11	1:C:215:VAL:CG2	2.34	0.41
2:B:19:ASP:OD1	2:B:19:ASP:N	2.54	0.41
1:C:162:SER:HA	1:C:242:PHE:O	2.20	0.41
1:C:180:HIS:CE1	1:C:182:PRO:HG3	2.55	0.41
1:C:219:LYS:HD2	1:C:222:GLU:HA	2.02	0.41
2:F:107:THR:O	2:F:110:PHE:HB3	2.21	0.41
1:A:5:VAL:O	2:B:10:ILE:HD13	2.21	0.41
1:C:79:ILE:HB	1:C:265:ILE:HD13	2.02	0.41
2:D:114:ASN:O	2:D:115:VAL:C	2.64	0.41
1:E:35:ASP:HA	1:E:294:ASN:OD1	2.21	0.41
2:B:88:PHE:CZ	2:D:87:GLY:HA3	2.57	0.40
1:C:171:LYS:HB2	1:C:256:ALA:HB1	2.02	0.40
1:C:177:TRP:CE2	1:C:201:VAL:HG21	2.56	0.40
2:F:5:ALA:HB1	2:F:115:VAL:CG2	2.51	0.40
1:C:19:ILE:HG22	2:D:105:GLU:HB2	2.02	0.40
1:E:178:GLY:HA2	1:E:228:ASN:O	2.21	0.40
1:E:110:SER:HB3	1:E:258:LYS:HB2	2.02	0.40
1:E:146:ARG:HH11	1:E:146:ARG:CG	2.34	0.40
1:A:8:HIS:NE2	1:A:10:ASN:HB3	2.36	0.40
1:C:134:VAL:HG23	1:C:142:ASN:OD1	2.22	0.40
1:E:2:THR:OG1	1:E:3:ILE:N	2.54	0.40
1:E:158:TYR:CZ	1:E:246:GLY:HA2	2.56	0.40
1:C:33:LEU:HB2	1:C:312:LEU:HD12	2.02	0.40
1:E:76:TRP:CZ3	1:E:111:PHE:CB	3.04	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:83:SER:N	1:E:269:ASP:OD1	2.54	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	319/321 (99%)	290 (91%)	24 (8%)	5 (2%)	7	27
1	C	319/321 (99%)	294 (92%)	23 (7%)	2 (1%)	21	51
1	E	319/321 (99%)	277 (87%)	38 (12%)	4 (1%)	9	31
2	B	154/156 (99%)	134 (87%)	17 (11%)	3 (2%)	6	22
2	D	154/156 (99%)	128 (83%)	23 (15%)	3 (2%)	6	22
2	F	154/156 (99%)	132 (86%)	19 (12%)	3 (2%)	6	22
All	All	1419/1431 (99%)	1255 (88%)	144 (10%)	20 (1%)	9	30

All (20) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	112	GLU
1	A	160	LYS
2	B	35	ALA
2	D	131	LYS
2	D	149	MET
1	E	139	SER
1	A	261	SER
2	B	67	GLY
1	C	170	GLY
1	E	142	ASN
2	B	118	LEU

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Mol	Chain	Res	Type
1	C	140	GLY
2	D	152	VAL
1	E	124	PRO
1	A	220	VAL
1	E	70	LEU
2	F	110	PHE
2	F	67	GLY
2	F	66	VAL
1	A	49	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 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	282/282 (100%)	255 (90%)	27 (10%)	8	26
1	C	282/282 (100%)	264 (94%)	18 (6%)	16	44
1	E	282/282 (100%)	248 (88%)	34 (12%)	5	16
2	B	134/134 (100%)	119 (89%)	15 (11%)	6	19
2	D	134/134 (100%)	116 (87%)	18 (13%)	4	13
2	F	134/134 (100%)	118 (88%)	16 (12%)	5	17
All	All	1248/1248 (100%)	1120 (90%)	128 (10%)	7	23

All (128) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	1	ASP
1	A	11	ASN
1	A	18	THR
1	A	30	VAL
1	A	36	SER
1	A	77	SER
1	A	107	THR
1	A	109	SER
1	A	110	SER

