



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 03:43 PM UTC

PDB ID : 6ZQ4 / pdb_00006zq4
Title : Crystal structure of Chaetomium thermophilum Glycerol Kinase in complex with substrate in P1 space group
Authors : Wilk, P.; Wator, E.; Grudnik, P.
Deposited on : 2020-07-09
Resolution : 2.02 Å(reported)

This is a Full wwPDB X-ray Structure Validation Report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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

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

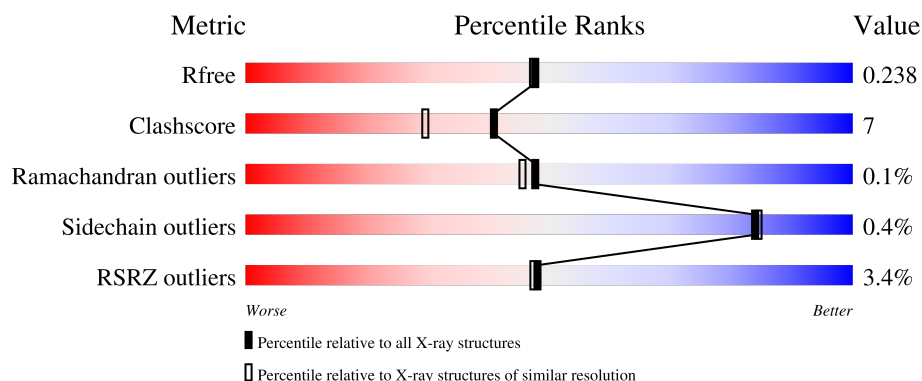
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

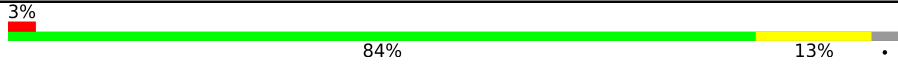
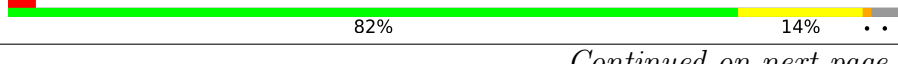
The reported resolution of this entry is 2.02 Å.

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	13299 (2.04-2.00)
Clashscore	190562	1022 (2.02-2.02)
Ramachandran outliers	187476	1014 (2.02-2.02)
Sidechain outliers	187428	1014 (2.02-2.02)
RSRZ outliers	180081	13314 (2.04-2.00)

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	526	
1	B	526	
1	C	526	
1	D	526	
1	E	526	

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Mol	Chain	Length	Quality of chain
1	F	526	
1	G	526	
1	H	526	

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
2	PO4	A	601	-	-	X	-

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 63968 atoms, of which 30941 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 Glycerol kinase-like protein.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	510	Total	C	H	N	O	S	0	4	0
			7817	2485	3890	681	745	16			
1	B	510	Total	C	H	N	O	S	0	1	0
			7773	2472	3868	677	740	16			
1	C	509	Total	C	H	N	O	S	0	0	0
			7748	2466	3854	673	739	16			
1	D	509	Total	C	H	N	O	S	0	0	0
			7745	2465	3852	673	739	16			
1	E	511	Total	C	H	N	O	S	0	0	0
			7762	2470	3860	675	741	16			
1	F	512	Total	C	H	N	O	S	0	0	0
			7776	2474	3866	677	743	16			
1	G	512	Total	C	H	N	O	S	0	0	0
			7777	2474	3867	677	743	16			
1	H	511	Total	C	H	N	O	S	0	0	0
			7762	2470	3860	675	741	16			

There are 16 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	65	GLY	-	expression tag	UNP G0SAG9
A	66	SER	-	expression tag	UNP G0SAG9
B	65	GLY	-	expression tag	UNP G0SAG9
B	66	SER	-	expression tag	UNP G0SAG9
C	65	GLY	-	expression tag	UNP G0SAG9
C	66	SER	-	expression tag	UNP G0SAG9
D	65	GLY	-	expression tag	UNP G0SAG9
D	66	SER	-	expression tag	UNP G0SAG9
E	65	GLY	-	expression tag	UNP G0SAG9
E	66	SER	-	expression tag	UNP G0SAG9
F	65	GLY	-	expression tag	UNP G0SAG9
F	66	SER	-	expression tag	UNP G0SAG9
G	65	GLY	-	expression tag	UNP G0SAG9

