



Full wwPDB X-ray Structure Validation Report ⓘ

Jul 5, 2016 – 10:58 AM EDT

PDB ID : 5JS9
Title : Uncleaved prefusion optimized gp140 trimer with an engineered 8-residue HR1 turn bound to broadly neutralizing antibodies 8ANC195 and PGT128
Authors : Kong, L.; Wilson, I.A.
Deposited on : 2016-05-07
Resolution : 6.92 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
<http://wwpdb.org/validation/2016/XrayValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

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

MolProbity : 4.02b-467
Mogul : 1.7.1 (RC1), CSD as537be (2016)
Xtriage (Phenix) : 1.9-1692
EDS : rb-20027790
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)
Refmac : 5.8.0135
CCP4 : 6.5.0
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : rb-20027790

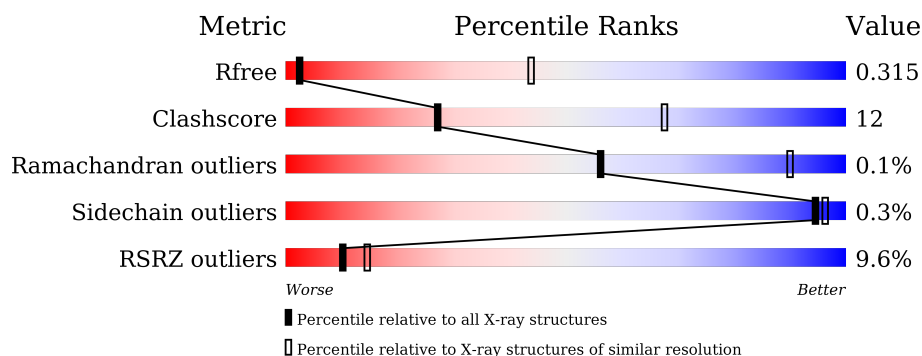
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 6.92 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}	91344	1014 (9.50-3.66)
Clashscore	102246	1063 (10.00-3.70)
Ramachandran outliers	100387	1035 (9.50-3.66)
Sidechain outliers	100360	1005 (9.50-3.66)
RSRZ outliers	91569	1013 (9.50-3.66)

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 on the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria. 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	239	<div> <div>18%</div> <div> <div>75%</div> <div>21%</div> <div>.</div> </div> </div>
2	B	211	<div> <div>23%</div> <div> <div>71%</div> <div>26%</div> <div>.</div> </div> </div>
3	C	480	<div> <div>6%</div> <div> <div>68%</div> <div>25%</div> <div>7%</div> </div> </div>
4	D	140	<div> <div>4%</div> <div> <div>66%</div> <div>26%</div> <div>7%</div> </div> </div>
5	E	238	<div> <div>5%</div> <div> <div>69%</div> <div>25%</div> <div>6%</div> </div> </div>
6	F	215	<div> <div>2%</div> <div> <div>74%</div> <div>25%</div> <div>.</div> </div> </div>

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
7	NAG	C	603	-	-	-	X
7	NAG	C	619	-	-	-	X
7	NAG	C	643	-	-	-	X
7	NAG	C	657	-	-	-	X
8	BMA	C	659	-	-	-	X
9	MAN	C	664	-	-	-	X
9	MAN	C	666	-	-	X	-
9	MAN	C	667	-	-	-	X

2 Entry composition

There are 9 unique types of molecules in this entry. The entry contains 12007 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 broadly neutralizing antibody PGT128 heavy chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	230	Total	C	N	O	S	0	0	0
			1735	1105	292	332	6			

- Molecule 2 is a protein called broadly neutralizing antibody PGT128 light chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	204	Total	C	N	O	S	0	0	0
			1514	950	254	306	4			

- Molecule 3 is a protein called gp120.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	C	447	Total	C	N	O	S	0	0	0
			3519	2210	622	659	28			

- Molecule 4 is a protein called gp41.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
4	D	130	Total	C	N	O	S	0	0	0
			1039	655	178	199	7			

- Molecule 5 is a protein called broadly neutralizing antibody 8ANC195 heavy chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
5	E	224	Total	C	N	O	S	0	0	0
			1686	1072	284	325	5			

- Molecule 6 is a protein called broadly neutralizing antibody 8ANC195 light chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
6	F	212	Total	C	N	O	S	0	0	0
			1626	1018	279	324	5			

- Molecule 7 is N-ACETYL-D-GLUCOSAMINE (three-letter code: NAG) (formula: $C_8H_{15}NO_6$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
7	C	1	Total	C	N	O	0	0
			14	8	1	5		
7	C	1	Total	C	N	O	0	0
			14	8	1	5		
7	C	1	Total	C	N	O	0	0
			14	8	1	5		
7	C	1	Total	C	N	O	0	0
			14	8	1	5		
7	C	1	Total	C	N	O	0	0
			14	8	1	5		
7	C	1	Total	C	N	O	0	0
			14	8	1	5		
7	C	1	Total	C	N	O	0	0
			14	8	1	5		
7	C	1	Total	C	N	O	0	0
			14	8	1	5		
7	C	1	Total	C	N	O	0	0
			14	8	1	5		

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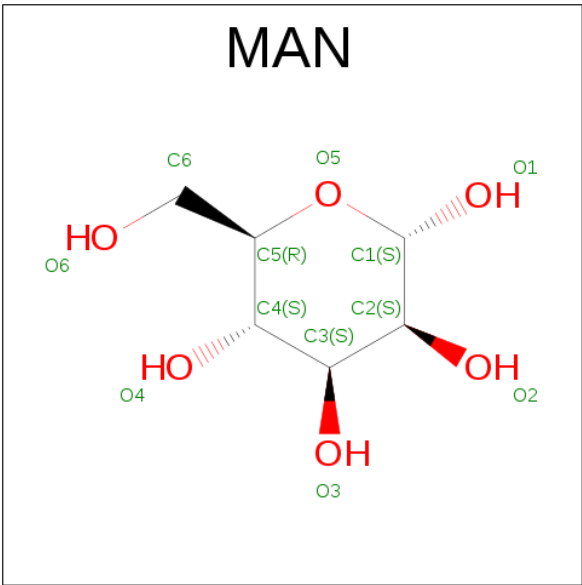
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
7	C	1	Total	C	N	O	0	0
			14	8	1	5		
7	C	1	Total	C	N	O	0	0
			14	8	1	5		
7	C	1	Total	C	N	O	0	0
			14	8	1	5		
7	C	1	Total	C	N	O	0	0
			14	8	1	5		
7	C	1	Total	C	N	O	0	0
			14	8	1	5		
7	C	1	Total	C	N	O	0	0
			14	8	1	5		
7	C	1	Total	C	N	O	0	0
			14	8	1	5		
7	C	1	Total	C	N	O	0	0
			14	8	1	5		
7	C	1	Total	C	N	O	0	0
			14	8	1	5		
7	C	1	Total	C	N	O	0	0
			14	8	1	5		
7	C	1	Total	C	N	O	0	0
			14	8	1	5		
7	C	1	Total	C	N	O	0	0
			14	8	1	5		
7	D	1	Total	C	N	O	0	0
			14	8	1	5		
7	D	1	Total	C	N	O	0	0
			14	8	1	5		
7	D	1	Total	C	N	O	0	0
			14	8	1	5		

- Molecule 8 is BETA-D-MANNOSE (three-letter code: BMA) (formula: $C_6H_{12}O_6$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
8	C	1	Total	C	O	0	0
			11	6	5		
8	C	1	Total	C	O	0	0
			11	6	5		
8	C	1	Total	C	O	0	0
			11	6	5		
8	C	1	Total	C	O	0	0
			11	6	5		
8	C	1	Total	C	O	0	0
			11	6	5		
8	C	1	Total	C	O	0	0
			11	6	5		
8	C	1	Total	C	O	0	0
			11	6	5		
8	D	1	Total	C	O	0	0
			11	6	5		

- Molecule 9 is ALPHA-D-MANNOSE (three-letter code: MAN) (formula: C₆H₁₂O₆).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
9	C	1	Total	C	O	0	0
			11	6	5		
9	C	1	Total	C	O	0	0
			11	6	5		
9	C	1	Total	C	O	0	0
			11	6	5		
9	C	1	Total	C	O	0	0
			11	6	5		
9	C	1	Total	C	O	0	0
			11	6	5		
9	C	1	Total	C	O	0	0
			11	6	5		
9	C	1	Total	C	O	0	0
			11	6	5		
9	C	1	Total	C	O	0	0
			11	6	5		
9	C	1	Total	C	O	0	0
			11	6	5		
9	C	1	Total	C	O	0	0
			11	6	5		
9	C	1	Total	C	O	0	0
			11	6	5		

