



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 14, 2026 – 10:22 AM UTC

PDB ID : 2BR2 / pdb_00002br2
Title : RNase PH core of the archaeal exosome
Authors : lorentzen, E.; Fribourg, S.; Conti, E.
Deposited on : 2005-04-30
Resolution : 2.80 Å(reported)

This is a wwPDB X-ray Structure Validation Summary 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
Xtrriage (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

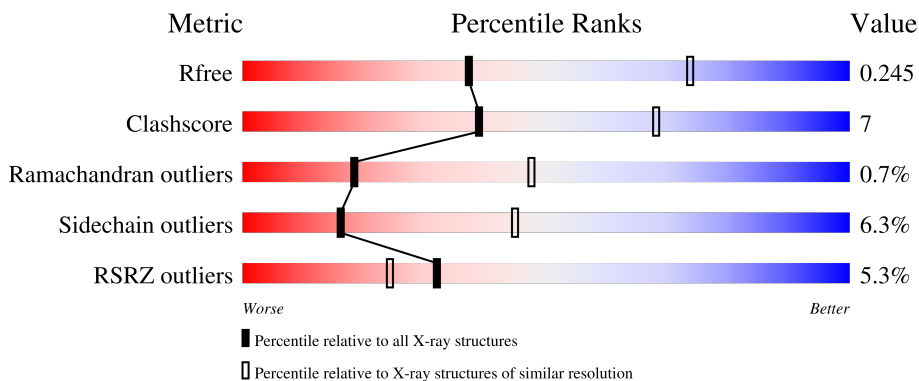
1 Overall quality at a glance

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	275	
1	C	275	
1	E	275	
1	G	275	
1	I	275	

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Mol	Chain	Length	Quality of chain
1	K	275	6% 79% 14% • 5%
1	M	275	6% 84% 10% • 5%
1	O	275	9% 84% 9% • 5%
1	Q	275	6% 80% 13% • 5%
1	S	275	5% 82% 11% • 5%
1	U	275	5% 83% 11% • 5%
1	W	275	6% 82% 11% • 5%
2	B	248	3% 74% 19% • •
2	D	248	4% 79% 17% •
2	F	248	4% 75% 18% • •
2	H	248	3% 72% 19% 6% •
2	J	248	4% 73% 21% • •
2	L	248	5% 78% 17% •
2	N	248	4% 75% 19% • •
2	P	248	2% 73% 22% 5%
2	R	248	4% 75% 18% • •
2	T	248	4% 78% 17% •
2	V	248	3% 76% 18% • •
2	X	248	2% 76% 17% • •

2 Entry composition [i](#)

There are 4 unique types of molecules in this entry. The entry contains 46287 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 EXOSOME COMPLEX EXONUCLEASE 2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	260	Total 1960	C 1248	N 323	O 384	S 5	0	0	0
1	C	260	Total 1972	C 1255	N 325	O 387	S 5	0	0	0
1	E	260	Total 1968	C 1253	N 324	O 386	S 5	0	0	0
1	G	260	Total 1964	C 1251	N 324	O 384	S 5	0	0	0
1	I	260	Total 1961	C 1250	N 323	O 383	S 5	0	0	0
1	K	260	Total 1964	C 1251	N 324	O 384	S 5	0	0	0
1	M	260	Total 1972	C 1255	N 325	O 387	S 5	0	0	0
1	O	260	Total 1968	C 1253	N 325	O 385	S 5	0	0	0
1	Q	260	Total 1968	C 1253	N 325	O 385	S 5	0	0	0
1	S	260	Total 1967	C 1253	N 324	O 385	S 5	0	0	0
1	U	260	Total 1968	C 1253	N 325	O 385	S 5	0	0	0
1	W	260	Total 1968	C 1253	N 324	O 386	S 5	0	0	0

- Molecule 2 is a protein called EXOSOME COMPLEX EXONUCLEASE 1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
2	B	241	Total 1863	C 1175	N 322	O 356	S 10	0	0	0
2	D	247	Total 1905	C 1202	N 329	O 363	S 11	0	0	0

