



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 10, 2026 – 05:10 AM UTC

PDB ID : 5CZA / pdb_00005cza
Title : Yeast 20S proteasome beta5-D166N mutant
Authors : Huber, E.M.; Groll, M.
Deposited on : 2015-07-31
Resolution : 2.50 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:

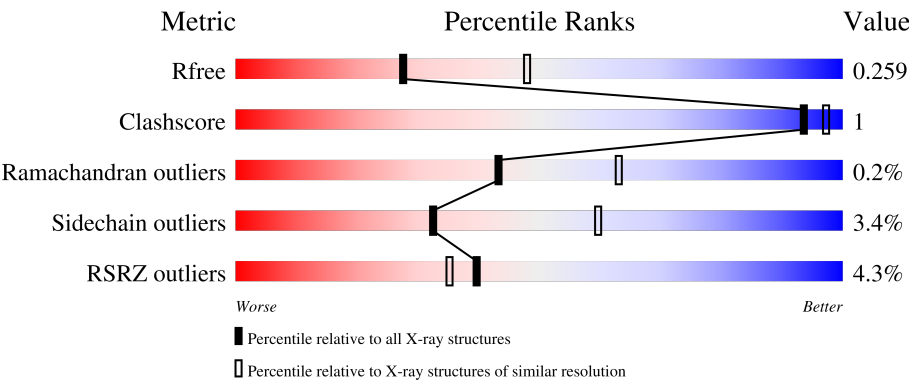
MolProbity	:	4-5-2 with Phenix2.0
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)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

1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:
X-RAY DIFFRACTION

The reported resolution of this entry is 2.50 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	5829 (2.50-2.50)
Clashscore	190562	6492 (2.50-2.50)
Ramachandran outliers	187476	6378 (2.50-2.50)
Sidechain outliers	187428	6380 (2.50-2.50)
RSRZ outliers	180081	5833 (2.50-2.50)

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	250	4% 97% .
1	O	250	4% 97% .
2	B	258	5% 87% 7% 5%
2	P	258	5% 88% 6% 5%
3	C	254	9% 87% 6% 6%

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Mol	Chain	Length	Quality of chain
3	Q	254	
4	D	260	
4	R	260	
5	E	234	
5	S	234	
6	F	288	
6	T	288	
7	G	252	
7	U	252	
8	H	232	
8	V	232	
9	I	205	
9	W	205	
10	J	198	
10	X	198	
11	K	212	
11	Y	212	
12	L	222	
12	Z	222	
13	M	246	
13	a	246	
14	N	196	
14	b	196	

2 Entry composition

There are 17 unique types of molecules in this entry. The entry contains 50531 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 Proteasome subunit alpha type-2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	250	Total	C	N	O	S	0	0	0
			1915	1219	315	377	4			
1	O	250	Total	C	N	O	S	0	0	0
			1915	1219	315	377	4			

- Molecule 2 is a protein called Proteasome subunit alpha type-3.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	244	Total	C	N	O	S	0	0	0
			1904	1201	321	379	3			
2	P	244	Total	C	N	O	S	0	0	0
			1904	1201	321	379	3			

- Molecule 3 is a protein called Proteasome subunit alpha type-4.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	C	240	Total	C	N	O	S	0	0	0
			1881	1176	329	372	4			
3	Q	240	Total	C	N	O	S	0	0	0
			1881	1176	329	372	4			

- Molecule 4 is a protein called Proteasome subunit alpha type-5.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
4	D	235	Total	C	N	O	S	0	0	0
			1813	1136	304	366	7			
4	R	235	Total	C	N	O	S	0	0	0
			1813	1136	304	366	7			

- Molecule 5 is a protein called Proteasome subunit alpha type-6.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
5	E	231	Total	C	N	O	S	0	0	0
			1773	1114	307	348	4			
5	S	231	Total	C	N	O	S	0	0	0
			1773	1114	307	348	4			

- Molecule 6 is a protein called Probable proteasome subunit alpha type-7.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
6	F	243	Total	C	N	O	S	0	0	0
			1892	1203	329	356	4			
6	T	243	Total	C	N	O	S	0	0	0
			1892	1203	329	356	4			

- Molecule 7 is a protein called Proteasome subunit alpha type-1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
7	G	241	Total	C	N	O	S	0	0	0
			1907	1214	320	365	8			
7	U	241	Total	C	N	O	S	0	0	0
			1907	1214	320	365	8			

- Molecule 8 is a protein called Proteasome subunit beta type-2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
8	H	226	Total	C	N	O	S	0	0	0
			1719	1082	298	332	7			
8	V	226	Total	C	N	O	S	0	0	0
			1719	1082	298	332	7			

- Molecule 9 is a protein called Proteasome subunit beta type-3.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
9	I	204	Total	C	N	O	S	0	0	0
			1581	1010	258	305	8			
9	W	204	Total	C	N	O	S	0	0	0
			1581	1010	258	305	8			

- Molecule 10 is a protein called Proteasome subunit beta type-4.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
10	J	195	Total	C	N	O	S	0	0	0
			1561	992	264	299	6			

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
10	X	195	Total	C	N	O	S	0	0	0
			1561	992	264	299	6			

- Molecule 11 is a protein called Proteasome subunit beta type-5.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
11	K	212	Total	C	N	O	S	0	0	0
			1644	1045	281	311	7			
11	Y	212	Total	C	N	O	S	0	0	0
			1644	1045	281	311	7			

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
K	168	ASN	ASP	engineered mutation	UNP P30656
Y	168	ASN	ASP	engineered mutation	UNP P30656

- Molecule 12 is a protein called Proteasome subunit beta type-6.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
12	L	222	Total	C	N	O	S	0	0	0
			1757	1115	303	335	4			
12	Z	222	Total	C	N	O	S	0	0	0
			1757	1115	303	335	4			

- Molecule 13 is a protein called Proteasome subunit beta type-7.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
13	M	229	Total	C	N	O	S	0	0	0
			1790	1133	306	344	7			
13	a	232	Total	C	N	O	S	0	0	0
			1815	1148	311	349	7			

- Molecule 14 is a protein called Proteasome subunit beta type-1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
14	N	196	Total	C	N	O	S	0	0	0
			1512	955	250	300	7			
14	b	196	Total	C	N	O	S	0	0	0
			1512	955	250	300	7			

- Molecule 15 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
15	G	1	Total Mg 1 1	0	0
15	I	2	Total Mg 2 2	0	0
15	K	1	Total Mg 1 1	0	0
15	L	1	Total Mg 1 1	0	0
15	N	1	Total Mg 1 1	0	0
15	W	1	Total Mg 1 1	0	0
15	Z	1	Total Mg 1 1	0	0

- Molecule 16 is CHLORIDE ION (CCD ID: CL) (formula: Cl).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
16	G	1	Total Cl 1 1	0	0
16	U	1	Total Cl 1 1	0	0

- Molecule 17 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
17	A	42	Total O 42 42	0	0
17	B	39	Total O 39 39	0	0
17	C	31	Total O 31 31	0	0
17	D	39	Total O 39 39	0	0
17	E	29	Total O 29 29	0	0
17	F	45	Total O 45 45	0	0
17	G	52	Total O 52 52	0	0
17	H	55	Total O 55 55	0	0
17	I	47	Total O 47 47	0	0

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
17	J	51	Total 51	O 51	0	0
17	K	50	Total 50	O 50	0	0
17	L	56	Total 56	O 56	0	0
17	M	62	Total 62	O 62	0	0
17	N	50	Total 50	O 50	0	0
17	O	23	Total 23	O 23	0	0
17	P	30	Total 30	O 30	0	0
17	Q	28	Total 28	O 28	0	0
17	R	23	Total 23	O 23	0	0
17	S	21	Total 21	O 21	0	0
17	T	33	Total 33	O 33	0	0
17	U	52	Total 52	O 52	0	0
17	V	35	Total 35	O 35	0	0
17	W	45	Total 45	O 45	0	0
17	X	29	Total 29	O 29	0	0
17	Y	61	Total 61	O 61	0	0
17	Z	56	Total 56	O 56	0	0
17	a	67	Total 67	O 67	0	0
17	b	47	Total 47	O 47	0	0