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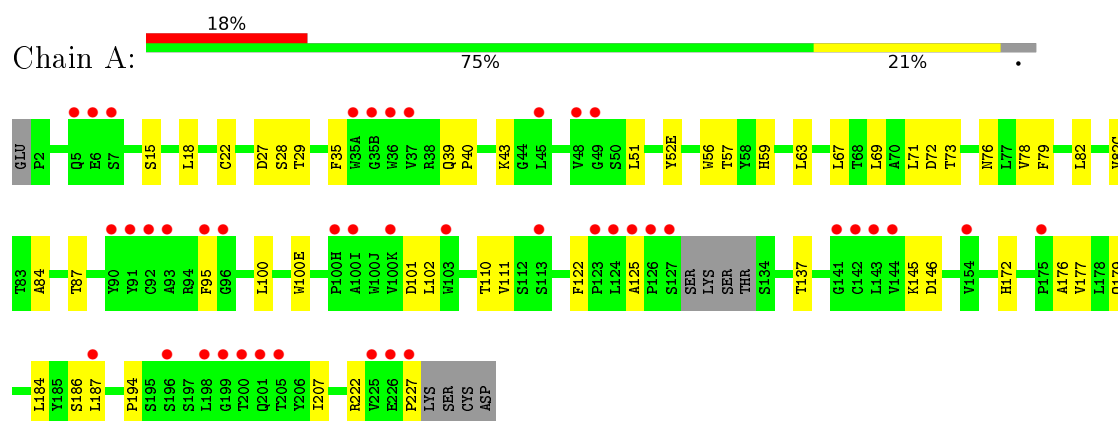
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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
9	C	1	Total	C	O	0	0
			11	6	5		
9	C	1	Total	C	O	0	0
			11	6	5		
9	C	1	Total	C	O	0	0
			11	6	5		
9	C	1	Total	C	O	0	0
			11	6	5		
9	C	1	Total	C	O	0	0
			11	6	5		
9	C	1	Total	C	O	0	0
			11	6	5		
9	C	1	Total	C	O	0	0
			11	6	5		
9	C	1	Total	C	O	0	0
			11	6	5		
9	C	1	Total	C	O	0	0
			11	6	5		
9	C	1	Total	C	O	0	0
			11	6	5		
9	C	1	Total	C	O	0	0
			11	6	5		
9	D	1	Total	C	O	0	0
			11	6	5		

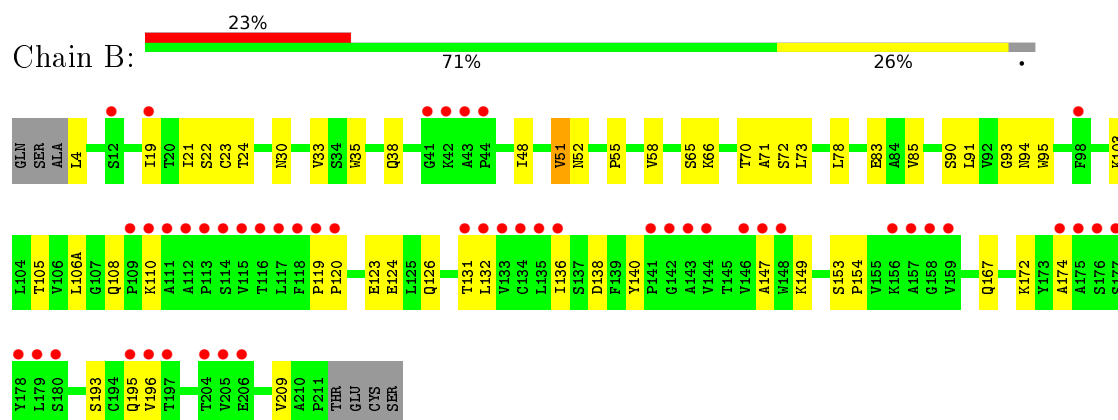
3 Residue-property plots

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors 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 ($\text{RSRZ} > 2$). 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.

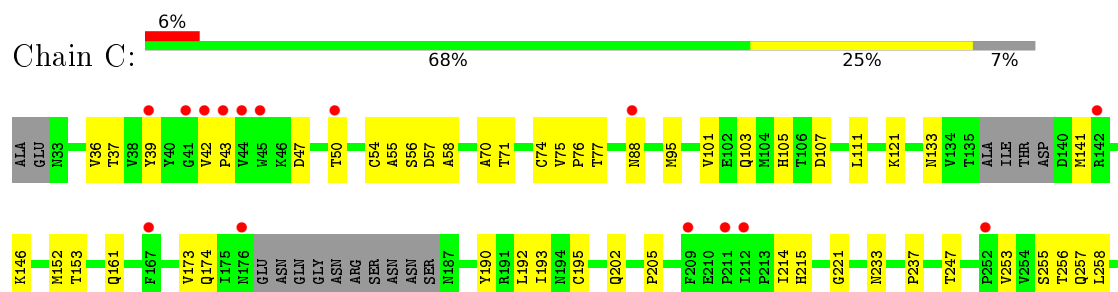
- Molecule 1: broadly neutralizing antibody PGT128 heavy chain

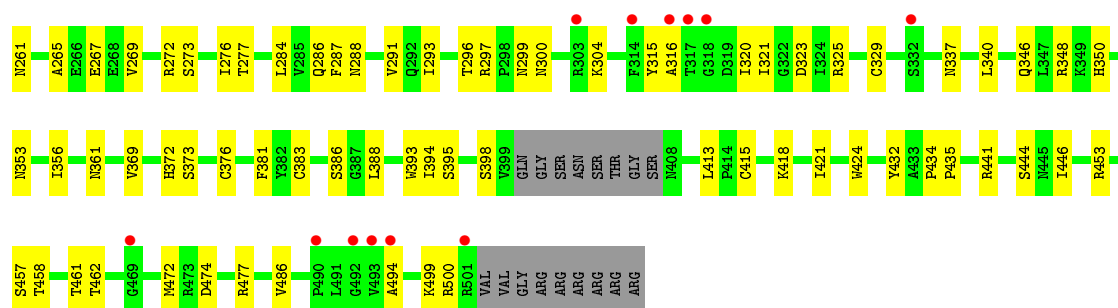


- Molecule 2: broadly neutralizing antibody PGT128 light chain

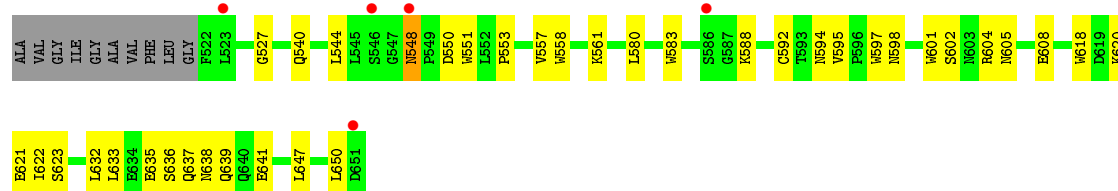


- Molecule 3: gp120

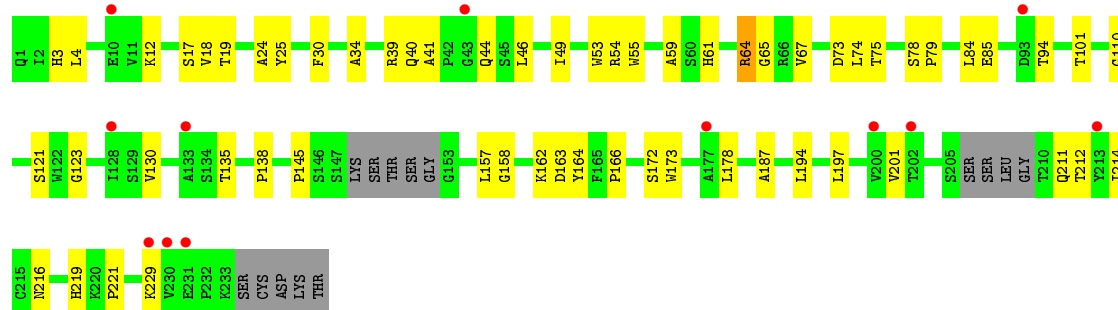




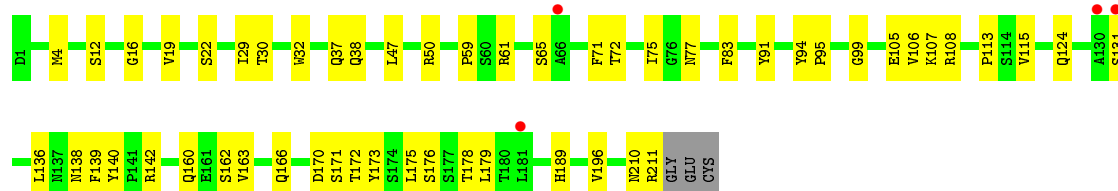
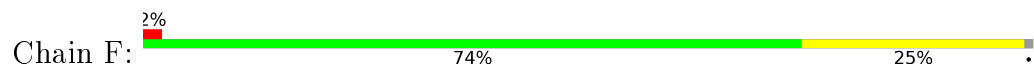
- Molecule 4: gp41



- Molecule 5: broadly neutralizing antibody 8ANC195 heavy chain



- Molecule 6: broadly neutralizing antibody 8ANC195 light chain



4 Data and refinement statistics

Property	Value	Source
Space group	I 2 3	Depositor
Cell constants a, b, c, α , β , γ	261.95Å 261.95Å 261.95Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	47.83 – 6.92 47.83 – 6.92	Depositor EDS
% Data completeness (in resolution range)	99.8 (47.83-6.92) 91.0 (47.83-6.92)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.99 (at 6.68Å)	Xtriage
Refinement program	PHENIX (phenix.refine: 1.9_1692)	Depositor
R, R_{free}	0.284 , 0.322 0.284 , 0.315	Depositor DCC
R_{free} test set	446 reflections (9.81%)	DCC
Wilson B-factor (Å ²)	342.3	Xtriage
Anisotropy	0.000	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.24 , 230.7	EDS
L-test for twinning ²	$\langle L \rangle = 0.44$, $\langle L^2 \rangle = 0.27$	Xtriage
Estimated twinning fraction	0.056 for -l,-k,-h	Xtriage
F_o, F_c correlation	0.83	EDS
Total number of atoms	12007	wwPDB-VP
Average B, all atoms (Å ²)	291.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.87% 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: BMA, NAG, MAN

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	0.21	0/1786	0.41	0/2449
2	B	0.22	0/1552	0.47	1/2121 (0.0%)
3	C	0.23	0/3592	0.44	0/4875
4	D	0.26	0/1061	0.51	0/1444
5	E	0.23	0/1730	0.44	0/2361
6	F	0.24	0/1661	0.44	0/2256
All	All	0.23	0/11382	0.45	1/15506 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	108	GLN	C-N-CD	-9.05	100.68	120.60

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	1735	0	1690	33	0
2	B	1514	0	1473	41	0
3	C	3519	0	3460	101	0
4	D	1039	0	1003	40	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
5	E	1686	0	1659	55	0
6	F	1626	0	1581	41	0
7	C	406	0	355	14	0
7	D	42	0	37	2	0
8	C	99	0	79	0	0
8	D	11	0	9	1	0
9	C	319	0	272	17	0
9	D	11	0	10	0	0
All	All	12007	0	11628	283	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 12.