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	F	241	Total	C	N	O	S	0	0	0
			1863	1175	322	356	10			
2	H	241	Total	C	N	O	S	0	0	0
			1863	1175	322	356	10			
2	J	241	Total	C	N	O	S	0	0	0
			1863	1175	322	356	10			
2	L	247	Total	C	N	O	S	0	0	0
			1909	1204	329	365	11			
2	N	241	Total	C	N	O	S	0	0	0
			1863	1175	322	356	10			
2	P	248	Total	C	N	O	S	0	0	0
			1907	1204	327	364	12			
2	R	245	Total	C	N	O	S	0	0	0
			1889	1192	327	359	11			
2	T	247	Total	C	N	O	S	0	0	0
			1905	1202	329	363	11			
2	V	244	Total	C	N	O	S	0	0	0
			1883	1189	325	359	10			
2	X	241	Total	C	N	O	S	0	0	0
			1863	1175	322	356	10			

- Molecule 3 is CHLORIDE ION (CCD ID: CL) (formula: Cl).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	B	1	Total	Cl	0	0
			1	1		
3	D	1	Total	Cl	0	0
			1	1		
3	F	1	Total	Cl	0	0
			1	1		
3	H	1	Total	Cl	0	0
			1	1		
3	J	1	Total	Cl	0	0
			1	1		
3	L	1	Total	Cl	0	0
			1	1		
3	M	1	Total	Cl	0	0
			1	1		
3	N	1	Total	Cl	0	0
			1	1		
3	P	1	Total	Cl	0	0
			1	1		

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Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	R	1	Total Cl 1 1	0	0
3	T	1	Total Cl 1 1	0	0
3	V	1	Total Cl 1 1	0	0
3	X	1	Total Cl 1 1	0	0

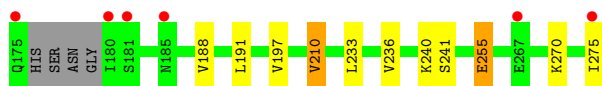
- Molecule 4 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	6	Total O 6 6	0	0
4	B	5	Total O 5 5	0	0
4	C	4	Total O 4 4	0	0
4	D	1	Total O 1 1	0	0
4	E	6	Total O 6 6	0	0
4	F	4	Total O 4 4	0	0
4	G	2	Total O 2 2	0	0
4	H	3	Total O 3 3	0	0
4	I	1	Total O 1 1	0	0
4	J	5	Total O 5 5	0	0
4	K	3	Total O 3 3	0	0
4	L	3	Total O 3 3	0	0
4	M	8	Total O 8 8	0	0
4	N	4	Total O 4 4	0	0
4	O	9	Total O 9 9	0	0

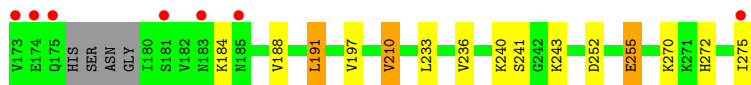
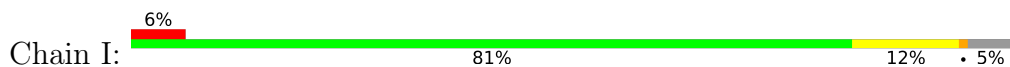
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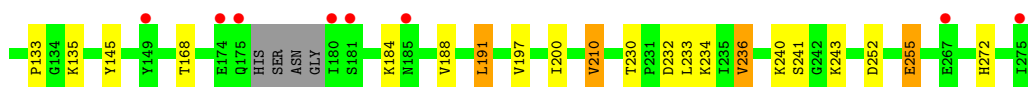
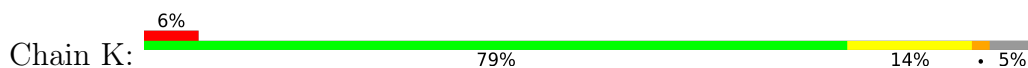
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	P	6	Total O 6 6	0	0
4	Q	4	Total O 4 4	0	0
4	R	5	Total O 5 5	0	0
4	S	6	Total O 6 6	0	0
4	T	4	Total O 4 4	0	0
4	U	3	Total O 3 3	0	0
4	V	3	Total O 3 3	0	0
4	W	2	Total O 2 2	0	0
4	X	1	Total O 1 1	0	0