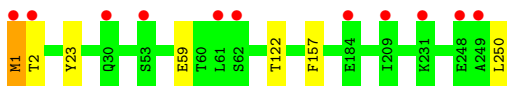
3 Residue-property plots

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

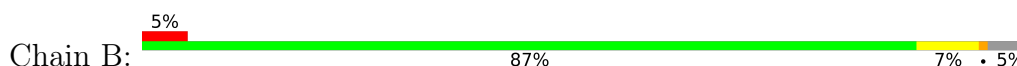
- Molecule 1: Proteasome subunit alpha type-2



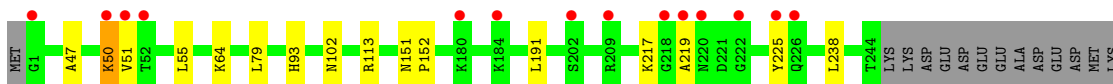
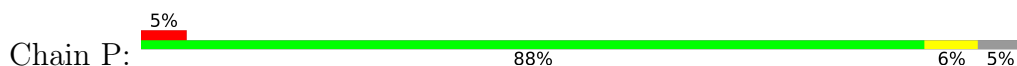
- Molecule 1: Proteasome subunit alpha type-2



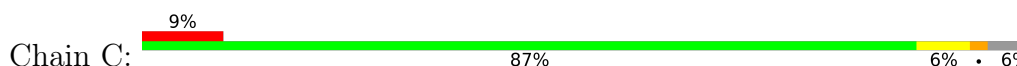
- Molecule 2: Proteasome subunit alpha type-3

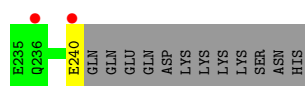


- Molecule 2: Proteasome subunit alpha type-3

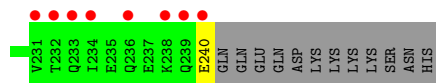
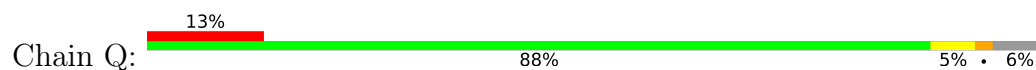


- Molecule 3: Proteasome subunit alpha type-4

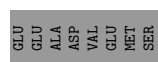
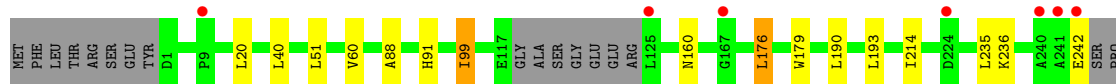
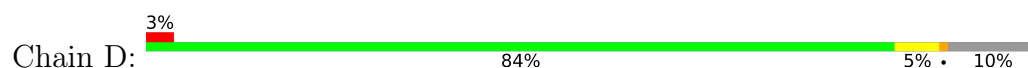




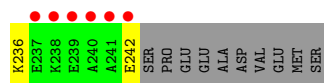
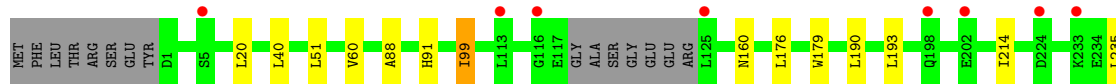
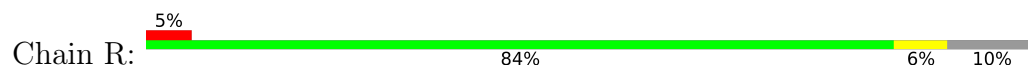
• Molecule 3: Proteasome subunit alpha type-4



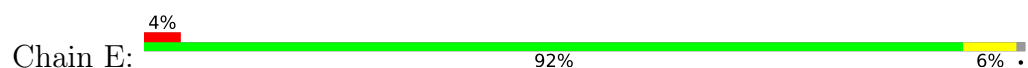
• Molecule 4: Proteasome subunit alpha type-5



• Molecule 4: Proteasome subunit alpha type-5

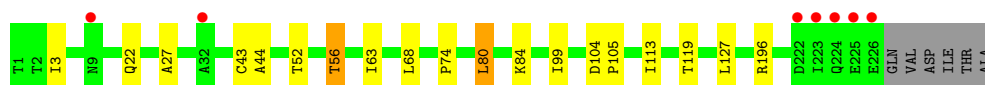
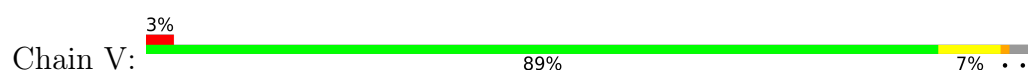


• Molecule 5: Proteasome subunit alpha type-6

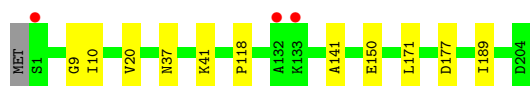


• Molecule 5: Proteasome subunit alpha type-6

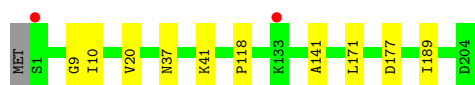




• Molecule 9: Proteasome subunit beta type-3



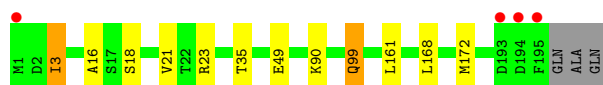
• Molecule 9: Proteasome subunit beta type-3



• Molecule 10: Proteasome subunit beta type-4



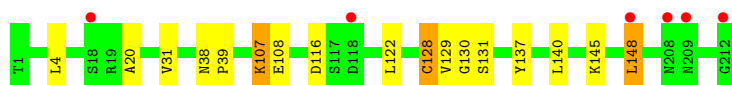
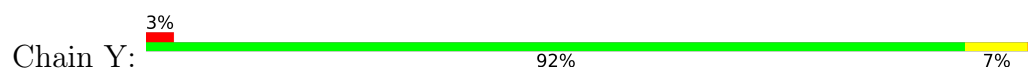
• Molecule 10: Proteasome subunit beta type-4



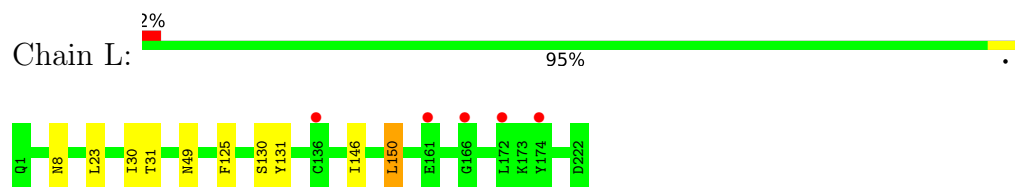
• Molecule 11: Proteasome subunit beta type-5



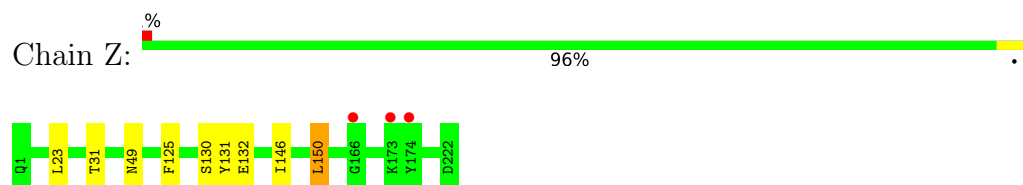
• Molecule 11: Proteasome subunit beta type-5