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Mol	Chain	Res	Type
1	A	111	PHE
1	A	112	GLU
1	A	119	LYS
1	A	121	THR
1	A	135	SER
1	A	143	SER
1	A	153	LYS
1	A	160	LYS
1	A	162	SER
1	A	169	LYS
1	A	185	ASP
1	A	187	ASP
1	A	219	LYS
1	A	232	THR
1	A	247	ASN
1	A	289	ASN
1	A	320	ASN
1	A	321	ILE
2	B	2	LEU
2	B	19	ASP
2	B	27	ARG
2	B	28	ASN
2	B	29	GLU
2	B	61	ILE
2	B	62	GLN
2	B	64	THR
2	B	70	PHE
2	B	72	SER
2	B	113	SER
2	B	116	LYS
2	B	120	GLU
2	B	156	THR
2	B	157	TYR
1	C	40	LYS
1	C	54	ASN
1	C	57	VAL
1	C	83	SER
1	C	95	PHE
1	C	111	PHE
1	C	129	THR
1	C	135	SER
1	C	171	LYS

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Mol	Chain	Res	Type
1	C	173	VAL
1	C	192	TYR
1	C	204	THR
1	C	217	ARG
1	C	219	LYS
1	C	255	PHE
1	C	257	LEU
1	C	259	LYS
1	C	308	LYS
2	D	2	LEU
2	D	19	ASP
2	D	24	TYR
2	D	25	HIS
2	D	40	SER
2	D	64	THR
2	D	66	VAL
2	D	72	SER
2	D	90	ASP
2	D	122	VAL
2	D	125	GLN
2	D	126	LEU
2	D	127	ARG
2	D	131	LYS
2	D	139	GLU
2	D	142	HIS
2	D	145	ASP
2	D	148	CYS
1	E	12	SER
1	E	23	ASN
1	E	36	SER
1	E	42	CYS
1	E	47	LYS
1	E	48	ILE
1	E	57	VAL
1	E	70	LEU
1	E	78	TYR
1	E	86	LYS
1	E	95	PHE
1	E	108	VAL
1	E	125	ASN
1	E	129	THR
1	E	134	VAL

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Mol	Chain	Res	Type
1	E	135	SER
1	E	139	SER
1	E	142	ASN
1	E	143	SER
1	E	154	LYS
1	E	160	LYS
1	E	164	SER
1	E	175	VAL
1	E	186	SER
1	E	192	TYR
1	E	211	THR
1	E	219	LYS
1	E	245	THR
1	E	274	ASN
1	E	276	THR
1	E	281	THR
1	E	296	HIS
1	E	298	VAL
1	E	302	LYS
2	F	22	TYR
2	F	24	TYR
2	F	48	ILE
2	F	56	ILE
2	F	60	ASN
2	F	64	THR
2	F	68	LYS
2	F	86	ASP
2	F	89	LEU
2	F	128	ASN
2	F	129	ASN
2	F	133	ILE
2	F	137	CYS
2	F	140	PHE
2	F	144	CYS
2	F	148	CYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (36) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	37	HIS
1	A	45	ASN
1	A	51	GLN

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Mol	Chain	Res	Type
1	A	87	ASN
1	A	125	ASN
1	A	193	GLN
1	A	236	GLN
1	A	273	HIS
1	A	280	GLN
1	A	296	HIS
1	A	320	ASN
2	B	26	HIS
2	B	28	ASN
2	B	117	ASN
2	B	129	ASN
1	C	8	HIS
1	C	87	ASN
1	C	126	HIS
1	C	138	HIS
1	C	168	ASN
1	C	193	GLN
2	D	125	GLN
1	E	51	GLN
1	E	126	HIS
1	E	138	HIS
1	E	142	ASN
1	E	167	ASN
1	E	168	ASN
1	E	193	GLN
1	E	194	ASN
1	E	253	HIS
1	E	311	GLN
2	F	38	GLN
2	F	117	ASN
2	F	142	HIS
2	F	154	ASN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

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](#)

12 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
3	NAG	C	403	-	14,14,15	0.21	0	17,19,21	0.45	0
3	NAG	A	404	1	14,14,15	0.27	0	17,19,21	0.55	0
3	NAG	C	402	1	14,14,15	0.63	0	17,19,21	0.72	1 (5%)
3	NAG	A	402	1	14,14,15	0.24	0	17,19,21	0.43	0
3	NAG	C	401	1	14,14,15	0.97	1 (7%)	17,19,21	0.50	0
3	NAG	A	403	1	14,14,15	0.17	0	17,19,21	0.52	0
3	NAG	E	402	1	14,14,15	0.51	0	17,19,21	0.77	1 (5%)
3	NAG	C	404	1	14,14,15	0.21	0	17,19,21	0.44	0
3	NAG	E	404	-	14,14,15	0.20	0	17,19,21	0.39	0
3	NAG	E	401	1	14,14,15	0.38	0	17,19,21	1.06	1 (5%)
3	NAG	E	403	1	14,14,15	0.22	0	17,19,21	0.41	0
3	NAG	A	401	1	14,14,15	0.99	1 (7%)	17,19,21	0.64	0