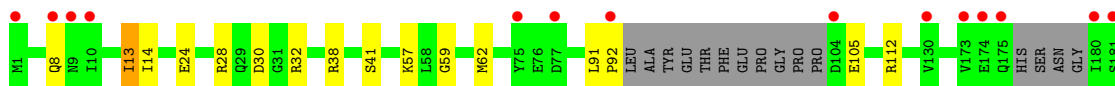
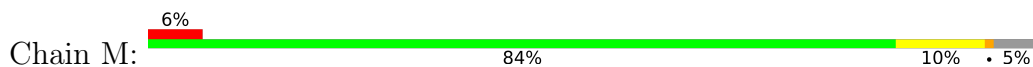
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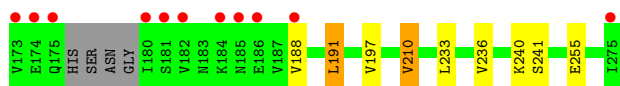
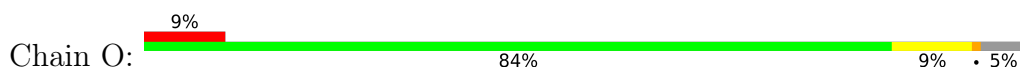
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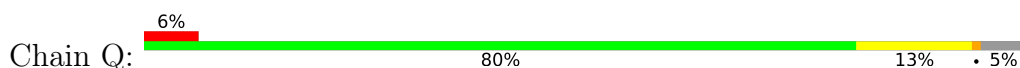
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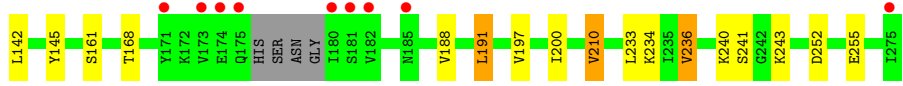
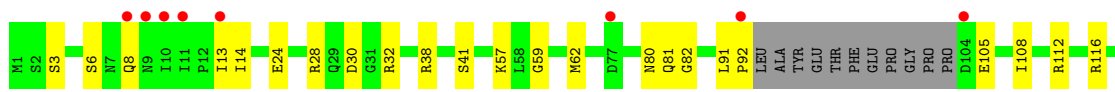


- Molecule 1: EXOSOME COMPLEX EXONUCLEASE 2

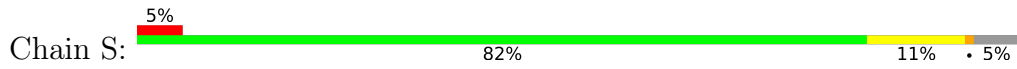


- Molecule 1: EXOSOME COMPLEX EXONUCLEASE 2

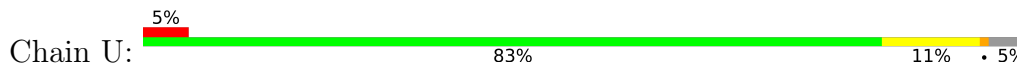




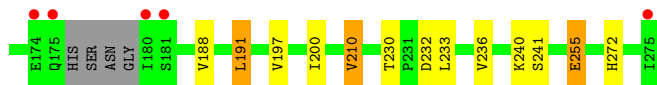
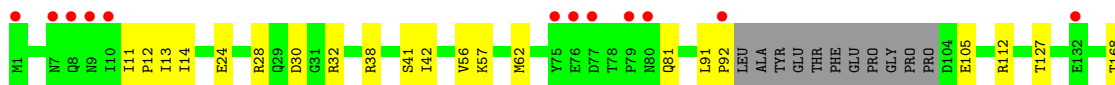
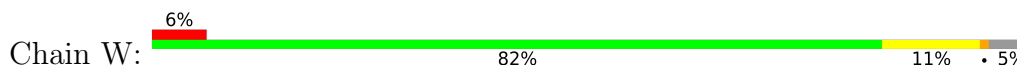
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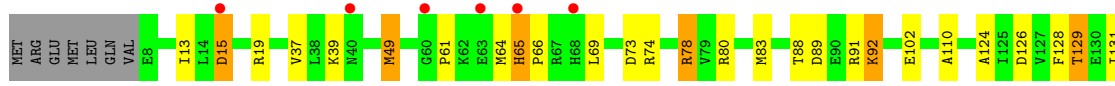
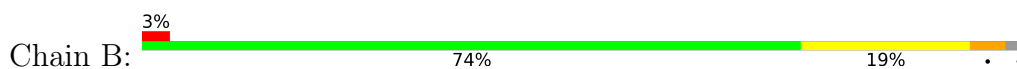
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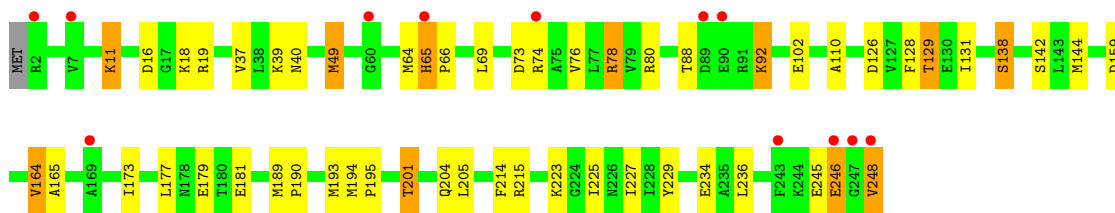