All (283) 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)
3:C:76:PRO:HD2	4:D:551:TRP:CE2	1.53	1.42
3:C:76:PRO:HG2	4:D:551:TRP:CZ2	1.53	1.41
3:C:76:PRO:HD2	4:D:551:TRP:NE1	1.44	1.31
3:C:76:PRO:CG	4:D:551:TRP:CZ2	2.26	1.18
3:C:76:PRO:HG2	4:D:551:TRP:CH2	1.80	1.15
9:C:666:MAN:H61	5:E:59:ALA:CB	1.78	1.14
3:C:76:PRO:CD	4:D:551:TRP:CE2	2.28	1.14
9:C:666:MAN:C6	5:E:59:ALA:HB3	1.81	1.09
3:C:58:ALA:HB2	3:C:76:PRO:HB3	1.32	1.05
9:C:666:MAN:O4	5:E:64:ARG:HA	1.66	0.96
2:B:95:TRP:HE1	9:C:629:MAN:HO4	0.94	0.94
9:C:666:MAN:H61	5:E:59:ALA:HB3	0.90	0.85
3:C:76:PRO:CD	4:D:551:TRP:CZ2	2.59	0.83
5:E:12:LYS:NZ	5:E:17:SER:O	2.10	0.83
7:C:609:NAG:H61	7:C:610:NAG:HN2	1.46	0.81
3:C:76:PRO:HD2	4:D:551:TRP:CZ2	2.16	0.80
3:C:55:ALA:HB3	3:C:215:HIS:HB2	1.66	0.78
4:D:548:ASN:HB2	4:D:550:ASP:HB3	1.66	0.76
3:C:499:LYS:HG2	3:C:500:ARG:H	1.52	0.75
3:C:76:PRO:CD	4:D:551:TRP:NE1	2.39	0.73
2:B:95:TRP:NE1	9:C:629:MAN:O4	2.10	0.73
3:C:394:ILE:HG22	3:C:395:SER:H	1.55	0.72
7:C:612:NAG:H2	5:E:25:TYR:HD1	1.55	0.71
3:C:291:VAL:HB	3:C:446:ILE:HB	1.71	0.71
3:C:329:CYS:HB3	3:C:413:LEU:HB2	1.72	0.71