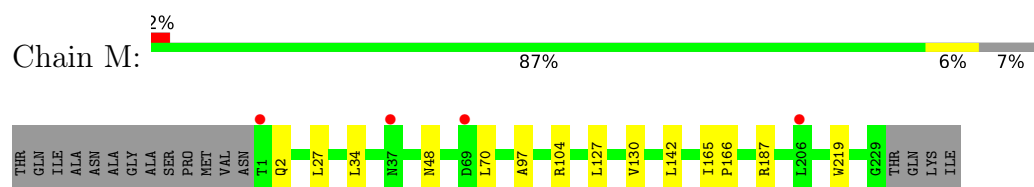
- Molecule 12: Proteasome subunit beta type-6



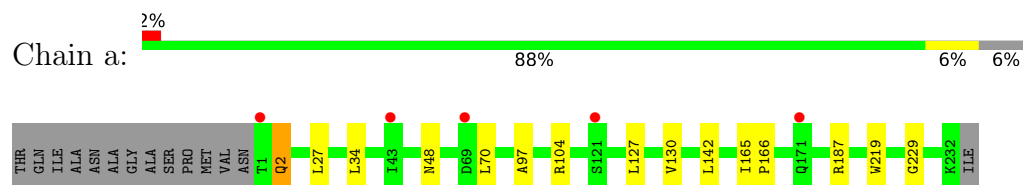
- Molecule 12: Proteasome subunit beta type-6



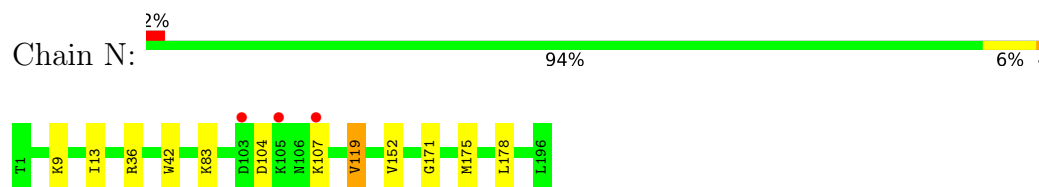
- Molecule 13: Proteasome subunit beta type-7



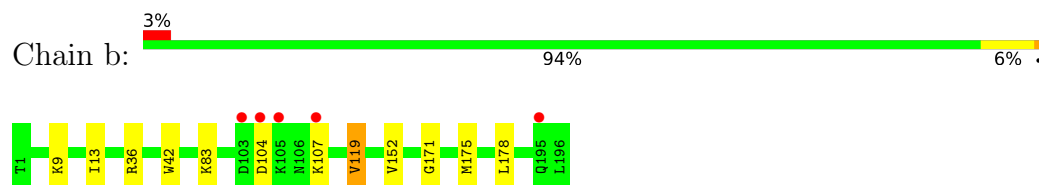
- Molecule 13: Proteasome subunit beta type-7



- Molecule 14: Proteasome subunit beta type-1



- Molecule 14: Proteasome subunit beta type-1



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	134.77Å 301.43Å 144.14Å 90.00° 112.84° 90.00°	Depositor
Resolution (Å)	15.00 – 2.50 15.00 – 2.50	Depositor EDS
% Data completeness (in resolution range)	97.5 (15.00-2.50) 97.0 (15.00-2.50)	Depositor EDS
R_{merge}	0.06	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.83 (at 2.51Å)	Xtriage
Refinement program	REFMAC 5.7.0032	Depositor
R, R_{free}	0.206 , 0.224 (Not available) , 0.259	Depositor DCC
R_{free} test set	17654 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å ²)	45.3	Xtriage
Anisotropy	0.067	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 53.3	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	50531	wwPDB-VP
Average B, all atoms (Å ²)	55.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.20% 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: CL, MG

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	0.38	0/1952	0.67	0/2642
1	O	0.38	0/1952	0.67	0/2642
2	B	0.39	0/1934	0.67	0/2618
2	P	0.39	0/1934	0.67	0/2618
3	C	0.38	0/1910	0.68	1/2586 (0.0%)
3	Q	0.38	0/1910	0.69	1/2586 (0.0%)
4	D	0.37	0/1837	0.65	0/2475
4	R	0.37	0/1837	0.65	0/2475
5	E	0.38	0/1800	0.64	0/2433
5	S	0.38	0/1800	0.64	0/2433
6	F	0.38	0/1932	0.69	0/2609
6	T	0.38	0/1932	0.69	0/2609
7	G	0.37	0/1945	0.66	0/2634
7	U	0.37	0/1945	0.67	0/2634
8	H	0.39	0/1750	0.65	0/2373
8	V	0.36	0/1750	0.65	0/2373
9	I	0.36	0/1611	0.66	0/2174
9	W	0.36	0/1611	0.66	0/2174
10	J	0.39	0/1589	0.66	0/2142
10	X	0.39	0/1589	0.65	0/2142
11	K	0.43	1/1681 (0.1%)	0.67	0/2274
11	Y	0.43	2/1681 (0.1%)	0.67	0/2274
12	L	0.36	0/1795	0.65	0/2420
12	Z	0.38	0/1795	0.65	0/2420
13	M	0.38	0/1821	0.67	0/2470
13	a	0.38	0/1846	0.67	0/2503
14	N	0.36	0/1541	0.64	0/2087
14	b	0.36	0/1541	0.64	0/2087
All	All	0.38	3/50221 (0.0%)	0.66	2/67907 (0.0%)

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
11	Y	130	GLY	C-O	-6.12	1.18	1.23
11	K	130	GLY	C-O	-5.98	1.17	1.23
11	Y	129	VAL	C-O	-5.67	1.18	1.24

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	Q	201	VAL	N-CA-C	6.13	116.29	110.53
3	C	201	VAL	N-CA-C	6.11	116.28	110.53

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	1915	0	1929	1	0
1	O	1915	0	1929	2	0
2	B	1904	0	1904	9	0
2	P	1904	0	1904	8	0
3	C	1881	0	1895	7	0
3	Q	1881	0	1895	5	0
4	D	1813	0	1797	5	0
4	R	1813	0	1797	4	0
5	E	1773	0	1775	6	0
5	S	1773	0	1775	3	0
6	F	1892	0	1883	4	0
6	T	1892	0	1883	3	0
7	G	1907	0	1901	4	0
7	U	1907	0	1901	5	0
8	H	1719	0	1719	10	0
8	V	1719	0	1719	11	0
9	I	1581	0	1574	6	0
9	W	1581	0	1574	5	0
10	J	1561	0	1569	4	0
10	X	1561	0	1569	6	0
11	K	1644	0	1597	7	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
11	Y	1644	0	1597	6	0
12	L	1757	0	1711	3	0
12	Z	1757	0	1711	2	0
13	M	1790	0	1793	5	0
13	a	1815	0	1821	6	0
14	N	1512	0	1481	6	0
14	b	1512	0	1481	6	0
15	G	1	0	0	0	0
15	I	2	0	0	0	0
15	K	1	0	0	0	0
15	L	1	0	0	0	0
15	N	1	0	0	0	0
15	W	1	0	0	0	0
15	Z	1	0	0	0	0
16	G	1	0	0	0	0
16	U	1	0	0	0	0
17	A	42	0	0	0	0
17	B	39	0	0	1	0
17	C	31	0	0	0	0
17	D	39	0	0	0	0
17	E	29	0	0	0	0
17	F	45	0	0	0	0
17	G	52	0	0	0	0
17	H	55	0	0	0	0
17	I	47	0	0	0	0
17	J	51	0	0	0	0
17	K	50	0	0	1	0
17	L	56	0	0	0	0
17	M	62	0	0	0	0
17	N	50	0	0	0	0
17	O	23	0	0	0	0
17	P	30	0	0	1	0
17	Q	28	0	0	0	0
17	R	23	0	0	0	0
17	S	21	0	0	0	0
17	T	33	0	0	0	0
17	U	52	0	0	0	0
17	V	35	0	0	0	0
17	W	45	0	0	0	0
17	X	29	0	0	0	0
17	Y	61	0	0	0	0
17	Z	56	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
17	a	67	0	0	1	0
17	b	47	0	0	0	0
All	All	50531	0	49084	135	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 1.