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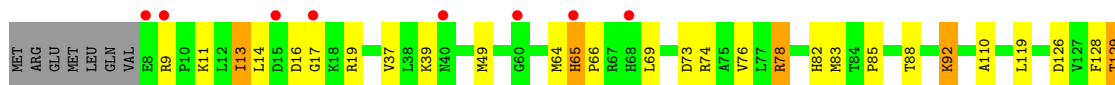


• Molecule 2: EXOSOME COMPLEX EXONUCLEASE 1

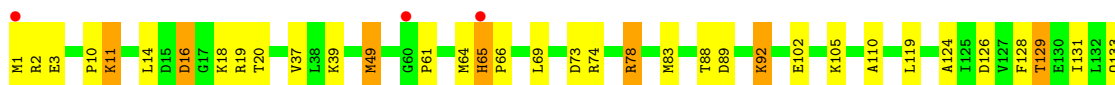




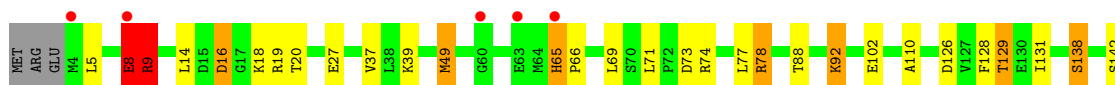
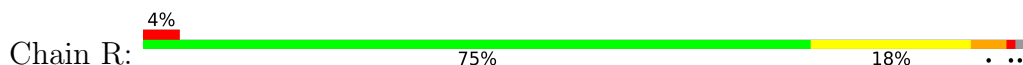
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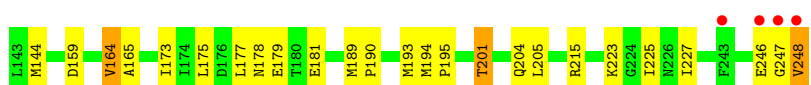
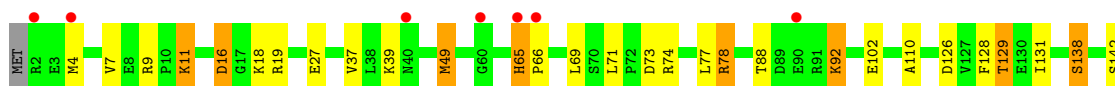
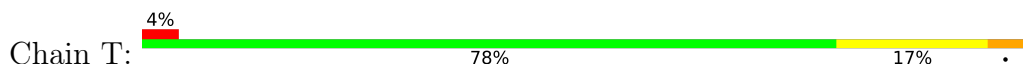
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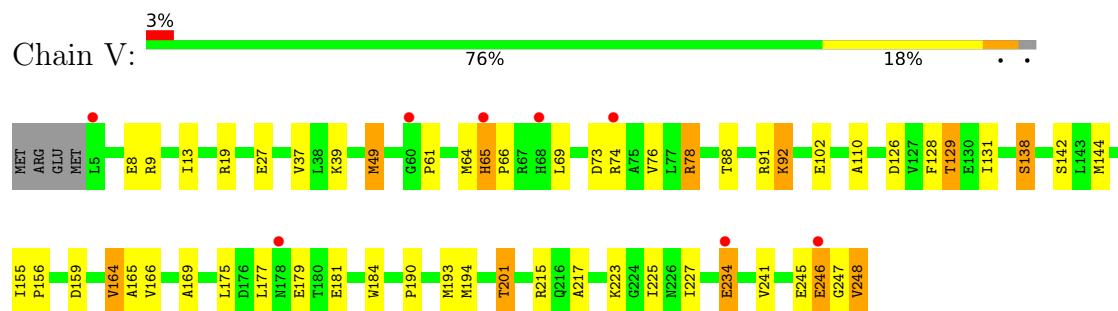
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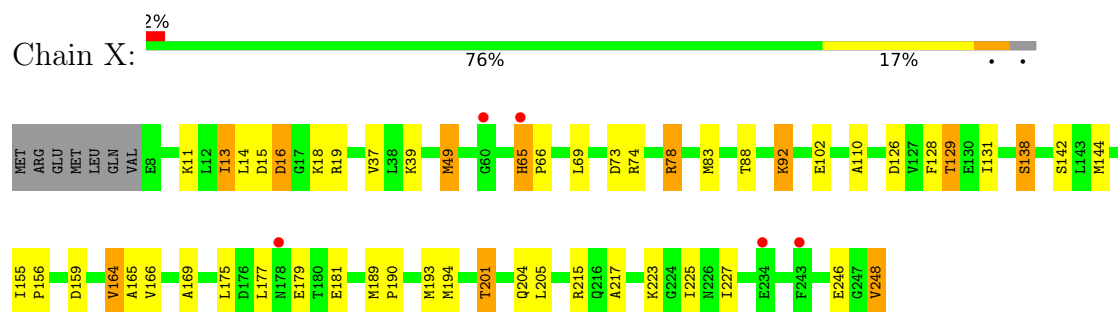
• Molecule 2: EXOSOME COMPLEX EXONUCLEASE 1