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Chain	Residue	Modelled	Actual	Comment	Reference
G	66	SER	-	expression tag	UNP G0SAG9
H	65	GLY	-	expression tag	UNP G0SAG9
H	66	SER	-	expression tag	UNP G0SAG9

- Molecule 2 is PHOSPHATE ION (CCD ID: PO4) (formula: O_4P).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	A	1	Total	O	P	0	0
			5	4	1		
2	B	1	Total	O	P	0	0
			5	4	1		
2	C	1	Total	O	P	0	0
			5	4	1		
2	D	1	Total	O	P	0	0
			5	4	1		
2	E	1	Total	O	P	0	0
			5	4	1		
2	F	1	Total	O	P	0	0
			5	4	1		

- Molecule 3 is GLYCEROL (CCD ID: GOL) (formula: $C_3H_8O_3$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	A	1	Total	C	H	O	0	0
			9	3	3	3		
3	B	1	Total	C	H	O	0	0
			9	3	3	3		
3	C	1	Total	C	H	O	0	0
			9	3	3	3		
3	D	1	Total	C	H	O	0	0
			9	3	3	3		
3	E	1	Total	C	H	O	0	0
			9	3	3	3		
3	F	1	Total	C	H	O	0	0
			9	3	3	3		
3	G	1	Total	C	H	O	0	0
			9	3	3	3		
3	H	1	Total	C	H	O	0	0
			9	3	3	3		

- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	192	Total	O	0	0
			192	192		
4	B	276	Total	O	0	0
			276	276		
4	C	243	Total	O	0	0
			243	243		
4	D	208	Total	O	0	0
			208	208		

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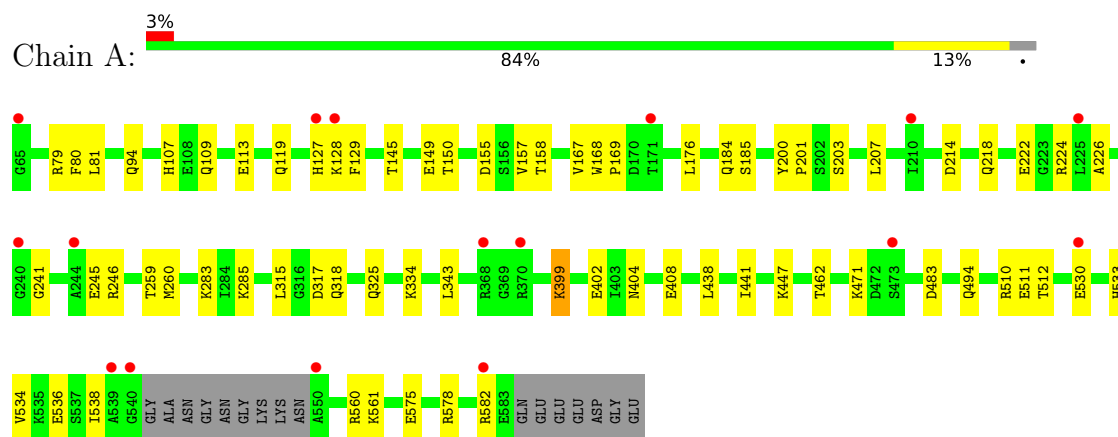
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	E	220	Total 220	O 220	0	0
4	F	234	Total 234	O 234	0	0
4	G	186	Total 186	O 186	0	0
4	H	147	Total 147	O 147	0	0

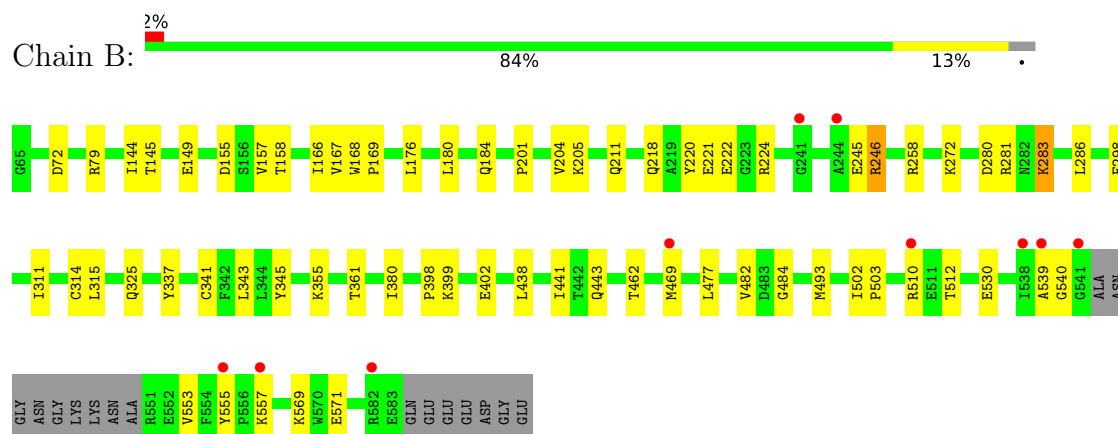
3 Residue-property plots [i](#)