All (135) 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)
8:V:52:THR:O	8:V:56:THR:OG1	2.04	0.75
8:H:52:THR:O	8:H:56:THR:OG1	2.05	0.73
14:N:152:VAL:HA	14:N:175:MET:HE1	1.85	0.59
14:b:152:VAL:HA	14:b:175:MET:HE1	1.84	0.59
2:P:217:LYS:C	2:P:219:ALA:H	2.13	0.56
8:V:80:LEU:HD13	8:V:119:THR:HG21	1.86	0.56
2:B:217:LYS:C	2:B:219:ALA:H	2.13	0.55
10:J:16:ALA:HB2	10:J:161:LEU:HD21	1.89	0.55
7:G:68:ARG:HH12	14:N:36:ARG:HH22	1.55	0.55
10:X:16:ALA:HB2	10:X:161:LEU:HD21	1.89	0.55
1:A:1:MET:HG3	6:F:122:TYR:CZ	2.43	0.54
8:V:3:ILE:HG22	8:V:99:ILE:HD12	1.89	0.54
2:P:93:HIS:HB3	17:P:301:HOH:O	2.08	0.51
3:Q:201:VAL:O	3:Q:202:GLN:CB	2.58	0.51
14:N:83:LYS:HG3	14:N:119:VAL:CG2	2.41	0.51
2:B:93:HIS:HB3	17:B:301:HOH:O	2.10	0.51
8:H:22:GLN:HG3	8:H:27:ALA:HB2	1.93	0.51
14:b:83:LYS:HG3	14:b:119:VAL:CG2	2.41	0.51
3:C:201:VAL:O	3:C:202:GLN:CB	2.58	0.50
7:U:23:PHE:O	7:U:26:THR:HB	2.11	0.50
8:V:22:GLN:HG3	8:V:27:ALA:HB2	1.94	0.50
8:H:3:ILE:HG13	8:H:99:ILE:HD12	1.94	0.50
7:G:23:PHE:O	7:G:26:THR:HB	2.12	0.50
2:P:47:ALA:HB1	2:P:64:LYS:HD2	1.94	0.50
3:Q:51:LYS:O	3:Q:52:LEU:HB2	2.12	0.49
2:B:47:ALA:HB1	2:B:64:LYS:HD2	1.94	0.49
3:C:51:LYS:O	3:C:52:LEU:HB2	2.12	0.48
3:C:160:GLN:HE21	3:C:160:GLN:HA	1.78	0.48
9:W:9:GLY:HA3	9:W:41:LYS:HE2	1.96	0.48
9:I:9:GLY:HA3	9:I:41:LYS:HE2	1.96	0.48
14:N:13:ILE:HG21	14:N:175:MET:HE2	1.96	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:12:PHE:H	3:C:17:GLN:HE22	1.60	0.47
8:V:3:ILE:HG21	8:V:44:ALA:HB3	1.95	0.47
11:K:128:CYS:HB2	11:K:137:TYR:CZ	2.49	0.47
9:I:10:ILE:HG21	9:I:141:ALA:HB3	1.97	0.47
2:P:50:LYS:O	2:P:51:VAL:C	2.57	0.47
3:Q:160:GLN:HE21	3:Q:160:GLN:HA	1.78	0.46
11:K:107:LYS:NZ	17:K:401:HOH:O	2.47	0.46
2:B:50:LYS:O	2:B:51:VAL:C	2.58	0.46
11:Y:20:ALA:HB2	11:Y:31:VAL:HG21	1.98	0.46
11:K:20:ALA:HB2	11:K:31:VAL:HG21	1.98	0.46
9:W:10:ILE:HG21	9:W:141:ALA:HB3	1.97	0.46
4:R:91:HIS:HB3	4:R:99:ILE:HG22	1.98	0.46
4:R:160:ASN:HB3	4:R:179:TRP:CE2	2.51	0.45
14:b:13:ILE:HG21	14:b:175:MET:HE2	1.97	0.45
11:Y:128:CYS:HB2	11:Y:137:TYR:CZ	2.51	0.45
4:D:91:HIS:HB3	4:D:99:ILE:HG22	1.99	0.45
5:S:87:LEU:HD21	5:S:107:ALA:HB1	1.98	0.45
14:b:36:ARG:HG3	14:b:42:TRP:CE2	2.51	0.45
3:C:35:LYS:HG2	3:C:158:SER:O	2.17	0.45
3:C:149:GLU:HB2	3:C:150:PRO:HD2	1.99	0.45
3:Q:149:GLU:HB2	3:Q:150:PRO:HD2	1.99	0.45
4:D:88:ALA:HA	4:D:99:ILE:HG21	1.99	0.45
14:N:36:ARG:HG3	14:N:42:TRP:CE2	2.51	0.45
4:R:91:HIS:HB3	4:R:99:ILE:CG2	2.47	0.45
8:V:104:ASP:HB2	8:V:105:PRO:HD2	1.99	0.45
4:D:91:HIS:HB3	4:D:99:ILE:CG2	2.47	0.44
4:D:160:ASN:HB3	4:D:179:TRP:CE2	2.52	0.44
10:X:3:ILE:HG23	10:X:18:SER:HB3	1.98	0.44
13:a:2:GLN:NE2	17:a:302:HOH:O	2.51	0.44
5:E:87:LEU:HD21	5:E:107:ALA:HB1	1.99	0.44
8:H:104:ASP:HB2	8:H:105:PRO:HD2	1.99	0.44
1:O:1:MET:HG3	6:T:122:TYR:CZ	2.53	0.44
4:R:88:ALA:HA	4:R:99:ILE:HG21	2.00	0.44
8:V:63:ILE:HG23	8:V:74:PRO:HB3	2.00	0.44
10:J:3:ILE:HG23	10:J:18:SER:HB3	1.99	0.44
8:H:63:ILE:HG23	8:H:74:PRO:HB3	2.00	0.44
3:Q:35:LYS:HG2	3:Q:158:SER:O	2.17	0.44
11:K:107:LYS:HG3	11:K:108:GLU:HG3	2.00	0.44
5:E:175:LEU:HA	5:E:178:PHE:CE2	2.53	0.43
8:H:43:CYS:SG	8:H:56:THR:HG23	2.58	0.43
8:H:196:ARG:NH2	9:I:150:GLU:OE2	2.51	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:S:175:LEU:HA	5:S:178:PHE:CE2	2.53	0.43
6:T:198:LEU:HD12	6:T:243:ILE:HG22	2.00	0.43
11:Y:107:LYS:HG3	11:Y:108:GLU:HG3	2.00	0.43
13:a:27:LEU:HD21	13:a:34:LEU:HD22	2.01	0.43
10:J:21:VAL:HG11	11:K:122:LEU:HD11	2.00	0.43
11:K:38:ASN:HB2	11:K:39:PRO:CD	2.49	0.43
2:B:50:LYS:HD3	2:B:50:LYS:HA	1.87	0.43
11:Y:38:ASN:HB2	11:Y:39:PRO:CD	2.49	0.43
2:B:151:ASN:HB2	2:B:152:PRO:CD	2.49	0.43
10:J:49:GLU:HB2	10:J:99:GLN:HB3	2.00	0.43
2:P:217:LYS:C	2:P:219:ALA:N	2.76	0.43
5:S:12:PHE:H	6:T:19:GLN:HE22	1.66	0.43
10:X:21:VAL:HG11	11:Y:122:LEU:HD11	2.01	0.43
8:H:43:CYS:SG	8:H:56:THR:CG2	3.07	0.42
9:I:20:VAL:HG13	9:I:118:PRO:HB3	2.01	0.42
9:I:141:ALA:HB2	9:I:177:ASP:HB2	2.01	0.42
13:M:127:LEU:HG	13:M:142:LEU:HD12	2.01	0.42
8:H:3:ILE:HD11	8:H:127:LEU:HB3	2.01	0.42
13:M:27:LEU:HD21	13:M:34:LEU:HD22	2.01	0.42
6:F:198:LEU:HD12	6:F:243:ILE:HG22	2.00	0.42
7:U:68:ARG:HH12	14:b:36:ARG:HH22	1.67	0.42
10:X:49:GLU:HB2	10:X:99:GLN:HB3	2.00	0.42
4:D:176:LEU:HD22	5:E:55:LEU:CD2	2.49	0.42
8:V:43:CYS:SG	8:V:56:THR:HG23	2.59	0.42
11:K:145:LYS:HB2	11:K:148:LEU:HD13	2.02	0.42
5:E:12:PHE:H	6:F:19:GLN:HE22	1.67	0.42
9:W:20:VAL:HG13	9:W:118:PRO:HB3	2.01	0.42
9:W:20:VAL:HG23	9:W:189:ILE:HB	2.02	0.42
8:V:43:CYS:SG	8:V:56:THR:CG2	3.08	0.42
11:Y:145:LYS:HB2	11:Y:148:LEU:HD13	2.02	0.41
7:U:78:ILE:N	7:U:79:PRO:CD	2.83	0.41
7:G:78:ILE:N	7:G:79:PRO:CD	2.83	0.41
8:V:104:ASP:HB2	8:V:105:PRO:CD	2.50	0.41
2:B:219:ALA:HB2	2:B:225:TYR:HB2	2.01	0.41
2:P:151:ASN:HB2	2:P:152:PRO:CD	2.50	0.41
9:W:141:ALA:HB2	9:W:177:ASP:HB2	2.01	0.41
7:G:73:VAL:HG12	7:G:133:THR:HB	2.01	0.41
8:H:104:ASP:HB2	8:H:105:PRO:CD	2.50	0.41
2:P:219:ALA:HB2	2:P:225:TYR:HB2	2.01	0.41
13:a:127:LEU:HG	13:a:142:LEU:HD12	2.02	0.41
12:L:8:ASN:HA	12:L:30:ILE:O	2.21	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:M:165:ILE:HB	13:M:166:PRO:HD3	2.03	0.41
7:U:73:VAL:HG12	7:U:133:THR:HB	2.01	0.41
12:Z:125:PHE:CD2	12:Z:131:TYR:HB3	2.56	0.41
2:P:151:ASN:HB2	2:P:152:PRO:HD2	2.03	0.41
12:L:146:ILE:HG22	12:L:150:LEU:HD22	2.03	0.41
13:a:97:ALA:HA	13:a:130:VAL:HG21	2.03	0.41
13:M:97:ALA:HA	13:M:130:VAL:HG21	2.03	0.40
5:E:68:HIS:HE1	5:E:102:LEU:O	2.04	0.40
6:F:123:ASN:HD22	6:F:123:ASN:C	2.30	0.40
12:L:125:PHE:CD2	12:L:131:TYR:HB3	2.56	0.40
13:M:219:TRP:CH2	14:b:171:GLY:HA2	2.56	0.40
14:N:171:GLY:HA2	13:a:219:TRP:CH2	2.56	0.40
13:a:165:ILE:HB	13:a:166:PRO:HD3	2.04	0.40
2:B:151:ASN:HB2	2:B:152:PRO:HD2	2.02	0.40
1:O:23:TYR:CD1	7:U:12:PRO:HA	2.56	0.40
3:C:147:GLN:NE2	3:C:160:GLN:OE1	2.55	0.40
5:E:77:ALA:N	5:E:78:PRO:CD	2.85	0.40
10:X:23:ARG:HD3	10:X:23:ARG:HA	1.95	0.40
12:Z:146:ILE:HG22	12:Z:150:LEU:HD22	2.03	0.40
9:I:20:VAL:HG23	9:I:189:ILE:HB	2.02	0.40
8:V:84:LYS:HA	8:V:113:ILE:HD11	2.04	0.40
10:X:168:LEU:O	10:X:172:MET:HB2	2.21	0.40