- Molecule 2: EXOSOME COMPLEX EXONUCLEASE 1



- Molecule 2: EXOSOME COMPLEX EXONUCLEASE 1



4 Data and refinement statistics i

Property	Value	Source
Space group	C 2 2 21	Depositor
Cell constants a, b, c, α , β , γ	206.88Å 212.72Å 434.05Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	218.22 – 2.80 217.03 – 2.80	Depositor EDS
% Data completeness (in resolution range)	99.7 (218.22-2.80) 99.8 (217.03-2.80)	Depositor EDS
R_{merge}	0.16	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.81 (at 2.82Å)	Xtrriage
Refinement program	REFMAC 5.2.0005	Depositor
R, R_{free}	0.215 , 0.237 0.227 , 0.245	Depositor DCC
R_{free} test set	7031 reflections (3.01%)	wwPDB-VP
Wilson B-factor (Å ²)	38.3	Xtrriage
Anisotropy	0.066	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 33.2	EDS
L-test for twinning ²	$\langle L \rangle = 0.46$, $\langle L^2 \rangle = 0.28$	Xtrriage
Estimated twinning fraction	0.033 for -k,-h,-l	Xtrriage
F_o, F_c correlation	0.90	EDS
Total number of atoms	46287	wwPDB-VP
Average B, all atoms (Å ²)	33.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 18.64% 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

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	0.56	0/1985	0.80	0/2697
1	C	0.62	1/1997 (0.1%)	0.83	3/2711 (0.1%)
1	E	0.57	0/1993	0.80	0/2706
1	G	0.58	0/1989	0.79	0/2701
1	I	0.57	0/1986	0.81	0/2697
1	K	0.63	1/1989 (0.1%)	0.82	3/2701 (0.1%)
1	M	0.57	0/1997	0.80	0/2711
1	O	0.65	2/1993 (0.1%)	0.83	0/2706
1	Q	0.61	1/1993 (0.1%)	0.82	1/2706 (0.0%)
1	S	0.60	0/1992	0.82	0/2706
1	U	0.58	0/1993	0.80	0/2706
1	W	0.57	0/1993	0.78	0/2706
2	B	0.57	0/1891	0.86	3/2553 (0.1%)
2	D	0.58	0/1933	0.88	4/2610 (0.2%)
2	F	0.58	0/1891	0.86	3/2553 (0.1%)
2	H	0.55	0/1891	0.85	1/2553 (0.0%)
2	J	0.57	0/1891	0.85	3/2553 (0.1%)
2	L	0.59	0/1937	0.88	4/2615 (0.2%)
2	N	0.56	0/1891	0.86	2/2553 (0.1%)
2	P	0.61	0/1935	0.87	3/2613 (0.1%)
2	R	0.61	0/1917	0.90	6/2588 (0.2%)
2	T	0.58	0/1933	0.88	1/2610 (0.0%)
2	V	0.58	0/1911	0.85	1/2581 (0.0%)
2	X	0.56	0/1891	0.85	1/2553 (0.0%)
All	All	0.59	5/46812 (0.0%)	0.84	39/63389 (0.1%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	O	0	1