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:50:THR:O	3:C:103:GLN:NE2	2.23	0.69
9:C:666:MAN:O4	5:E:64:ARG:CA	2.40	0.69
2:B:138:ASP:HA	2:B:172:LYS:HB3	1.75	0.69
5:E:178:LEU:HD21	5:E:201:VAL:HG11	1.75	0.68
5:E:40:GLN:HE22	6:F:38:GLN:HE22	1.41	0.68
5:E:172:SER:HB3	5:E:216:ASN:HB2	1.76	0.67
3:C:273:SER:HB3	3:C:276:ILE:HG12	1.78	0.66
4:D:637:GLN:O	4:D:641:GLU:N	2.24	0.65
9:C:662:MAN:HO3	5:E:19:THR:HG1	1.43	0.65
9:C:666:MAN:O4	5:E:65:GLY:N	2.27	0.65
3:C:350:HIS:O	5:E:75:THR:OG1	2.14	0.65
9:C:662:MAN:O3	5:E:19:THR:OG1	2.12	0.65
1:A:52(E):TYR:O	3:C:441:ARG:NH1	2.30	0.64
3:C:88:ASN:ND2	4:D:527:GLY:O	2.30	0.64
5:E:187:ALA:HB2	5:E:197:LEU:HD23	1.81	0.63
6:F:189:HIS:O	6:F:211:ARG:NH2	2.32	0.62
7:C:654:NAG:O7	7:C:654:NAG:O3	2.13	0.62
3:C:36:VAL:HG12	4:D:597:TRP:HE3	1.64	0.62
1:A:28:SER:HA	1:A:76:ASN:HD21	1.65	0.61
5:E:163:ASP:HA	5:E:194:LEU:HB3	1.82	0.60
7:C:612:NAG:H2	5:E:25:TYR:CD1	2.35	0.60
1:A:100:LEU:HD12	3:C:321:ILE:HG23	1.84	0.60
1:A:72:ASP:HB2	1:A:79:PHE:HE1	1.67	0.60
3:C:418:LYS:HE3	3:C:421:ILE:HG22	1.83	0.59
2:B:23:CYS:N	2:B:71:ALA:O	2.36	0.59
9:C:666:MAN:C6	5:E:59:ALA:CB	2.61	0.59
3:C:36:VAL:HG22	4:D:595:VAL:HB	1.84	0.59
1:A:125:ALA:HB1	1:A:227:PRO:HA	1.84	0.59
3:C:37:THR:HG22	4:D:592:CYS:HA	1.85	0.59
3:C:47:ASP:HA	3:C:486:VAL:HG12	1.83	0.59
5:E:30:PHE:HB2	5:E:55:TRP:CH2	2.38	0.58
1:A:100(E):TRP:NE1	2:B:94:ASN:O	2.35	0.58
2:B:93:GLY:HA3	9:C:623:MAN:O2	2.04	0.58
6:F:113:PRO:HB3	6:F:139:PHE:HB3	1.85	0.58
2:B:65:SER:O	2:B:72:SER:N	2.27	0.58
7:C:658:NAG:H61	5:E:55:TRP:CZ3	2.39	0.57
6:F:37:GLN:HB2	6:F:47:LEU:HD11	1.87	0.57
6:F:12:SER:HB3	6:F:107:LYS:HD3	1.86	0.57
6:F:160:GLN:O	6:F:178:THR:N	2.29	0.57
7:C:601:NAG:O3	7:C:601:NAG:H83	2.05	0.57
7:C:638:NAG:H61	7:C:639:NAG:N2	2.20	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:51:LEU:HB3	1:A:57:THR:HG23	1.87	0.56
2:B:105:THR:HG22	2:B:106(A):LEU:H	1.69	0.56
3:C:300:ASN:HB3	3:C:321:ILE:O	2.06	0.56
6:F:136:LEU:HD11	6:F:196:VAL:HG11	1.88	0.56
4:D:583:TRP:O	4:D:638:ASN:ND2	2.37	0.56
3:C:174:GLN:HA	3:C:190:TYR:HA	1.86	0.56
5:E:4:LEU:HB2	5:E:123:GLY:HA2	1.87	0.56
4:D:620:LYS:HG3	6:F:32:TRP:HH2	1.71	0.55
3:C:284:LEU:HD21	3:C:474:ASP:HB3	1.87	0.55
3:C:101:VAL:HG21	3:C:477:ARG:HG2	1.89	0.55
3:C:215:HIS:ND1	3:C:247:THR:O	2.33	0.55
2:B:83:GLU:HG3	2:B:105:THR:HA	1.89	0.55
3:C:55:ALA:HA	3:C:75:VAL:O	2.07	0.55
7:D:702:NAG:H83	7:D:702:NAG:H3	1.88	0.55
5:E:135:THR:HG22	5:E:166:PRO:HD3	1.89	0.55
3:C:202:GLN:HG3	3:C:432:TYR:HD2	1.72	0.55
1:A:40:PRO:HB2	1:A:43:LYS:HD2	1.90	0.54
3:C:141:MET:N	3:C:141:MET:SD	2.80	0.54
3:C:152:MET:O	3:C:161:GLN:N	2.40	0.54
3:C:267:GLU:O	3:C:288:ASN:ND2	2.41	0.54
3:C:57:ASP:HA	3:C:77:THR:HB	1.89	0.54
7:C:601:NAG:C3	7:C:601:NAG:H83	2.37	0.54
6:F:59:PRO:HB2	6:F:61:ARG:HG2	1.89	0.54
2:B:85:VAL:HG22	2:B:103:LYS:HG2	1.89	0.54
3:C:237:PRO:HB3	5:E:54:ARG:HH11	1.72	0.54
2:B:119:PRO:HD3	2:B:209:VAL:HG11	1.90	0.53
4:D:557:VAL:O	4:D:558:TRP:HB3	2.08	0.53
2:B:110:LYS:HG2	2:B:140:TYR:CD2	2.44	0.53
2:B:136:ILE:HG12	2:B:196:VAL:HG11	1.90	0.53
5:E:110:GLY:HA3	6:F:50:ARG:HG3	1.91	0.53
3:C:152:MET:SD	3:C:153:THR:N	2.81	0.52
3:C:500:ARG:HB2	4:D:594:ASN:OD1	2.10	0.52
3:C:76:PRO:CB	4:D:551:TRP:CZ2	2.91	0.52
1:A:84:ALA:HA	1:A:111:VAL:HB	1.91	0.52
4:D:602:SER:H	6:F:30:THR:HG21	1.74	0.52
6:F:107:LYS:HA	6:F:140:TYR:OH	2.08	0.52
6:F:115:VAL:HG21	6:F:196:VAL:HG21	1.91	0.52
1:A:176:ALA:HA	1:A:187:LEU:HB3	1.91	0.52
3:C:221:GLY:HA2	4:D:544:LEU:HD11	1.91	0.52
3:C:361:ASN:HB3	3:C:386:SER:HA	1.90	0.52
3:C:71:THR:HA	3:C:74:CYS:HB2	1.92	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:F:105:GLU:OE2	6:F:166:GLN:NE2	2.43	0.52
3:C:388:LEU:HD11	3:C:413:LEU:HD11	1.91	0.52
3:C:296:THR:HG22	3:C:441:ARG:HA	1.91	0.52
2:B:147:ALA:HB3	2:B:195:GLN:HB3	1.92	0.52
5:E:219:HIS:CD2	5:E:221:PRO:HD2	2.45	0.52
5:E:67:VAL:HG13	5:E:84:LEU:HD11	1.92	0.51
1:A:137:THR:HG22	1:A:194:PRO:HA	1.92	0.51
2:B:120:PRO:HD3	2:B:132:LEU:HG	1.91	0.51
3:C:257:GLN:NE2	3:C:369:VAL:O	2.42	0.51
4:D:623:SER:HB2	6:F:50:ARG:HH12	1.76	0.51
6:F:65:SER:HB3	6:F:72:THR:HG23	1.93	0.51
5:E:187:ALA:HA	5:E:197:LEU:HB3	1.93	0.51
6:F:108:ARG:HE	6:F:171:SER:HG	1.55	0.51
5:E:25:TYR:CD1	5:E:79:PRO:HG3	2.45	0.50
1:A:22:CYS:HB3	1:A:78:VAL:HB	1.93	0.50
3:C:133:ASN:OD1	3:C:146:LYS:NZ	2.42	0.50
4:D:620:LYS:HG3	6:F:32:TRP:CH2	2.46	0.50
3:C:37:THR:OG1	3:C:494:ALA:O	2.26	0.50
6:F:83:PHE:CE1	6:F:106:VAL:HA	2.47	0.50
3:C:393:TRP:CD2	3:C:398:SER:HB3	2.46	0.50
2:B:19:ILE:HG13	2:B:78:LEU:HD11	1.94	0.50
5:E:94:THR:HG22	5:E:130:VAL:H	1.76	0.50
1:A:18:LEU:HD23	1:A:82:LEU:HD12	1.93	0.50
3:C:299:ASN:HB3	3:C:320:ILE:HD13	1.93	0.50
3:C:205:PRO:HG3	3:C:315:TYR:CE2	2.47	0.50
5:E:40:GLN:HB2	5:E:46:LEU:HD23	1.92	0.50
5:E:34:ALA:HB2	5:E:53:TRP:CD1	2.47	0.50
5:E:162:LYS:NZ	6:F:131:SER:OG	2.44	0.50
1:A:51:LEU:HD23	1:A:69:LEU:HB3	1.93	0.49
3:C:258:LEU:HD12	3:C:372:HIS:CD2	2.46	0.49
5:E:3:HIS:HB2	5:E:25:TYR:HB2	1.93	0.49
1:A:27:ASP:OD1	1:A:28:SER:N	2.45	0.49
2:B:24:THR:HG22	2:B:70:THR:HG22	1.95	0.49
2:B:123:GLU:HA	2:B:126:GLN:OE1	2.12	0.49
4:D:605:ASN:HB3	4:D:608:GLU:HB2	1.95	0.49
5:E:163:ASP:HB3	5:E:194:LEU:HD13	1.95	0.49
9:C:666:MAN:O6	5:E:67:VAL:O	2.19	0.49
6:F:162:SER:HB3	6:F:176:SER:HB2	1.94	0.48
7:C:658:NAG:H2	5:E:55:TRP:CG	2.48	0.48
3:C:107:ASP:OD1	4:D:561:LYS:HE2	2.14	0.48
1:A:87:THR:HG23	1:A:110:THR:HA	1.93	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:E:24:ALA:O	5:E:79:PRO:HB2	2.13	0.48
5:E:39:ARG:HB3	5:E:49:ILE:HD11	1.95	0.48
1:A:63:LEU:HB3	1:A:67:LEU:HD23	1.94	0.48
3:C:272:ARG:O	3:C:284:LEU:N	2.47	0.48
6:F:166:GLN:HB2	6:F:173:TYR:CZ	2.49	0.48
3:C:277:THR:OG1	5:E:75:THR:O	2.28	0.48
1:A:146:ASP:HB3	1:A:184:LEU:HD13	1.93	0.48
3:C:388:LEU:HG	3:C:413:LEU:HD21	1.94	0.48
5:E:41:ALA:HB3	5:E:44:GLN:HB2	1.95	0.48
2:B:149:LYS:HB2	2:B:193:SER:HB2	1.96	0.48
3:C:95:MET:SD	3:C:272:ARG:HD3	2.53	0.48
3:C:36:VAL:HG12	4:D:597:TRP:CE3	2.48	0.48
9:C:662:MAN:O4	5:E:85:GLU:HB2	2.14	0.48
1:A:59:HIS:N	9:C:629:MAN:O3	2.45	0.48
3:C:192:LEU:HB2	3:C:195:CYS:SG	2.55	0.47
4:D:633:LEU:O	4:D:637:GLN:HB2	2.14	0.47
5:E:145:PRO:HG3	5:E:157:LEU:HB3	1.96	0.47
3:C:474:ASP:OD1	3:C:477:ARG:NH1	2.48	0.47
3:C:56:SER:O	3:C:57:ASP:HB2	2.13	0.47
3:C:304:LYS:HB2	3:C:316:ALA:HB3	1.97	0.47
6:F:138:ASN:HB3	6:F:172:THR:HG21	1.95	0.47
7:D:702:NAG:O3	8:D:703:BMA:O5	2.23	0.47
5:E:12:LYS:HD3	5:E:18:VAL:HB	1.97	0.47
6:F:136:LEU:HB2	6:F:175:LEU:HB3	1.96	0.47
6:F:4:MET:HB2	6:F:99:GLY:HA2	1.97	0.47
1:A:177:VAL:N	1:A:186:SER:O	2.46	0.46
1:A:172:HIS:NE2	2:B:167:GLN:OE1	2.48	0.46
6:F:124:GLN:OE1	6:F:131:SER:N	2.47	0.46
4:D:602:SER:N	6:F:30:THR:HG21	2.29	0.46
1:A:146:ASP:OD1	1:A:179:GLN:NE2	2.38	0.46
7:C:608:NAG:H61	7:C:649:NAG:H5	1.97	0.46
3:C:348:ARG:HD3	3:C:353:ASN:O	2.16	0.46
2:B:33:VAL:HA	2:B:90:SER:HB2	1.98	0.46
6:F:142:ARG:HB2	6:F:173:TYR:CD2	2.51	0.46
6:F:94:TYR:HA	6:F:95:PRO:HA	1.79	0.46
3:C:277:THR:O	3:C:453:ARG:NH2	2.48	0.45
6:F:32:TRP:HE3	6:F:91:TYR:HE2	1.63	0.45
1:A:35:PHE:HB2	1:A:95:PHE:HB2	1.98	0.45
2:B:30:ASN:ND2	2:B:91:LEU:O	2.49	0.45
2:B:51:VAL:HG12	2:B:52:ASN:N	2.31	0.45
7:C:609:NAG:H83	7:C:638:NAG:H62	1.99	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:356:ILE:O	3:C:462:THR:OG1	2.31	0.45
3:C:376:CYS:HB3	3:C:381:PHE:CE1	2.52	0.45
1:A:100(E):TRP:CD1	2:B:95:TRP:HE3	2.35	0.45
6:F:29:ILE:HB	6:F:71:PHE:HZ	1.81	0.45
3:C:272:ARG:HH12	3:C:286:GLN:HB2	1.82	0.45
1:A:57:THR:O	9:C:628:MAN:O3	2.18	0.45
2:B:30:ASN:OD1	2:B:90:SER:OG	2.35	0.44
3:C:383:CYS:HA	3:C:415:CYS:HA	1.99	0.44
2:B:35:TRP:HB2	2:B:48:ILE:HG22	1.99	0.44
2:B:65:SER:N	2:B:72:SER:O	2.46	0.44
3:C:499:LYS:HG2	3:C:500:ARG:N	2.27	0.44
4:D:647:LEU:HA	4:D:650:LEU:HD23	2.00	0.44
3:C:255:SER:HA	3:C:373:SER:O	2.17	0.44
3:C:461:THR:OG1	3:C:462:THR:N	2.49	0.44
3:C:329:CYS:O	3:C:413:LEU:N	2.51	0.44
5:E:61:HIS:HA	5:E:64:ARG:HG2	2.00	0.44
2:B:22:SER:OG	2:B:23:CYS:N	2.51	0.44
2:B:66:LYS:HA	2:B:71:ALA:HA	1.99	0.44
3:C:340:LEU:HB3	3:C:393:TRP:CZ2	2.53	0.44
7:C:638:NAG:H61	7:C:639:NAG:HN2	1.83	0.44
2:B:124:GLU:OE1	2:B:131:THR:N	2.51	0.43
1:A:39:GLN:NE2	2:B:38:GLN:OE1	2.47	0.43
3:C:54:CYS:HB2	3:C:214:ILE:HG23	2.00	0.43
3:C:39:TYR:CE1	3:C:494:ALA:HB3	2.53	0.43
4:D:551:TRP:HB3	4:D:553:PRO:HD2	2.00	0.43
3:C:276:ILE:H	5:E:74:LEU:HD21	1.84	0.43
1:A:207:ILE:HG13	1:A:222:ARG:HA	1.98	0.43
3:C:434:PRO:HA	3:C:435:PRO:HD3	1.83	0.43
3:C:173:VAL:HG12	3:C:193:ILE:HA	2.00	0.43
2:B:23:CYS:O	2:B:71:ALA:N	2.38	0.43
3:C:70:ALA:HB2	3:C:111:LEU:HD11	2.01	0.43
3:C:424:TRP:HE1	3:C:472:MET:HG3	1.84	0.43
3:C:42:VAL:HA	3:C:43:PRO:HD3	1.89	0.43
6:F:170:ASP:HB2	6:F:172:THR:HG22	2.01	0.43
5:E:12:LYS:O	5:E:130:VAL:HA	2.18	0.43
7:C:657:NAG:N2	5:E:73:ASP:OD2	2.49	0.43
1:A:101:ASP:OD1	1:A:102:LEU:N	2.52	0.43
1:A:56:TRP:HE3	9:C:628:MAN:H62	1.83	0.43
3:C:253:VAL:HG21	3:C:261:ASN:HB2	2.00	0.43
6:F:16:GLY:HA2	6:F:77:ASN:OD1	2.19	0.42
1:A:29:THR:OG1	1:A:73:THR:HA	2.19	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:323:ASP:HB3	3:C:325:ARG:HD2	2.01	0.42
4:D:598:ASN:HB3	4:D:601:TRP:CD2	2.54	0.42
5:E:75:THR:HG23	5:E:78:SER:H	1.84	0.42
6:F:22:SER:HA	6:F:72:THR:HA	2.01	0.42
2:B:51:VAL:HG12	2:B:52:ASN:H	1.84	0.42
6:F:19:VAL:N	6:F:75:ILE:O	2.45	0.42
5:E:214:ILE:HG22	5:E:229:LYS:HG2	2.01	0.42
6:F:108:ARG:NE	6:F:171:SER:OG	2.28	0.42
3:C:287:PHE:HE2	3:C:446:ILE:HG22	1.85	0.42
4:D:604:ARG:NH1	4:D:608:GLU:OE2	2.52	0.42
6:F:210:ASN:O	6:F:211:ARG:HG2	2.19	0.42
5:E:138:PRO:HB3	5:E:164:TYR:HB3	2.02	0.42
6:F:142:ARG:HB2	6:F:173:TYR:CE2	2.54	0.42
4:D:632:LEU:O	4:D:636:SER:HB3	2.20	0.42
5:E:158:GLY:HA2	5:E:173:TRP:CH2	2.55	0.42
1:A:122:PHE:HE2	1:A:145:LYS:HD3	1.85	0.41
1:A:15:SER:N	1:A:82(C):VAL:O	2.39	0.41
3:C:55:ALA:HB1	3:C:77:THR:OG1	2.20	0.41
4:D:580:LEU:HD21	4:D:588:LYS:HA	2.01	0.41
5:E:211:GLN:O	5:E:212:THR:OG1	2.36	0.41
3:C:297:ARG:C	3:C:299:ASN:H	2.24	0.41
3:C:457:SER:HA	3:C:458:THR:OG1	2.20	0.41
2:B:147:ALA:O	2:B:195:GLN:N	2.44	0.41
2:B:167:GLN:NE2	2:B:174:ALA:HB2	2.35	0.41
6:F:163:VAL:HG22	6:F:175:LEU:HD12	2.02	0.41
3:C:293:ILE:HD12	3:C:446:ILE:HD11	2.02	0.41
5:E:101:THR:HG22	5:E:121:SER:HB2	2.03	0.41
3:C:121:LYS:H	3:C:121:LYS:HG2	1.62	0.41
4:D:621:GLU:HG2	6:F:32:TRP:HE1	1.84	0.41
2:B:55:PRO:HG2	2:B:58:VAL:HG21	2.02	0.41
3:C:76:PRO:HB2	4:D:551:TRP:HZ2	1.86	0.41
4:D:618:TRP:O	4:D:622:ILE:HG12	2.20	0.41
6:F:131:SER:HA	6:F:179:LEU:O	2.20	0.41
1:A:51:LEU:HD11	1:A:71:LEU:HB2	2.02	0.41
2:B:4:LEU:HB3	2:B:23:CYS:SG	2.60	0.41
3:C:269:VAL:HG12	3:C:288:ASN:N	2.35	0.41
3:C:293:ILE:HG22	3:C:444:SER:O	2.21	0.41
2:B:153:SER:HA	2:B:154:PRO:HD3	1.87	0.41
2:B:35:TRP:H	2:B:48:ILE:HG22	1.85	0.41
3:C:54:CYS:O	3:C:75:VAL:HB	2.21	0.41
3:C:265:ALA:HB2	3:C:286:GLN:HG2	2.03	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:E:138:PRO:HD3	5:E:219:HIS:ND1	2.36	0.41
3:C:105:HIS:CE1	3:C:472:MET:HB2	2.56	0.41
3:C:353:ASN:HD22	7:C:606:NAG:H83	1.86	0.41
3:C:71:THR:HG23	3:C:74:CYS:HB3	2.03	0.41
2:B:110:LYS:HG2	2:B:140:TYR:HD2	1.84	0.40
3:C:269:VAL:HG23	3:C:346:GLN:HG3	2.02	0.40
3:C:107:ASP:O	3:C:111:LEU:HB2	2.22	0.40
4:D:635:GLU:O	4:D:639:GLN:HB3	2.21	0.40
4:D:540:GLN:NE2	4:D:540:GLN:HA	2.36	0.40
2:B:21:ILE:HD11	2:B:73:LEU:HD23	2.03	0.40
3:C:256:THR:O	3:C:372:HIS:ND1	2.39	0.40
5:E:25:TYR:CE1	5:E:79:PRO:HG3	2.56	0.40