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all 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	248/250 (99%)	239 (96%)	8 (3%)	1 (0%)	30	49
1	O	82/250 (33%)	79 (96%)	2 (2%)	1 (1%)	10	20
2	B	242/258 (94%)	236 (98%)	2 (1%)	4 (2%)	7	13

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	P	8/258 (3%)	8 (100%)	0	0	100	100
3	C	238/254 (94%)	232 (98%)	3 (1%)	3 (1%)	9	18
3	Q	108/254 (42%)	107 (99%)	1 (1%)	0	100	100
4	D	32/260 (12%)	31 (97%)	1 (3%)	0	100	100
4	R	68/260 (26%)	67 (98%)	1 (2%)	0	100	100
6	F	129/288 (45%)	127 (98%)	2 (2%)	0	100	100
7	G	239/252 (95%)	237 (99%)	2 (1%)	0	100	100
7	U	18/252 (7%)	18 (100%)	0	0	100	100
8	H	224/232 (97%)	219 (98%)	5 (2%)	0	100	100
8	V	116/232 (50%)	113 (97%)	3 (3%)	0	100	100
9	I	202/205 (98%)	196 (97%)	6 (3%)	0	100	100
9	W	121/205 (59%)	116 (96%)	5 (4%)	0	100	100
10	J	160/198 (81%)	155 (97%)	5 (3%)	0	100	100
10	X	193/198 (98%)	188 (97%)	5 (3%)	0	100	100
11	K	210/212 (99%)	206 (98%)	4 (2%)	0	100	100
11	Y	210/212 (99%)	206 (98%)	4 (2%)	0	100	100
12	L	220/222 (99%)	215 (98%)	5 (2%)	0	100	100
12	Z	220/222 (99%)	215 (98%)	5 (2%)	0	100	100
13	M	227/246 (92%)	221 (97%)	6 (3%)	0	100	100
13	a	230/246 (94%)	223 (97%)	6 (3%)	1 (0%)	30	49
14	N	194/196 (99%)	190 (98%)	4 (2%)	0	100	100
14	b	194/196 (99%)	190 (98%)	4 (2%)	0	100	100
All	All	4133/5858 (71%)	4034 (98%)	89 (2%)	10 (0%)	43	63

All (10) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	B	51	VAL
2	B	221	ASP
3	C	202	GLN
1	A	2	THR
2	B	218	GLY
2	B	220	ASN
1	O	2	THR

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Mol	Chain	Res	Type
3	C	205	ALA
3	C	183	PRO
13	a	229	GLY