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	O	25	LYS	C-N	6.69	1.42	1.33
1	C	234	LYS	C-N	5.82	1.41	1.33
1	K	234	LYS	C-N	5.65	1.41	1.33
1	Q	234	LYS	C-N	5.64	1.41	1.33
1	O	24	GLU	C-N	5.39	1.40	1.33

The worst 5 of 39 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	R	8	GLU	CA-C-N	7.44	135.09	121.70
2	R	8	GLU	C-N-CA	7.44	135.09	121.70
1	C	236	VAL	CB-CA-C	6.66	117.30	110.70
2	L	18	LYS	N-CA-C	6.52	120.17	110.52
1	Q	236	VAL	CB-CA-C	6.12	116.76	110.70

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	O	24	GLU	Mainchain

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	1960	0	1996	20	0
1	C	1972	0	2017	23	0
1	E	1968	0	2011	22	0
1	G	1964	0	2007	15	0
1	I	1961	0	2003	26	0
1	K	1964	0	2007	30	0
1	M	1972	0	2017	16	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	O	1968	0	2013	17	0
1	Q	1968	0	2013	26	0
1	S	1967	0	2011	22	0
1	U	1968	0	2013	16	0
1	W	1968	0	2011	16	0
2	B	1863	0	1895	38	0
2	D	1905	0	1936	34	0
2	F	1863	0	1895	38	0
2	H	1863	0	1895	40	0
2	J	1863	0	1895	50	0
2	L	1909	0	1940	37	0
2	N	1863	0	1895	36	0
2	P	1907	0	1937	44	0
2	R	1889	0	1921	43	0
2	T	1905	0	1936	40	0
2	V	1883	0	1917	37	0
2	X	1863	0	1895	31	0
3	B	1	0	0	0	0
3	D	1	0	0	0	0
3	F	1	0	0	0	0
3	H	1	0	0	0	0
3	J	1	0	0	0	0
3	L	1	0	0	0	0
3	M	1	0	0	1	0
3	N	1	0	0	0	0
3	P	1	0	0	0	0
3	R	1	0	0	0	0
3	T	1	0	0	0	0
3	V	1	0	0	0	0
3	X	1	0	0	0	0
4	A	6	0	0	2	0
4	B	5	0	0	2	0
4	C	4	0	0	1	0
4	D	1	0	0	0	0
4	E	6	0	0	1	0
4	F	4	0	0	0	0
4	G	2	0	0	0	0
4	H	3	0	0	0	0
4	I	1	0	0	1	0
4	J	5	0	0	0	0
4	K	3	0	0	1	0
4	L	3	0	0	2	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	M	8	0	0	2	0
4	N	4	0	0	0	0
4	O	9	0	0	1	0
4	P	6	0	0	0	0
4	Q	4	0	0	1	0
4	R	5	0	0	0	0
4	S	6	0	0	0	0
4	T	4	0	0	0	0
4	U	3	0	0	0	0
4	V	3	0	0	0	0
4	W	2	0	0	1	0
4	X	1	0	0	0	0
All	All	46287	0	47076	638	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 7.

The worst 5 of 638 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:O:62:MET:HE3	4:O:2003:HOH:O	1.59	1.02
2:P:110:ALA:HB1	2:P:201:THR:HG23	1.45	0.99
1:A:272:HIS:HD2	4:A:2001:HOH:O	1.49	0.94
2:T:110:ALA:HB1	2:T:201:THR:HG23	1.50	0.91
2:N:110:ALA:HB1	2:N:201:THR:HG23	1.50	0.91