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

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	226/239 (95%)	212 (94%)	14 (6%)	0	100	100
2	B	202/211 (96%)	193 (96%)	8 (4%)	1 (0%)	34	77
3	C	439/480 (92%)	417 (95%)	22 (5%)	0	100	100
4	D	128/140 (91%)	118 (92%)	10 (8%)	0	100	100
5	E	218/238 (92%)	209 (96%)	9 (4%)	0	100	100
6	F	210/215 (98%)	205 (98%)	5 (2%)	0	100	100
All	All	1423/1523 (93%)	1354 (95%)	68 (5%)	1 (0%)	56	90

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	B	51	VAL

5.3.2 Protein sidechains [i](#)

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	194/203 (96%)	194 (100%)	0	100	100
2	B	171/177 (97%)	171 (100%)	0	100	100
3	C	399/426 (94%)	397 (100%)	2 (0%)	92	96
4	D	113/118 (96%)	112 (99%)	1 (1%)	84	93
5	E	192/204 (94%)	191 (100%)	1 (0%)	92	96
6	F	180/182 (99%)	180 (100%)	0	100	100
All	All	1249/1310 (95%)	1245 (100%)	4 (0%)	94	96

All (4) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
3	C	233	ASN
3	C	337	ASN
4	D	548	ASN
5	E	64	ARG

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (1) such sidechains are listed below:

Mol	Chain	Res	Type
5	E	40	GLN

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

There are no carbohydrates in this entry.