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	209/209 (100%)	203 (97%)	6 (3%)	37	65
1	O	209/209 (100%)	204 (98%)	5 (2%)	43	70
2	B	203/216 (94%)	196 (97%)	7 (3%)	32	60
2	P	203/216 (94%)	196 (97%)	7 (3%)	32	60
3	C	212/226 (94%)	201 (95%)	11 (5%)	21	42
3	Q	212/226 (94%)	201 (95%)	11 (5%)	21	42
4	D	194/215 (90%)	182 (94%)	12 (6%)	16	34
4	R	194/215 (90%)	182 (94%)	12 (6%)	16	34
5	E	190/193 (98%)	184 (97%)	6 (3%)	34	62
5	S	190/193 (98%)	184 (97%)	6 (3%)	34	62
6	F	201/239 (84%)	194 (96%)	7 (4%)	32	58
6	T	201/239 (84%)	194 (96%)	7 (4%)	32	58
7	G	206/210 (98%)	198 (96%)	8 (4%)	28	55
7	U	206/210 (98%)	198 (96%)	8 (4%)	28	55
8	H	185/190 (97%)	179 (97%)	6 (3%)	34	62
8	V	185/190 (97%)	180 (97%)	5 (3%)	39	67
9	I	172/173 (99%)	170 (99%)	2 (1%)	63	83
9	W	172/173 (99%)	170 (99%)	2 (1%)	63	83
10	J	173/175 (99%)	169 (98%)	4 (2%)	44	72
10	X	173/175 (99%)	169 (98%)	4 (2%)	44	72
11	K	169/169 (100%)	162 (96%)	7 (4%)	27	53

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
11	Y	169/169 (100%)	162 (96%)	7 (4%)	27	53
12	L	185/185 (100%)	180 (97%)	5 (3%)	39	67
12	Z	185/185 (100%)	179 (97%)	6 (3%)	34	62
13	M	195/208 (94%)	190 (97%)	5 (3%)	40	68
13	a	198/208 (95%)	193 (98%)	5 (2%)	42	69
14	N	162/162 (100%)	157 (97%)	5 (3%)	35	62
14	b	162/162 (100%)	157 (97%)	5 (3%)	35	62
All	All	5315/5540 (96%)	5134 (97%)	181 (3%)	32	60

All (181) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	1	MET
1	A	59	GLU
1	A	62	SER
1	A	122	THR
1	A	157	PHE
1	A	250	LEU
2	B	50	LYS
2	B	55	LEU
2	B	79	LEU
2	B	102	ASN
2	B	113	ARG
2	B	191	LEU
2	B	238	LEU
3	C	4	ARG
3	C	38	ASN
3	C	50	LEU
3	C	51	LYS
3	C	52	LEU
3	C	147	GLN
3	C	160	GLN
3	C	169	VAL
3	C	180	LYS
3	C	213	VAL
3	C	240	GLU
4	D	20	LEU
4	D	40	LEU
4	D	51	LEU
4	D	60	VAL

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Mol	Chain	Res	Type
4	D	99	ILE
4	D	176	LEU
4	D	190	LEU
4	D	193	LEU
4	D	214	ILE
4	D	235	LEU
4	D	236	LYS
4	D	242	GLU
5	E	9	THR
5	E	29	LYS
5	E	55	LEU
5	E	71	LEU
5	E	188	LEU
5	E	231	LYS
6	F	123	ASN
6	F	172	LEU
6	F	181	GLU
6	F	201	GLU
6	F	207	ASP
6	F	221	ASN
6	F	240	GLN
7	G	26	THR
7	G	75	ASN
7	G	83	ASN
7	G	115	LEU
7	G	122	ARG
7	G	125	MET
7	G	235	ARG
7	G	236	LEU
8	H	3	ILE
8	H	56	THR
8	H	68	LEU
8	H	80	LEU
8	H	127	LEU
8	H	196	ARG
9	I	37	ASN
9	I	171	LEU
10	J	3	ILE
10	J	35	THR
10	J	90	LYS
10	J	99	GLN
11	K	4	LEU

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Mol	Chain	Res	Type
11	K	107	LYS
11	K	116	ASP
11	K	128	CYS
11	K	131	SER
11	K	140	LEU
11	K	148	LEU
12	L	23	LEU
12	L	31	THR
12	L	49	ASN
12	L	130	SER
12	L	150	LEU
13	M	2	GLN
13	M	48	ASN
13	M	70	LEU
13	M	104	ARG
13	M	187	ARG
14	N	9	LYS
14	N	104	ASP
14	N	107	LYS
14	N	119	VAL
14	N	178	LEU
1	O	1	MET
1	O	59	GLU
1	O	122	THR
1	O	157	PHE
1	O	250	LEU
2	P	50	LYS
2	P	55	LEU
2	P	79	LEU
2	P	102	ASN
2	P	113	ARG
2	P	191	LEU
2	P	238	LEU
3	Q	4	ARG
3	Q	38	ASN
3	Q	50	LEU
3	Q	51	LYS
3	Q	52	LEU
3	Q	147	GLN
3	Q	160	GLN
3	Q	169	VAL
3	Q	180	LYS

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Mol	Chain	Res	Type
3	Q	213	VAL
3	Q	240	GLU
4	R	20	LEU
4	R	40	LEU
4	R	51	LEU
4	R	60	VAL
4	R	99	ILE
4	R	176	LEU
4	R	190	LEU
4	R	193	LEU
4	R	214	ILE
4	R	235	LEU
4	R	236	LYS
4	R	242	GLU
5	S	9	THR
5	S	29	LYS
5	S	55	LEU
5	S	71	LEU
5	S	188	LEU
5	S	231	LYS
6	T	123	ASN
6	T	172	LEU
6	T	181	GLU
6	T	201	GLU
6	T	207	ASP
6	T	221	ASN
6	T	240	GLN
7	U	26	THR
7	U	75	ASN
7	U	83	ASN
7	U	115	LEU
7	U	122	ARG
7	U	125	MET
7	U	235	ARG
7	U	236	LEU
8	V	56	THR
8	V	68	LEU
8	V	80	LEU
8	V	127	LEU
8	V	196	ARG
9	W	37	ASN
9	W	171	LEU

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Mol	Chain	Res	Type
10	X	3	ILE
10	X	35	THR
10	X	90	LYS
10	X	99	GLN
11	Y	4	LEU
11	Y	107	LYS
11	Y	116	ASP
11	Y	128	CYS
11	Y	131	SER
11	Y	140	LEU
11	Y	148	LEU
12	Z	23	LEU
12	Z	31	THR
12	Z	49	ASN
12	Z	130	SER
12	Z	132	GLU
12	Z	150	LEU
13	a	2	GLN
13	a	48	ASN
13	a	70	LEU
13	a	104	ARG
13	a	187	ARG
14	b	9	LYS
14	b	104	ASP
14	b	107	LYS
14	b	119	VAL
14	b	178	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (124) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	94	HIS
1	A	149	GLN
2	B	119	GLN
2	B	123	GLN
2	B	124	HIS
2	B	176	GLN
2	B	220	ASN
2	B	232	GLN
3	C	17	GLN
3	C	116	GLN
3	C	120	GLN

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Mol	Chain	Res	Type
3	C	147	GLN
3	C	160	GLN
4	D	15	GLN
4	D	100	ASN
4	D	225	ASN
5	E	68	HIS
5	E	92	ASN
5	E	99	ASN
5	E	116	GLN
5	E	118	ASN
5	E	120	GLN
5	E	184	ASN
6	F	19	GLN
6	F	86	ASN
6	F	117	GLN
6	F	123	ASN
6	F	143	HIS
7	G	30	ASN
7	G	83	ASN
7	G	114	ASN
7	G	117	GLN
7	G	121	GLN
7	G	175	ASN
7	G	212	ASN
8	H	22	GLN
8	H	86	HIS
9	I	37	ASN
9	I	63	ASN
9	I	88	GLN
9	I	203	GLN
10	J	55	GLN
10	J	63	ASN
10	J	146	HIS
10	J	147	HIS
11	K	9	GLN
11	K	85	ASN
11	K	143	ASN
11	K	168	ASN
11	K	176	ASN
11	K	190	ASN
11	K	208	ASN
12	L	49	ASN