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	254/275 (92%)	245 (96%)	7 (3%)	2 (1%)	16	44
1	C	254/275 (92%)	245 (96%)	7 (3%)	2 (1%)	16	44
1	E	254/275 (92%)	247 (97%)	6 (2%)	1 (0%)	30	60
1	G	254/275 (92%)	247 (97%)	5 (2%)	2 (1%)	16	44
1	I	254/275 (92%)	243 (96%)	9 (4%)	2 (1%)	16	44
1	K	254/275 (92%)	245 (96%)	8 (3%)	1 (0%)	30	60
1	M	254/275 (92%)	244 (96%)	9 (4%)	1 (0%)	30	60
1	O	254/275 (92%)	245 (96%)	8 (3%)	1 (0%)	30	60
1	Q	254/275 (92%)	243 (96%)	9 (4%)	2 (1%)	16	44
1	S	254/275 (92%)	248 (98%)	5 (2%)	1 (0%)	30	60
1	U	254/275 (92%)	244 (96%)	8 (3%)	2 (1%)	16	44
1	W	254/275 (92%)	247 (97%)	6 (2%)	1 (0%)	30	60
2	B	239/248 (96%)	227 (95%)	11 (5%)	1 (0%)	30	60
2	D	245/248 (99%)	231 (94%)	12 (5%)	2 (1%)	16	44
2	F	239/248 (96%)	228 (95%)	9 (4%)	2 (1%)	16	44
2	H	239/248 (96%)	227 (95%)	11 (5%)	1 (0%)	30	60
2	J	239/248 (96%)	228 (95%)	10 (4%)	1 (0%)	30	60
2	L	245/248 (99%)	230 (94%)	13 (5%)	2 (1%)	16	44
2	N	239/248 (96%)	227 (95%)	11 (5%)	1 (0%)	30	60
2	P	246/248 (99%)	232 (94%)	12 (5%)	2 (1%)	16	44
2	R	243/248 (98%)	226 (93%)	13 (5%)	4 (2%)	7	27
2	T	245/248 (99%)	229 (94%)	14 (6%)	2 (1%)	16	44
2	V	242/248 (98%)	229 (95%)	11 (4%)	2 (1%)	16	44
2	X	239/248 (96%)	227 (95%)	11 (5%)	1 (0%)	30	60
All	All	5948/6276 (95%)	5684 (96%)	225 (4%)	39 (1%)	18	47

5 of 39 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	105	GLU
1	C	105	GLU
1	E	105	GLU
1	G	105	GLU
1	I	105	GLU

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	216/242 (89%)	205 (95%)	11 (5%)	21	54
1	C	219/242 (90%)	206 (94%)	13 (6%)	18	48
1	E	218/242 (90%)	207 (95%)	11 (5%)	22	54
1	G	217/242 (90%)	208 (96%)	9 (4%)	27	62
1	I	216/242 (89%)	207 (96%)	9 (4%)	26	61
1	K	217/242 (90%)	206 (95%)	11 (5%)	21	54
1	M	219/242 (90%)	208 (95%)	11 (5%)	22	54
1	O	218/242 (90%)	209 (96%)	9 (4%)	27	62
1	Q	218/242 (90%)	206 (94%)	12 (6%)	19	51
1	S	218/242 (90%)	206 (94%)	12 (6%)	19	51
1	U	218/242 (90%)	206 (94%)	12 (6%)	19	51
1	W	218/242 (90%)	208 (95%)	10 (5%)	24	58
2	B	199/208 (96%)	184 (92%)	15 (8%)	12	37
2	D	203/208 (98%)	187 (92%)	16 (8%)	11	35
2	F	199/208 (96%)	183 (92%)	16 (8%)	11	34
2	H	199/208 (96%)	181 (91%)	18 (9%)	9	28
2	J	199/208 (96%)	185 (93%)	14 (7%)	14	40
2	L	204/208 (98%)	188 (92%)	16 (8%)	11	35
2	N	199/208 (96%)	183 (92%)	16 (8%)	11	34
2	P	203/208 (98%)	186 (92%)	17 (8%)	10	32
2	R	201/208 (97%)	187 (93%)	14 (7%)	14	40
2	T	203/208 (98%)	187 (92%)	16 (8%)	11	35
2	V	201/208 (97%)	188 (94%)	13 (6%)	15	43
2	X	199/208 (96%)	183 (92%)	16 (8%)	11	34
All	All	5021/5400 (93%)	4704 (94%)	317 (6%)	16	45