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

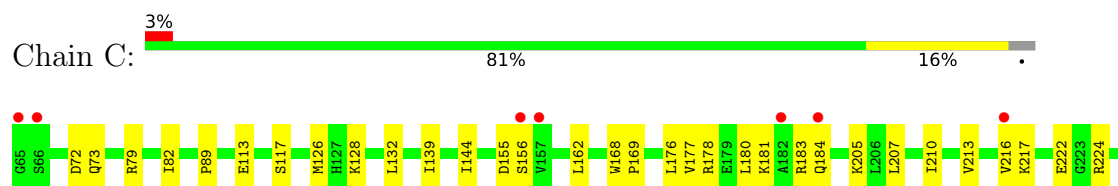
- Molecule 1: Glycerol kinase-like protein

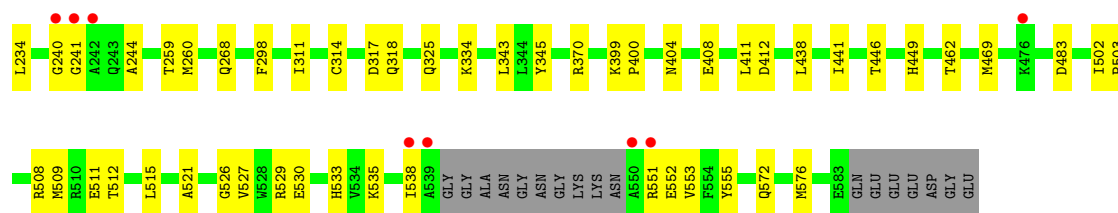


- Molecule 1: Glycerol kinase-like protein

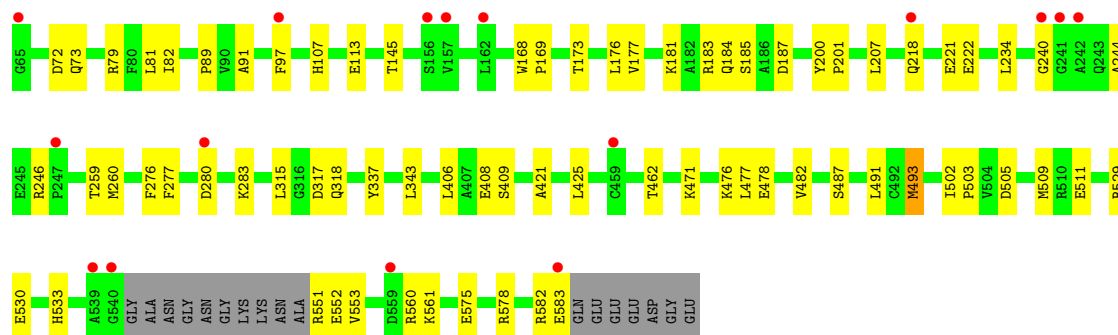
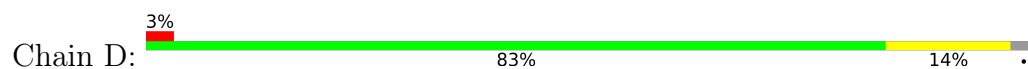