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Mol	Chain	Res	Type
12	L	70	ASN
12	L	79	HIS
12	L	135	GLN
12	L	153	GLN
12	L	155	ASN
12	L	158	ASN
12	L	197	GLN
13	M	48	ASN
13	M	108	ASN
13	M	149	HIS
13	M	194	ASN
13	M	213	GLN
2	P	119	GLN
2	P	123	GLN
2	P	124	HIS
2	P	176	GLN
2	P	232	GLN
3	Q	17	GLN
3	Q	115	GLN
3	Q	116	GLN
3	Q	120	GLN
3	Q	147	GLN
3	Q	160	GLN
4	R	15	GLN
4	R	91	HIS
4	R	100	ASN
4	R	225	ASN
5	S	68	HIS
5	S	92	ASN
5	S	99	ASN
5	S	120	GLN
5	S	184	ASN
6	T	19	GLN
6	T	86	ASN
6	T	117	GLN
6	T	123	ASN
7	U	30	ASN
7	U	114	ASN
7	U	117	GLN
7	U	121	GLN
7	U	166	GLN
7	U	175	ASN

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Mol	Chain	Res	Type
8	V	22	GLN
8	V	66	HIS
8	V	86	HIS
9	W	37	ASN
9	W	63	ASN
9	W	88	GLN
9	W	203	GLN
10	X	10	GLN
10	X	55	GLN
10	X	63	ASN
10	X	146	HIS
10	X	147	HIS
11	Y	9	GLN
11	Y	85	ASN
11	Y	176	ASN
11	Y	208	ASN
12	Z	49	ASN
12	Z	70	ASN
12	Z	79	HIS
12	Z	135	GLN
12	Z	153	GLN
12	Z	155	ASN
12	Z	158	ASN
12	Z	197	GLN
13	a	48	ASN
13	a	108	ASN
13	a	149	HIS
13	a	194	ASN
13	a	213	GLN

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 ⓘ

There are no oligosaccharides in this entry.

5.6 Ligand geometry

Of 10 ligands modelled in this entry, 10 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers

There are no such residues in this entry.

5.8 Polymer linkage issues

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	250/250 (100%)	0.16	10 (4%)	42	38	32, 45, 81, 116	0
1	O	250/250 (100%)	0.23	11 (4%)	39	34	37, 53, 99, 128	0
2	B	244/258 (94%)	0.37	14 (5%)	29	26	31, 51, 91, 143	0
2	P	244/258 (94%)	0.38	14 (5%)	29	26	37, 54, 98, 145	0
3	C	240/254 (94%)	0.46	23 (9%)	13	11	31, 56, 118, 148	0
3	Q	240/254 (94%)	0.79	33 (13%)	6	5	40, 69, 151, 186	0
4	D	235/260 (90%)	0.34	7 (2%)	52	48	38, 57, 89, 131	0
4	R	235/260 (90%)	0.48	14 (5%)	27	24	39, 60, 103, 143	0
5	E	231/234 (98%)	0.34	9 (3%)	43	38	38, 57, 93, 136	0
5	S	231/234 (98%)	0.69	23 (9%)	12	10	44, 68, 108, 151	0
6	F	243/288 (84%)	0.23	17 (6%)	22	20	34, 50, 103, 132	0
6	T	243/288 (84%)	0.49	17 (6%)	22	20	39, 63, 118, 149	0
7	G	241/252 (95%)	0.08	6 (2%)	58	54	26, 46, 80, 131	0
7	U	241/252 (95%)	0.26	16 (6%)	24	21	37, 51, 81, 126	0
8	H	226/232 (97%)	0.18	7 (3%)	51	47	28, 44, 77, 137	0
8	V	226/232 (97%)	0.27	7 (3%)	51	47	35, 49, 80, 153	0
9	I	204/205 (99%)	-0.10	3 (1%)	72	68	28, 40, 69, 92	0
9	W	204/205 (99%)	-0.07	2 (0%)	79	76	31, 42, 73, 95	0
10	J	195/198 (98%)	-0.01	1 (0%)	87	85	29, 44, 70, 122	0
10	X	195/198 (98%)	0.06	4 (2%)	63	59	31, 46, 69, 131	0
11	K	212/212 (100%)	-0.02	3 (1%)	73	70	26, 43, 67, 85	0
11	Y	212/212 (100%)	-0.00	6 (2%)	55	50	32, 45, 69, 89	0
12	L	222/222 (100%)	0.02	5 (2%)	61	57	28, 45, 77, 111	0
12	Z	222/222 (100%)	-0.01	3 (1%)	73	70	29, 44, 78, 114	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2		OWAB(Å ²)	Q<0.9
13	M	229/246 (93%)	-0.05	4 (1%)	69 65	26, 44, 67, 84	0
13	a	232/246 (94%)	-0.01	5 (2%)	62 58	27, 45, 65, 83	0
14	N	196/196 (100%)	-0.15	3 (1%)	72 68	28, 39, 66, 93	0
14	b	196/196 (100%)	-0.06	5 (2%)	57 52	28, 40, 68, 98	0
All	All	6339/6614 (95%)	0.20	272 (4%)	40 35	26, 49, 95, 186	0

All (272) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
3	Q	50	LEU	8.2
8	V	223	ILE	8.1
2	P	218	GLY	6.1
10	X	1	MET	5.9
2	B	219	ALA	5.8
3	Q	205	ALA	5.7
8	H	223	ILE	5.6
2	B	51	VAL	5.3
8	V	224	GLN	5.0
3	Q	49	THR	4.9
10	J	1	MET	4.8
1	O	53	SER	4.5
2	P	219	ALA	4.4
4	D	241	ALA	4.4
6	T	243	ILE	4.3
14	N	103	ASP	4.1
2	P	222	GLY	4.1
3	Q	48	SER	4.1
4	D	240	ALA	4.1
3	C	205	ALA	4.0
1	A	2	THR	4.0
14	b	103	ASP	3.9
2	P	52	THR	3.9
8	H	224	GLN	3.9
3	Q	223	SER	3.8
13	a	69	ASP	3.8
2	B	221	ASP	3.7
1	O	249	ALA	3.7
6	F	202	ASP	3.7
12	L	174	TYR	3.7
2	B	220	ASN	3.6
13	a	1	THR	3.6

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Mol	Chain	Res	Type	RSRZ
5	S	52	ALA	3.6
1	A	1	MET	3.6
6	T	244	ASN	3.6
3	Q	208	ILE	3.5
3	C	236	GLN	3.5
7	U	188	GLU	3.4
11	Y	118	ASP	3.4
5	E	209	ASN	3.4
7	U	222	ASP	3.4
13	M	1	THR	3.4
3	Q	234	ILE	3.4
11	K	208	ASN	3.4
1	O	1	MET	3.3
6	T	14	ASP	3.3
6	T	204	LYS	3.3
3	C	206	LYS	3.3
1	O	2	THR	3.3
6	T	206	LYS	3.3
1	A	62	SER	3.2
5	E	122	TYR	3.2
2	B	52	THR	3.2
5	S	173	ARG	3.2
4	R	224	ASP	3.2
5	S	209	ASN	3.2
7	U	242	GLN	3.1
6	T	178	HIS	3.1
11	Y	208	ASN	3.1
3	C	207	ASN	3.1
2	P	1	GLY	3.1
3	C	203	THR	3.1
5	S	58	TYR	3.1
8	V	222	ASP	3.1
2	B	218	GLY	3.1
7	U	179	LYS	3.0
14	N	107	LYS	3.0
6	F	243	ILE	3.0
3	Q	51	LYS	3.0
3	Q	231	VAL	3.0
5	S	122	TYR	3.0
5	E	54	GLU	3.0
13	M	69	ASP	3.0
5	S	3	ASN	3.0