5.6 Ligand geometry

72 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	$\# Z > 2$
7	NAG	C	601	3,7	14,14,15	0.28	0	15,19,21	0.55	0
7	NAG	C	602	7	14,14,15	0.18	0	15,19,21	0.28	0
7	NAG	C	603	3	14,14,15	0.26	0	15,19,21	0.36	0
7	NAG	C	604	3,7	14,14,15	0.20	0	15,19,21	0.34	0
7	NAG	C	605	7	14,14,15	0.26	0	15,19,21	0.32	0
7	NAG	C	606	3	14,14,15	0.34	0	15,19,21	0.46	0
7	NAG	C	607	3,7	14,14,15	0.21	0	15,19,21	1.04	1 (6%)
7	NAG	C	608	7	14,14,15	0.23	0	15,19,21	0.26	0
7	NAG	C	609	3,7	14,14,15	0.28	0	15,19,21	0.45	0
7	NAG	C	610	7	14,14,15	0.25	0	15,19,21	0.25	0
7	NAG	C	611	3,7	14,14,15	0.59	0	15,19,21	0.42	0
7	NAG	C	612	8,7	14,14,15	0.56	0	15,19,21	0.43	0
8	BMA	C	613	9,7	11,11,12	0.55	0	15,15,17	0.71	0
9	MAN	C	614	9,8	11,11,12	0.68	0	15,15,17	1.06	1 (6%)
9	MAN	C	615	9	11,11,12	0.57	0	15,15,17	1.00	1 (6%)
9	MAN	C	616	9,8	11,11,12	0.87	0	15,15,17	0.90	1 (6%)
9	MAN	C	617	9	11,11,12	0.76	1 (9%)	15,15,17	1.41	2 (13%)
9	MAN	C	618	9	11,11,12	0.62	0	15,15,17	0.99	2 (13%)
7	NAG	C	619	3	14,14,15	0.35	0	15,19,21	0.27	0
7	NAG	C	620	3,7	14,14,15	0.24	0	15,19,21	0.38	0
7	NAG	C	621	8,7	14,14,15	0.21	0	15,19,21	0.29	0
9	MAN	C	622	9	11,11,12	0.64	0	15,15,17	1.22	2 (13%)
9	MAN	C	623	9	11,11,12	0.66	0	15,15,17	0.90	1 (6%)
8	BMA	C	624	9,7	11,11,12	0.79	0	15,15,17	0.89	0
9	MAN	C	625	9,8	11,11,12	0.72	1 (9%)	15,15,17	1.11	2 (13%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
9	MAN	C	626	9,8	11,11,12	0.67	0	15,15,17	1.02	2 (13%)
9	MAN	C	627	9	11,11,12	0.66	0	15,15,17	0.98	2 (13%)
9	MAN	C	628	9	11,11,12	0.67	0	15,15,17	1.12	2 (13%)
9	MAN	C	629	9	11,11,12	0.79	0	15,15,17	0.96	1 (6%)
7	NAG	C	630	3,7	14,14,15	0.48	0	15,19,21	0.55	0
7	NAG	C	631	8,7	14,14,15	0.19	0	15,19,21	0.65	0
8	BMA	C	632	9,7	11,11,12	0.79	0	15,15,17	1.07	0
9	MAN	C	633	9,8	11,11,12	0.69	0	15,15,17	0.96	2 (13%)
9	MAN	C	634	9	11,11,12	0.65	0	15,15,17	0.96	1 (6%)
9	MAN	C	635	9,8	11,11,12	0.74	0	15,15,17	1.28	2 (13%)
9	MAN	C	636	9	11,11,12	0.58	0	15,15,17	1.09	2 (13%)
9	MAN	C	637	9	11,11,12	0.56	0	15,15,17	1.09	2 (13%)
7	NAG	C	638	3,7	14,14,15	0.29	0	15,19,21	0.42	0
7	NAG	C	639	8,7	14,14,15	0.41	0	15,19,21	0.43	0
8	BMA	C	640	9,7	11,11,12	0.65	0	15,15,17	0.99	1 (6%)
9	MAN	C	641	8	11,11,12	0.74	1 (9%)	15,15,17	1.15	2 (13%)
9	MAN	C	642	8	11,11,12	0.67	0	15,15,17	1.27	1 (6%)
7	NAG	C	643	3,7	14,14,15	0.44	0	15,19,21	0.36	0
7	NAG	C	644	8,7	14,14,15	0.23	0	15,19,21	0.56	0
8	BMA	C	645	9,7	11,11,12	0.66	0	15,15,17	1.26	1 (6%)
9	MAN	C	646	9,8	11,11,12	0.59	0	15,15,17	1.30	2 (13%)
9	MAN	C	647	9	11,11,12	0.22	0	15,15,17	0.53	0
7	NAG	C	648	3,7	14,14,15	0.39	0	15,19,21	0.29	0
7	NAG	C	649	8,7	14,14,15	0.26	0	15,19,21	0.59	0
8	BMA	C	650	7	11,11,12	0.62	0	15,15,17	0.77	0
7	NAG	C	651	3,7	14,14,15	0.32	0	15,19,21	0.44	0
7	NAG	C	652	8,7	14,14,15	0.38	0	15,19,21	0.58	0
8	BMA	C	653	7	11,11,12	0.65	0	15,15,17	0.79	0
7	NAG	C	654	3,7	14,14,15	0.31	0	15,19,21	0.66	0
7	NAG	C	655	8,7	14,14,15	0.22	0	15,19,21	0.63	0
8	BMA	C	656	7	11,11,12	0.63	0	15,15,17	0.74	0
7	NAG	C	657	3,7	14,14,15	0.17	0	15,19,21	0.28	0
7	NAG	C	658	8,7	14,14,15	0.37	0	15,19,21	0.37	0
8	BMA	C	659	9,7	11,11,12	0.51	0	15,15,17	0.70	0
9	MAN	C	660	9,8	11,11,12	0.50	0	15,15,17	1.08	2 (13%)
9	MAN	C	661	9	11,11,12	0.72	0	15,15,17	1.07	0
9	MAN	C	662	9	11,11,12	0.51	0	15,15,17	0.97	2 (13%)
9	MAN	C	663	9,8	11,11,12	0.56	0	15,15,17	1.14	2 (13%)
9	MAN	C	664	9	11,11,12	0.61	0	15,15,17	1.17	2 (13%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
9	MAN	C	665	9	11,11,12	0.83	0	15,15,17	1.41	3 (20%)
9	MAN	C	666	9	11,11,12	0.63	0	15,15,17	0.94	2 (13%)
9	MAN	C	667	9	11,11,12	0.56	0	15,15,17	1.01	2 (13%)
7	NAG	D	701	4,7	14,14,15	0.24	0	15,19,21	0.32	0
7	NAG	D	702	8,7	14,14,15	0.40	0	15,19,21	1.43	2 (13%)
8	BMA	D	703	9,7	11,11,12	0.76	0	15,15,17	1.00	0
9	MAN	D	704	8	11,11,12	1.55	3 (27%)	15,15,17	1.34	2 (13%)
7	NAG	D	705	4	14,14,15	0.20	0	15,19,21	0.32	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
7	NAG	C	601	3,7	-	1/6/23/26	0/1/1/1
7	NAG	C	602	7	-	0/6/23/26	0/1/1/1
7	NAG	C	603	3	-	0/6/23/26	0/1/1/1
7	NAG	C	604	3,7	-	0/6/23/26	0/1/1/1
7	NAG	C	605	7	-	0/6/23/26	0/1/1/1
7	NAG	C	606	3	-	0/6/23/26	0/1/1/1
7	NAG	C	607	3,7	-	0/6/23/26	0/1/1/1
7	NAG	C	608	7	-	0/6/23/26	0/1/1/1
7	NAG	C	609	3,7	-	0/6/23/26	0/1/1/1
7	NAG	C	610	7	-	0/6/23/26	0/1/1/1
7	NAG	C	611	3,7	-	0/6/23/26	0/1/1/1
7	NAG	C	612	8,7	-	0/6/23/26	0/1/1/1
8	BMA	C	613	9,7	-	0/2/19/22	0/1/1/1
9	MAN	C	614	9,8	-	0/2/19/22	0/1/1/1
9	MAN	C	615	9	-	0/2/19/22	0/1/1/1
9	MAN	C	616	9,8	-	0/2/19/22	0/1/1/1
9	MAN	C	617	9	-	0/2/19/22	0/1/1/1
9	MAN	C	618	9	-	0/2/19/22	0/1/1/1
7	NAG	C	619	3	-	0/6/23/26	0/1/1/1
7	NAG	C	620	3,7	-	0/6/23/26	0/1/1/1
7	NAG	C	621	8,7	-	0/6/23/26	0/1/1/1
9	MAN	C	622	9	-	0/2/19/22	0/1/1/1
9	MAN	C	623	9	-	0/2/19/22	0/1/1/1
8	BMA	C	624	9,7	-	0/2/19/22	0/1/1/1
9	MAN	C	625	9,8	-	0/2/19/22	0/1/1/1
9	MAN	C	626	9,8	-	0/2/19/22	0/1/1/1

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
9	MAN	C	627	9	-	0/2/19/22	0/1/1/1
9	MAN	C	628	9	-	0/2/19/22	0/1/1/1
9	MAN	C	629	9	-	0/2/19/22	0/1/1/1
7	NAG	C	630	3,7	-	0/6/23/26	0/1/1/1
7	NAG	C	631	8,7	-	0/6/23/26	0/1/1/1
8	BMA	C	632	9,7	-	0/2/19/22	0/1/1/1
9	MAN	C	633	9,8	-	0/2/19/22	0/1/1/1
9	MAN	C	634	9	-	0/2/19/22	0/1/1/1
9	MAN	C	635	9,8	-	0/2/19/22	0/1/1/1
9	MAN	C	636	9	-	0/2/19/22	0/1/1/1
9	MAN	C	637	9	-	0/2/19/22	0/1/1/1
7	NAG	C	638	3,7	-	0/6/23/26	0/1/1/1
7	NAG	C	639	8,7	-	0/6/23/26	0/1/1/1
8	BMA	C	640	9,7	-	0/2/19/22	0/1/1/1
9	MAN	C	641	8	-	0/2/19/22	0/1/1/1
9	MAN	C	642	8	-	0/2/19/22	0/1/1/1
7	NAG	C	643	3,7	-	0/6/23/26	0/1/1/1
7	NAG	C	644	8,7	-	0/6/23/26	0/1/1/1
8	BMA	C	645	9,7	-	0/2/19/22	0/1/1/1
9	MAN	C	646	9,8	-	0/2/19/22	0/1/1/1
9	MAN	C	647	9	-	0/2/19/22	0/1/1/1
7	NAG	C	648	3,7	-	0/6/23/26	0/1/1/1
7	NAG	C	649	8,7	-	0/6/23/26	0/1/1/1
8	BMA	C	650	7	-	0/2/19/22	0/1/1/1
7	NAG	C	651	3,7	-	0/6/23/26	0/1/1/1
7	NAG	C	652	8,7	-	0/6/23/26	0/1/1/1
8	BMA	C	653	7	-	0/2/19/22	0/1/1/1
7	NAG	C	654	3,7	-	0/6/23/26	0/1/1/1
7	NAG	C	655	8,7	-	0/6/23/26	0/1/1/1
8	BMA	C	656	7	-	0/2/19/22	0/1/1/1
7	NAG	C	657	3,7	-	0/6/23/26	0/1/1/1
7	NAG	C	658	8,7	-	0/6/23/26	0/1/1/1
8	BMA	C	659	9,7	-	0/2/19/22	0/1/1/1
9	MAN	C	660	9,8	-	0/2/19/22	0/1/1/1
9	MAN	C	661	9	-	0/2/19/22	0/1/1/1
9	MAN	C	662	9	-	0/2/19/22	0/1/1/1
9	MAN	C	663	9,8	-	0/2/19/22	0/1/1/1
9	MAN	C	664	9	-	0/2/19/22	0/1/1/1
9	MAN	C	665	9	-	0/2/19/22	0/1/1/1
9	MAN	C	666	9	-	0/2/19/22	0/1/1/1
9	MAN	C	667	9	-	0/2/19/22	0/1/1/1
7	NAG	D	701	4,7	-	0/6/23/26	0/1/1/1