5 of 317 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	R	138	SER
2	V	177	LEU
1	S	13	ILE
2	T	164	VAL
1	W	255	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 70 such sidechains are listed below:

Mol	Chain	Res	Type
2	T	198	ASN
1	U	80	ASN
1	W	183	ASN
1	I	272	HIS
1	I	253	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 [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 13 ligands modelled in this entry, 13 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 [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 [i](#)

6.1 Protein, DNA and RNA chains [i](#)

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	260/275 (94%)	0.38	21 (8%) 18 13	23, 32, 46, 60	0
1	C	260/275 (94%)	0.33	17 (6%) 25 18	24, 32, 46, 58	0
1	E	260/275 (94%)	0.24	15 (5%) 29 22	24, 32, 46, 57	0
1	G	260/275 (94%)	0.49	19 (7%) 21 15	24, 32, 46, 58	0
1	I	260/275 (94%)	0.26	16 (6%) 26 20	24, 32, 46, 57	0
1	K	260/275 (94%)	0.30	17 (6%) 25 18	24, 32, 46, 58	0
1	M	260/275 (94%)	0.26	17 (6%) 25 18	24, 32, 46, 58	0
1	O	260/275 (94%)	0.39	24 (9%) 14 10	24, 32, 46, 59	0
1	Q	260/275 (94%)	0.28	17 (6%) 25 18	24, 32, 46, 59	0
1	S	260/275 (94%)	0.28	15 (5%) 29 22	24, 32, 46, 57	0
1	U	260/275 (94%)	0.31	15 (5%) 29 22	24, 32, 46, 58	0
1	W	260/275 (94%)	0.31	17 (6%) 25 18	24, 32, 46, 57	0
2	B	241/248 (97%)	0.16	8 (3%) 49 39	25, 31, 46, 59	0
2	D	247/248 (99%)	0.26	9 (3%) 46 37	22, 30, 46, 59	0
2	F	241/248 (97%)	0.14	10 (4%) 41 33	25, 31, 47, 59	0
2	H	241/248 (97%)	0.25	8 (3%) 49 39	25, 31, 46, 59	0
2	J	241/248 (97%)	0.20	9 (3%) 45 36	25, 31, 46, 59	0
2	L	247/248 (99%)	0.27	12 (4%) 35 27	22, 31, 46, 59	0
2	N	241/248 (97%)	0.18	11 (4%) 37 29	25, 31, 46, 59	0
2	P	248/248 (100%)	0.18	6 (2%) 59 49	23, 30, 46, 59	0
2	R	245/248 (98%)	0.24	11 (4%) 38 30	23, 31, 46, 59	0
2	T	247/248 (99%)	0.16	11 (4%) 38 30	22, 31, 46, 59	0
2	V	244/248 (98%)	0.09	8 (3%) 49 39	25, 31, 46, 59	0
2	X	241/248 (97%)	0.12	5 (2%) 63 54	25, 31, 46, 59	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
All	All	6044/6276 (96%)	0.26	318 (5%) 32 24	22, 31, 47, 60	0

The worst 5 of 318 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	S	175	GLN	5.6
1	S	181	SER	5.5
2	R	60	GLY	5.3
2	P	60	GLY	5.3
2	L	60	GLY	5.3

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(Å ²)	Q<0.9
3	CL	B	1249	1/1	0.88	0.14	67,67,67,67	0
3	CL	D	1249	1/1	0.90	0.11	49,49,49,49	0
3	CL	J	1249	1/1	0.90	0.10	47,47,47,47	0
3	CL	V	1249	1/1	0.90	0.11	52,52,52,52	0
3	CL	P	1249	1/1	0.91	0.12	59,59,59,59	0
3	CL	N	1249	1/1	0.91	0.14	56,56,56,56	0
3	CL	T	1249	1/1	0.92	0.10	50,50,50,50	0
3	CL	L	1249	1/1	0.93	0.07	45,45,45,45	0
3	CL	X	1249	1/1	0.94	0.10	43,43,43,43	0
3	CL	R	1249	1/1	0.95	0.07	46,46,46,46	0
3	CL	F	1249	1/1	0.95	0.08	48,48,48,48	0
3	CL	H	1249	1/1	0.97	0.05	52,52,52,52	0
3	CL	M	1276	1/1	0.97	0.08	45,45,45,45	0

6.5 Other polymers [i](#)

There are no such residues in this entry.