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Mol	Chain	Res	Type	RSRZ
3	Q	239	GLN	3.0
2	B	243	ILE	2.9
1	O	184	GLU	2.9
6	F	206	LYS	2.9
6	F	215	CYS	2.9
1	A	3	ASP	2.9
7	U	183	ASP	2.9
3	C	229	GLN	2.9
3	Q	236	GLN	2.9
3	Q	201	VAL	2.9
6	T	235	ALA	2.9
7	G	68	ARG	2.9
6	F	204	LYS	2.9
7	G	242	GLN	2.9
3	Q	61	LYS	2.8
5	S	233	ILE	2.8
5	S	229	VAL	2.8
6	F	2	THR	2.8
3	C	3	ASP	2.8
2	B	93	HIS	2.8
3	Q	232	THR	2.8
6	F	244	ASN	2.8
7	U	168	GLU	2.8
5	S	207	VAL	2.8
1	O	61	LEU	2.8
8	V	226	GLU	2.8
5	S	225	ASP	2.8
10	X	195	PHE	2.8
8	H	214	LYS	2.7
3	Q	47	ARG	2.7
1	O	30	GLN	2.7
3	C	202	GLN	2.7
2	P	51	VAL	2.7
3	Q	238	LYS	2.7
5	E	200	LEU	2.7
4	D	242	GLU	2.7
4	R	239	GLU	2.7
4	D	224	ASP	2.7
5	S	216	GLY	2.7
3	C	51	LYS	2.7
3	Q	52	LEU	2.7
2	P	225	TYR	2.7

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Mol	Chain	Res	Type	RSRZ
3	C	53	GLN	2.7
7	G	2	GLY	2.6
3	Q	58	THR	2.6
3	Q	46	ARG	2.6
12	Z	174	TYR	2.6
3	Q	3	ASP	2.6
12	L	166	GLY	2.6
14	N	105	LYS	2.6
2	B	125	GLY	2.6
11	K	118	ASP	2.6
3	C	240	GLU	2.6
6	F	178	HIS	2.6
3	C	204	GLY	2.5
8	H	222	ASP	2.5
2	B	50	LYS	2.5
4	R	238	LYS	2.5
13	M	37	ASN	2.5
6	T	2	THR	2.5
6	T	205	GLU	2.5
5	S	180	LYS	2.5
5	S	40	ASN	2.5
9	I	1	SER	2.5
11	Y	212	GLY	2.5
3	C	12	ASP	2.5
1	A	231	LYS	2.4
6	T	50	ILE	2.4
5	E	3	ASN	2.4
7	U	171	THR	2.4
4	D	167	GLY	2.4
6	T	241	LYS	2.4
7	U	203	ASP	2.4
3	Q	198	LEU	2.4
14	b	195	GLN	2.4
7	U	68	ARG	2.4
6	T	203	ASN	2.4
5	S	56	SER	2.4
8	V	225	GLU	2.4
3	C	50	LEU	2.4
4	R	113	LEU	2.4
3	Q	189	CYS	2.4
6	T	238	PHE	2.4
12	Z	173	LYS	2.4

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Mol	Chain	Res	Type	RSRZ
4	R	242	GLU	2.4
9	W	1	SER	2.3
13	a	121	SER	2.3
2	P	209	ARG	2.3
3	C	46	ARG	2.3
3	C	234	ILE	2.3
7	U	3	TYR	2.3
8	V	9	ASN	2.3
5	E	207	VAL	2.3
4	R	202	GLU	2.3
4	R	237	GLU	2.3
2	B	222	GLY	2.3
3	Q	233	GLN	2.3
7	U	2	GLY	2.3
8	H	216	SER	2.3
3	Q	210	ILE	2.3
6	T	59	LYS	2.3
7	U	230	GLU	2.3
1	A	240	SER	2.3
2	B	2	SER	2.3
3	Q	224	SER	2.3
12	L	172	LEU	2.3
1	O	231	LYS	2.3
2	P	180	LYS	2.3
2	B	209	ARG	2.3
6	T	39	ASN	2.2
11	K	209	ASN	2.2
12	L	136	CYS	2.3
3	Q	55	THR	2.2
1	A	58	SER	2.2
4	R	125	LEU	2.2
6	T	198	LEU	2.2
4	R	240	ALA	2.2
4	R	241	ALA	2.2
2	P	226	GLN	2.2
3	Q	222	LEU	2.2
5	S	200	LEU	2.2
13	M	206	LEU	2.2
3	Q	240	GLU	2.2
1	A	4	ARG	2.2
6	F	39	ASN	2.2
11	Y	209	ASN	2.2

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Mol	Chain	Res	Type	RSRZ
7	G	3	TYR	2.2
9	W	133	LYS	2.2
14	b	105	LYS	2.2
3	Q	204	GLY	2.2
5	S	54	GLU	2.2
2	P	50	LYS	2.2
3	Q	206	LYS	2.2
4	R	233	LYS	2.2
8	V	32	ALA	2.2
13	a	171	GLN	2.2
7	U	153	TYR	2.2
5	E	233	ILE	2.2
12	L	161	GLU	2.2
4	D	9	PRO	2.2
6	F	59	LYS	2.2
6	F	241	LYS	2.2
3	C	186	VAL	2.1
3	C	201	VAL	2.1
3	Q	203	THR	2.1
3	C	209	GLU	2.1
9	I	133	LYS	2.1
14	b	107	LYS	2.1
3	C	58	THR	2.1
5	S	161	GLY	2.1
5	S	175	LEU	2.1
13	a	43	ILE	2.1
2	B	217	LYS	2.1
7	U	177	PHE	2.1
6	T	199	ALA	2.1
2	P	220	ASN	2.1
3	Q	38	ASN	2.1
4	D	125	LEU	2.1
6	F	182	GLY	2.1
6	F	205	GLU	2.1
5	E	217	LYS	2.1
1	O	62	SER	2.1
2	P	202	SER	2.1
11	Y	18	SER	2.1
11	Y	148	LEU	2.1
1	A	59	GLU	2.1
5	E	227	GLU	2.1
5	S	181	ILE	2.1

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Mol	Chain	Res	Type	RSRZ
6	F	207	ASP	2.1
7	G	222	ASP	2.1
7	U	40	ASP	2.1
3	C	48	SER	2.1
4	R	5	SER	2.1
7	U	180	SER	2.1
8	H	27	ALA	2.0
9	I	132	ALA	2.0
5	S	210	LEU	2.0
6	F	183	LEU	2.0
6	F	203	ASN	2.0
1	O	248	GLU	2.0
6	F	242	GLU	2.0
12	Z	166	GLY	2.0
1	O	209	ILE	2.0
3	Q	175	LYS	2.0
5	S	169	THR	2.0
7	G	40	ASP	2.0
10	X	193	ASP	2.0
4	R	198	GLN	2.0
3	C	117	ARG	2.0
8	H	196	ARG	2.0
1	A	184	GLU	2.0
3	C	52	LEU	2.0
5	S	230	ALA	2.0
2	P	184	LYS	2.0
4	R	116	GLY	2.0
5	S	166	GLY	2.0
10	X	194	ASP	2.0
14	b	104	ASP	2.0

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

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

6.3 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

6.4 Ligands

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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
15	MG	Z	301	1/1	0.84	0.11	64,64,64,64	0
15	MG	I	302	1/1	0.92	0.13	40,40,40,40	0
15	MG	K	301	1/1	0.95	0.12	41,41,41,41	0
15	MG	W	301	1/1	0.96	0.05	49,49,49,49	0
15	MG	I	301	1/1	0.97	0.05	46,46,46,46	0
15	MG	G	301	1/1	0.98	0.09	34,34,34,34	0
15	MG	L	301	1/1	0.99	0.11	41,41,41,41	0
15	MG	N	201	1/1	0.99	0.06	41,41,41,41	0
16	CL	G	302	1/1	0.99	0.05	33,33,33,33	0
16	CL	U	301	1/1	0.99	0.04	37,37,37,37	0

6.5 Other polymers

There are no such residues in this entry.