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
7	NAG	D	702	8,7	-	0/6/23/26	0/1/1/1
8	BMA	D	703	9,7	-	0/2/19/22	0/1/1/1
9	MAN	D	704	8	-	0/2/19/22	0/1/1/1
7	NAG	D	705	4	-	0/6/23/26	0/1/1/1

All (6) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
9	C	625	MAN	C1-C2	2.01	1.57	1.52
9	C	617	MAN	C1-C2	2.08	1.57	1.52
9	C	641	MAN	C1-C2	2.17	1.57	1.52
9	D	704	MAN	C1-C2	2.47	1.58	1.52
9	D	704	MAN	O2-C2	2.60	1.49	1.43
9	D	704	MAN	C2-C3	3.30	1.57	1.52

All (55) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
9	C	665	MAN	O2-C2-C3	-3.31	103.52	110.19
9	C	628	MAN	O2-C2-C3	-3.13	103.89	110.19
9	C	622	MAN	O2-C2-C3	-3.01	104.12	110.19
8	C	640	BMA	C1-C2-C3	-2.78	106.18	109.55
9	C	665	MAN	C1-C2-C3	-2.52	106.50	109.55
9	C	667	MAN	O2-C2-C3	-2.47	105.21	110.19
9	C	625	MAN	O2-C2-C3	-2.44	105.27	110.19
9	C	626	MAN	O2-C2-C3	-2.30	105.54	110.19
9	C	662	MAN	O2-C2-C3	-2.26	105.62	110.19
9	C	663	MAN	O2-C2-C3	-2.26	105.63	110.19
9	C	637	MAN	O2-C2-C3	-2.25	105.65	110.19
9	C	634	MAN	O2-C2-C3	-2.25	105.66	110.19
9	C	633	MAN	O2-C2-C3	-2.24	105.67	110.19
9	C	623	MAN	O2-C2-C3	-2.23	105.69	110.19
9	C	636	MAN	O2-C2-C3	-2.23	105.70	110.19
9	C	618	MAN	O2-C2-C3	-2.21	105.73	110.19
9	C	666	MAN	O2-C2-C3	-2.21	105.74	110.19
9	C	660	MAN	O2-C2-C3	-2.18	105.79	110.19
9	C	627	MAN	O2-C2-C3	-2.18	105.80	110.19
9	C	616	MAN	O2-C2-C3	-2.17	105.81	110.19
9	C	629	MAN	O2-C2-C3	-2.16	105.84	110.19
9	C	617	MAN	O2-C2-C3	-2.14	105.87	110.19
9	C	664	MAN	O2-C2-C3	-2.11	105.93	110.19
9	C	641	MAN	O2-C2-C3	-2.11	105.93	110.19

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
9	C	635	MAN	O2-C2-C3	-2.10	105.96	110.19
9	C	666	MAN	C1-O5-C5	2.07	115.18	112.14
9	C	627	MAN	C1-O5-C5	2.11	115.24	112.14
9	C	633	MAN	C1-O5-C5	2.14	115.29	112.14
9	C	614	MAN	C1-O5-C5	2.15	115.30	112.14
9	C	628	MAN	C1-O5-C5	2.28	115.49	112.14
9	D	704	MAN	C1-O5-C5	2.36	115.61	112.14
7	D	702	NAG	C1-O5-C5	2.38	115.65	112.14
9	C	667	MAN	C1-O5-C5	2.43	115.71	112.14
9	C	618	MAN	C1-O5-C5	2.43	115.72	112.14
9	C	662	MAN	C1-O5-C5	2.47	115.78	112.14
9	C	626	MAN	C1-O5-C5	2.48	115.78	112.14
9	C	641	MAN	C1-O5-C5	2.63	116.00	112.14
9	C	664	MAN	C1-O5-C5	2.65	116.03	112.14
9	C	615	MAN	C1-O5-C5	2.70	116.11	112.14
9	C	646	MAN	C1-O5-C5	2.73	116.15	112.14
9	C	665	MAN	C1-O5-C5	2.84	116.32	112.14
9	C	625	MAN	C1-O5-C5	2.85	116.33	112.14
9	C	622	MAN	C1-O5-C5	2.86	116.35	112.14
9	D	704	MAN	O2-C2-C1	2.92	115.08	109.23
9	C	663	MAN	C1-O5-C5	3.00	116.55	112.14
9	C	660	MAN	C1-O5-C5	3.02	116.59	112.14
9	C	637	MAN	C1-O5-C5	3.04	116.61	112.14
8	C	645	BMA	C1-C2-C3	3.17	113.39	109.55
9	C	636	MAN	C1-O5-C5	3.22	116.88	112.14
9	C	646	MAN	O2-C2-C1	3.33	115.91	109.23
7	C	607	NAG	C2-N2-C7	3.43	127.56	123.11
9	C	635	MAN	C1-O5-C5	4.03	118.07	112.14
9	C	642	MAN	C1-O5-C5	4.15	118.25	112.14
9	C	617	MAN	C1-O5-C5	4.30	118.47	112.14
7	D	702	NAG	C2-N2-C7	4.77	129.31	123.11

There are no chirality outliers.

All (1) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
7	C	601	NAG	O7-C7-N2-C2

There are no ring outliers.

19 monomers are involved in 33 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
7	C	601	NAG	2	0
7	C	606	NAG	1	0
7	C	608	NAG	1	0
7	C	609	NAG	2	0
7	C	610	NAG	1	0
7	C	612	NAG	2	0
9	C	623	MAN	1	0
9	C	628	MAN	2	0
9	C	629	MAN	3	0
7	C	638	NAG	3	0
7	C	639	NAG	2	0
7	C	649	NAG	1	0
7	C	654	NAG	1	0
7	C	657	NAG	1	0
7	C	658	NAG	2	0
9	C	662	MAN	3	0
9	C	666	MAN	8	0
7	D	702	NAG	2	0
8	D	703	BMA	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(Å ²)	Q<0.9
1	A	230/239 (96%)	0.93	42 (18%) 2 7	294, 318, 478, 494	0
2	B	204/211 (96%)	1.00	49 (24%) 1 6	282, 349, 452, 467	0
3	C	447/480 (93%)	0.37	27 (6%) 25 26	198, 274, 313, 343	0
4	D	130/140 (92%)	0.11	5 (3%) 44 42	196, 219, 291, 311	0
5	E	224/238 (94%)	0.24	12 (5%) 29 30	215, 252, 299, 317	0
6	F	212/215 (98%)	0.08	4 (1%) 70 65	204, 243, 286, 291	0
All	All	1447/1523 (95%)	0.46	139 (9%) 10 14	196, 282, 457, 494	0

All (139) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	B	179	LEU	9.6
2	B	158	GLY	9.6
1	A	35(B)	GLY	9.5
2	B	177	SER	8.9
3	C	43	PRO	8.6
2	B	118	PHE	8.6
1	A	200	THR	8.5
2	B	119	PRO	7.3
1	A	93	ALA	7.1
2	B	132	LEU	6.8
2	B	157	ALA	6.7
1	A	123	PRO	6.4
1	A	199	GLY	6.4
2	B	116	THR	6.4
1	A	100(H)	PRO	6.2
1	A	226	GLU	5.9
2	B	176	SER	5.8
1	A	36	TRP	5.7
3	C	42	VAL	5.6

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Mol	Chain	Res	Type	RSRZ
2	B	175	ALA	5.5
3	C	41	GLY	5.5
2	B	109	PRO	5.2
2	B	117	LEU	5.0
1	A	100(I)	ALA	5.0
2	B	110	LYS	5.0
2	B	133	VAL	5.0
1	A	49	GLY	4.9
3	C	317	THR	4.8
1	A	124	LEU	4.8
3	C	44	VAL	4.5
1	A	227	PRO	4.5
1	A	92	CYS	4.5
2	B	206	GLU	4.4
3	C	316	ALA	4.4
1	A	141	GLY	4.4
4	D	548	ASN	4.3
2	B	131	THR	4.3
2	B	204	THR	4.1
2	B	115	VAL	4.1
2	B	205	VAL	4.0
1	A	37	VAL	3.9
2	B	120	PRO	3.9
2	B	134	CYS	3.8
1	A	48	VAL	3.7
3	C	318	GLY	3.7
2	B	178	TYR	3.7
3	C	492	GLY	3.4
2	B	111	ALA	3.4
2	B	148	TRP	3.4
3	C	469	GLY	3.4
1	A	125	ALA	3.3
2	B	136	ILE	3.3
2	B	195	GLN	3.2
2	B	114	SER	3.2
6	F	131	SER	3.0
3	C	493	VAL	3.0
5	E	43	GLY	3.0
3	C	303	ARG	3.0
4	D	651	ASP	3.0
3	C	252	PRO	2.9
1	A	95	PHE	2.9