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
3	NAG	C	403	-	-	0/6/23/26	0/1/1/1
3	NAG	A	404	1	-	2/6/23/26	0/1/1/1
3	NAG	C	402	1	-	4/6/23/26	0/1/1/1
3	NAG	A	402	1	-	2/6/23/26	0/1/1/1
3	NAG	C	401	1	-	3/6/23/26	0/1/1/1
3	NAG	A	403	1	-	0/6/23/26	0/1/1/1

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	NAG	E	402	1	-	0/6/23/26	0/1/1/1
3	NAG	C	404	1	-	2/6/23/26	0/1/1/1
3	NAG	E	404	-	-	2/6/23/26	0/1/1/1
3	NAG	E	401	1	-	2/6/23/26	0/1/1/1
3	NAG	E	403	1	-	2/6/23/26	0/1/1/1
3	NAG	A	401	1	-	4/6/23/26	0/1/1/1

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	401	NAG	C1-C2	3.04	1.56	1.52
3	C	401	NAG	C1-C2	2.91	1.56	1.52

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	E	401	NAG	C1-O5-C5	3.75	117.21	112.19
3	E	402	NAG	C1-O5-C5	2.37	115.36	112.19
3	C	402	NAG	C2-N2-C7	2.29	125.97	122.90

There are no chirality outliers.

All (23) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	C	401	NAG	O5-C5-C6-O6
3	C	401	NAG	C4-C5-C6-O6
3	C	402	NAG	C4-C5-C6-O6
3	C	402	NAG	O5-C5-C6-O6
3	A	401	NAG	O5-C5-C6-O6
3	A	401	NAG	C4-C5-C6-O6
3	A	404	NAG	C4-C5-C6-O6
3	A	404	NAG	O5-C5-C6-O6
3	A	402	NAG	C4-C5-C6-O6
3	A	401	NAG	C1-C2-N2-C7
3	E	401	NAG	C4-C5-C6-O6
3	A	401	NAG	C3-C2-N2-C7
3	C	402	NAG	C3-C2-N2-C7
3	E	401	NAG	O5-C5-C6-O6
3	A	402	NAG	O5-C5-C6-O6
3	C	404	NAG	C4-C5-C6-O6

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Mol	Chain	Res	Type	Atoms
3	C	402	NAG	C1-C2-N2-C7
3	C	404	NAG	C1-C2-N2-C7
3	E	403	NAG	C1-C2-N2-C7
3	E	404	NAG	C4-C5-C6-O6
3	C	401	NAG	C3-C2-N2-C7
3	E	403	NAG	C4-C5-C6-O6
3	E	404	NAG	O5-C5-C6-O6

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	C	402	NAG	1	0

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(Å²)	Q<0.9
1	A	321/321 (100%)	0.37	15 (4%)	36	29	15, 47, 74, 100	0
1	C	321/321 (100%)	0.21	16 (4%)	34	26	17, 46, 72, 139	0
1	E	321/321 (100%)	0.71	35 (10%)	10	8	22, 56, 88, 116	0
2	B	156/156 (100%)	0.16	8 (5%)	33	25	12, 47, 79, 117	0
2	D	156/156 (100%)	0.91	32 (20%)	2	2	16, 60, 117, 136	0
2	F	156/156 (100%)	0.45	11 (7%)	22	16	16, 56, 96, 122	0
All	All	1431/1431 (100%)	0.46	117 (8%)	17	13	12, 51, 91, 139	0

All (117) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	D	130	ALA	7.0
2	D	141	TYR	6.3
2	D	131	LYS	5.3
2	D	142	HIS	5.1
2	D	127	ARG	4.7
2	D	138	PHE	4.6
2	D	63	PHE	4.4
2	D	128	ASN	4.4
1	E	152	VAL	4.3
2	F	4	GLY	4.2
2	D	144	CYS	4.2
1	A	192	TYR	4.0
1	E	120	ALA	4.0
2	F	64	THR	3.9
1	E	108	VAL	3.7
1	A	112	GLU	3.7
1	A	131	GLY	3.7
2	B	63	PHE	3.7
2	D	129	ASN	3.5