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Mol	Chain	Res	Type	RSRZ
1	A	175	PRO	2.9
1	A	91	TYR	2.9
2	B	135	LEU	2.9
2	B	156	LYS	2.9
2	B	141	PRO	2.9
2	B	113	PRO	2.8
3	C	490	PRO	2.8
3	C	176	ASN	2.8
2	B	41	GLY	2.7
2	B	197	THR	2.7
2	B	159	VAL	2.7
2	B	196	VAL	2.7
3	C	50	THR	2.7
1	A	225	VAL	2.7
2	B	174	ALA	2.6
3	C	39	TYR	2.6
3	C	211	PRO	2.6
5	E	10	GLU	2.6
1	A	7	SER	2.5
1	A	205	THR	2.5
2	B	98	PHE	2.5
5	E	133	ALA	2.5
4	D	546	SER	2.5
2	B	12	SER	2.5
3	C	88	ASN	2.5
1	A	126	PRO	2.5
2	B	43	ALA	2.5
2	B	144	VAL	2.5
3	C	314	PHE	2.4
1	A	142	CYS	2.4
1	A	90	TYR	2.4
3	C	167	PHE	2.4
1	A	45	LEU	2.4
1	A	103	TRP	2.4
2	B	143	ALA	2.4
1	A	143	LEU	2.4
1	A	144	VAL	2.4
1	A	187	LEU	2.3
2	B	42	LYS	2.3
1	A	35(A)	TRP	2.3
1	A	100(K)	VAL	2.3
3	C	209	PHE	2.3

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Mol	Chain	Res	Type	RSRZ
3	C	142	ARG	2.3
2	B	146	VAL	2.3
1	A	127	SER	2.3
2	B	44	PRO	2.3
4	D	586	SER	2.2
3	C	501	ARG	2.2
6	F	181	LEU	2.2
5	E	230	VAL	2.2
2	B	112	ALA	2.2
3	C	45	TRP	2.2
5	E	128	ILE	2.2
2	B	147	ALA	2.2
5	E	231	GLU	2.2
6	F	66	ALA	2.2
6	F	130	ALA	2.1
3	C	494	ALA	2.1
5	E	202	THR	2.1
3	C	212	ILE	2.1
5	E	93	ASP	2.1
5	E	177	ALA	2.1
2	B	180	SER	2.1
4	D	523	LEU	2.1
1	A	154	VAL	2.1
1	A	201	GLN	2.1
1	A	113	SER	2.1
1	A	198	LEU	2.1
3	C	332	SER	2.1
1	A	196	SER	2.1
1	A	96	GLY	2.1
5	E	229	LYS	2.1
1	A	5	GLN	2.1
2	B	142	GLY	2.0
1	A	6	GLU	2.0
2	B	19	ILE	2.0
5	E	213	TYR	2.0
5	E	200	VAL	2.0

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

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

6.3 Carbohydrates

There are no carbohydrates 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. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. 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	LLDF	B-factors(Å ²)	Q<0.9
9	MAN	C	667	11/12	0.64	0.48	5.95	264,264,264,264	0
8	BMA	C	659	11/12	0.61	0.69	5.35	249,249,249,249	0
7	NAG	C	603	14/15	0.36	0.55	3.16	301,301,301,301	0
7	NAG	C	657	14/15	0.76	0.57	2.06	254,254,254,254	0
9	MAN	C	664	11/12	0.91	0.45	1.70	238,238,238,238	0
7	NAG	C	619	14/15	0.17	0.79	1.66	326,326,326,326	0
7	NAG	C	620	14/15	0.77	0.32	0.65	297,297,297,297	0
7	NAG	C	643	14/15	0.61	0.43	0.21	302,302,302,302	0
7	NAG	C	630	14/15	0.78	0.40	0.10	296,296,296,296	0
7	NAG	D	701	14/15	0.75	0.26	-0.11	212,212,212,212	0
9	MAN	C	662	11/12	0.80	0.32	-0.15	257,257,257,257	0
7	NAG	C	638	14/15	0.85	0.40	-0.20	276,276,276,276	0
9	MAN	C	628	11/12	0.60	0.27	-0.26	294,294,294,294	0
9	MAN	C	666	11/12	0.82	0.30	-0.28	235,235,235,235	0
9	MAN	C	661	11/12	0.88	0.24	-0.48	248,248,248,248	0
7	NAG	C	606	14/15	0.97	0.18	-0.61	272,272,272,272	0
7	NAG	C	611	14/15	0.92	0.17	-0.85	261,261,261,261	0
7	NAG	C	612	14/15	0.90	0.16	-0.98	259,259,259,259	0
9	MAN	C	629	11/12	0.87	0.13	-1.07	295,295,295,295	0
9	MAN	C	623	11/12	0.96	0.11	-2.39	284,284,284,284	0
7	NAG	C	607	14/15	0.93	0.28	-	272,272,272,272	0
8	BMA	C	650	11/12	0.73	0.37	-	271,271,271,271	0
9	MAN	C	633	11/12	0.92	0.21	-	298,298,298,298	0
9	MAN	C	634	11/12	0.84	0.39	-	305,305,305,305	0
7	NAG	C	652	14/15	0.67	0.29	-	343,343,343,343	0
7	NAG	C	621	14/15	0.86	0.35	-	305,305,305,305	0
8	BMA	C	613	11/12	0.81	0.10	-	273,273,273,273	0
7	NAG	C	658	14/15	0.86	0.54	-	250,250,250,250	0
9	MAN	C	615	11/12	0.88	0.37	-	293,293,293,293	0
7	NAG	C	648	14/15	0.82	0.32	-	270,270,270,270	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
9	MAN	C	647	11/12	0.79	0.32	-	369,369,369,369	0
9	MAN	C	663	11/12	0.86	0.57	-	244,244,244,244	0
9	MAN	D	704	11/12	0.84	0.38	-	247,247,247,247	0
7	NAG	C	655	14/15	0.79	0.45	-	324,324,324,324	0
7	NAG	C	605	14/15	0.56	0.53	-	329,329,329,329	0
9	MAN	C	617	11/12	0.81	0.35	-	305,305,305,305	0
9	MAN	C	626	11/12	0.80	0.27	-	303,303,303,303	0
8	BMA	C	656	11/12	0.44	0.37	-	334,334,334,334	0
8	BMA	C	653	11/12	0.72	0.30	-	363,363,363,363	0
7	NAG	C	604	14/15	0.51	0.52	-	318,318,318,318	0
8	BMA	C	640	11/12	0.86	0.65	-	314,314,314,314	0
8	BMA	D	703	11/12	0.76	0.19	-	227,227,227,227	0
7	NAG	C	644	14/15	0.73	0.45	-	330,330,330,330	0
7	NAG	C	610	14/15	0.85	0.31	-	318,318,318,318	0
9	MAN	C	622	11/12	0.90	0.20	-	290,290,290,290	0
8	BMA	C	645	11/12	0.73	0.37	-	354,354,354,354	0
9	MAN	C	642	11/12	0.35	1.05	-	321,321,321,321	0
9	MAN	C	618	11/12	0.91	0.18	-	311,311,311,311	0
9	MAN	C	635	11/12	0.93	0.24	-	308,308,308,308	0
7	NAG	C	601	14/15	0.86	0.34	-	318,318,318,318	0
9	MAN	C	616	11/12	0.76	0.24	-	292,292,292,292	0
9	MAN	C	641	11/12	0.78	0.72	-	314,314,314,314	0
7	NAG	C	649	14/15	0.81	0.29	-	270,270,270,270	0
7	NAG	C	631	14/15	0.82	0.26	-	295,295,295,295	0
7	NAG	D	702	14/15	0.88	0.18	-	219,219,219,219	0
9	MAN	C	636	11/12	0.93	0.19	-	317,317,317,317	0
7	NAG	C	651	14/15	0.70	0.37	-	311,311,311,311	0
7	NAG	C	639	14/15	0.90	0.47	-	296,296,296,296	0
9	MAN	C	637	11/12	0.90	0.28	-	323,323,323,323	0
9	MAN	C	614	11/12	0.92	0.13	-	281,281,281,281	0
9	MAN	C	665	11/12	0.71	0.74	-	253,253,253,253	0
9	MAN	C	627	11/12	0.84	0.34	-	301,301,301,301	0
9	MAN	C	660	11/12	0.92	0.29	-	242,242,242,242	0
7	NAG	C	609	14/15	0.80	0.34	-	292,292,292,292	0
7	NAG	C	602	14/15	0.62	0.43	-	325,325,325,325	0
7	NAG	C	654	14/15	0.52	0.42	-	315,315,315,315	0
7	NAG	C	608	14/15	0.85	0.33	-	275,275,275,275	0
9	MAN	C	646	11/12	0.88	0.26	-	372,372,372,372	0
7	NAG	D	705	14/15	0.84	0.30	-	225,225,225,225	0
9	MAN	C	625	11/12	0.92	0.48	-	296,296,296,296	0
8	BMA	C	632	11/12	0.93	0.14	-	299,299,299,299	0
8	BMA	C	624	11/12	0.72	0.31	-	300,300,300,300	0

6.5 Other polymers

There are no such residues in this entry.