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Mol	Chain	Res	Type	RSRZ
2	D	140	PHE	3.5
1	E	284	GLY	3.4
2	F	3	PHE	3.3
2	D	64	THR	3.3
2	F	63	PHE	3.2
1	C	218	PRO	3.1
1	E	164	SER	3.1
2	D	66	VAL	3.1
1	C	321	ILE	3.1
2	D	34	TYR	3.0
2	D	4	GLY	3.0
1	C	320	ASN	2.9
2	B	150	GLU	2.9
1	E	39	GLY	2.9
2	D	152	VAL	2.9
2	D	67	GLY	2.9
1	C	2	THR	2.9
1	E	151	ILE	2.9
1	A	220	VAL	2.9
1	E	130	ARG	2.8
2	B	20	GLY	2.8
1	A	183	PRO	2.8
2	D	126	LEU	2.8
1	C	217	ARG	2.7
2	F	23	GLY	2.7
1	E	114	PHE	2.7
1	E	285	ALA	2.7
2	B	34	TYR	2.7
2	B	62	GLN	2.7
2	D	133	ILE	2.7
2	D	33	GLY	2.7
1	E	254	ALA	2.6
2	D	157	TYR	2.6
1	A	160	LYS	2.6
2	F	62	GLN	2.6
1	E	126	HIS	2.6
1	A	132	THR	2.6
1	C	300	ILE	2.6
2	D	62	GLN	2.6
1	A	224	ALA	2.6
2	D	61	ILE	2.5
1	E	139	SER	2.5

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Mol	Chain	Res	Type	RSRZ
1	E	255	PHE	2.5
1	A	221	ARG	2.5
1	E	116	ILE	2.5
1	E	173	VAL	2.5
1	A	185	ASP	2.5
2	F	61	ILE	2.5
1	A	223	GLN	2.5
2	D	139	GLU	2.4
2	F	24	TYR	2.4
2	B	64	THR	2.4
2	F	138	PHE	2.4
1	E	250	ALA	2.4
1	E	287	LYS	2.3
1	C	255	PHE	2.3
2	D	109	ASP	2.3
2	D	148	CYS	2.3
2	F	18	VAL	2.3
1	C	111	PHE	2.3
1	A	222	GLU	2.3
2	D	25	HIS	2.3
2	F	140	PHE	2.3
1	E	138	HIS	2.3
1	E	279	CYS	2.3
2	D	23	GLY	2.3
2	D	134	GLY	2.3
1	E	72	THR	2.2
1	C	262	SER	2.2
1	E	278	LYS	2.2
1	A	225	GLY	2.2
2	B	154	ASN	2.2
1	E	65	PRO	2.2
1	C	219	LYS	2.2
2	D	119	TYR	2.2
2	D	65	SER	2.2
1	A	216	ALA	2.2
1	E	176	ILE	2.1
1	C	153	LYS	2.1
1	E	2	THR	2.1
1	C	110	SER	2.1
1	E	262	SER	2.1
2	D	32	SER	2.1
1	C	223	GLN	2.1

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Mol	Chain	Res	Type	RSRZ
1	E	239	THR	2.1
1	E	113	ARG	2.1
1	E	295	VAL	2.1
2	B	40	SER	2.0
1	E	253	HIS	2.0
1	E	296	HIS	2.0
1	C	1	ASP	2.0
1	C	3	ILE	2.0
1	C	138	HIS	2.0
1	E	283	HIS	2.0
1	E	286	LEU	2.0
1	E	127	ASP	2.0
1	A	219	LYS	2.0
1	E	153	LYS	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 [i](#)

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(\AA^2)	Q<0.9
3	NAG	C	401	14/15	0.49	0.17	98,122,135,136	0
3	NAG	A	402	14/15	-	-	51,53,54,54	14
3	NAG	A	403	14/15	-	-	74,75,76,77	14
3	NAG	A	404	14/15	-	-	35,37,39,40	14
3	NAG	E	402	14/15	0.51	0.16	77,77,77,77	0
3	NAG	C	402	14/15	0.54	0.16	72,91,109,111	0
3	NAG	C	403	14/15	-	-	43,43,45,45	14
3	NAG	C	404	14/15	-	-	48,50,52,52	14
3	NAG	A	401	14/15	0.59	0.19	65,114,128,129	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
3	NAG	E	401	14/15	0.76	0.12	49,74,82,86	0
3	NAG	E	403	14/15	-	-	57,59,60,61	14
3	NAG	E	404	14/15	-	-	87,96,98,99	14

6.5 Other polymers [i](#)

There are no such residues in this entry.