- Molecule 1: Glycerol kinase-like protein

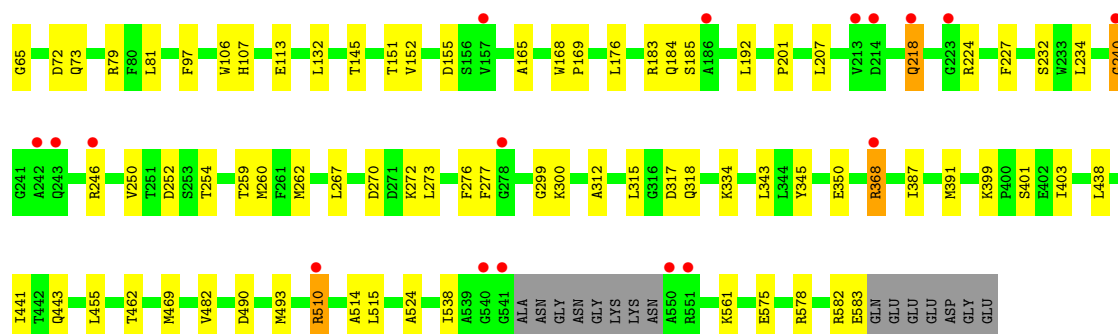
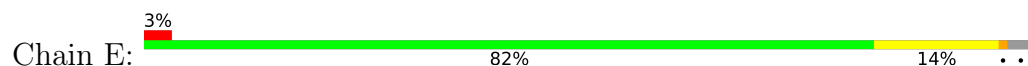




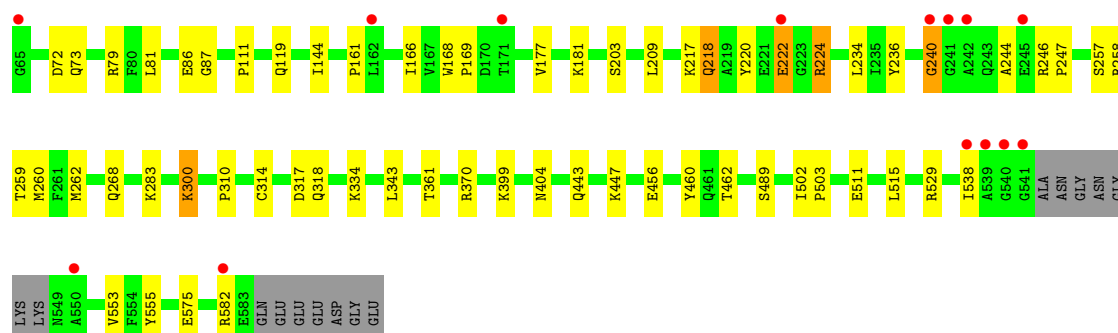
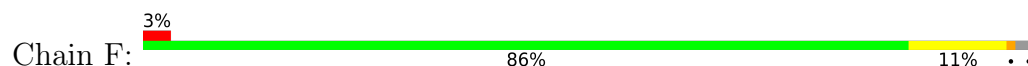
• Molecule 1: Glycerol kinase-like protein



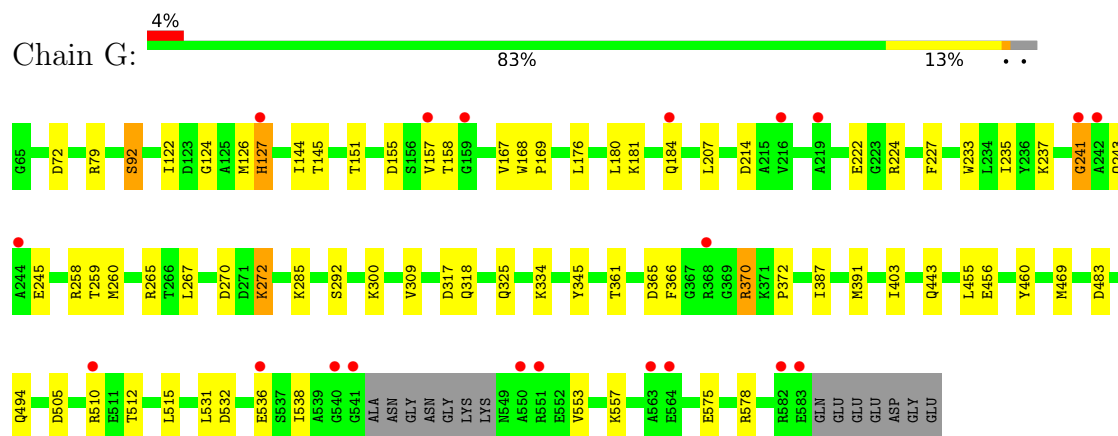
• Molecule 1: Glycerol kinase-like protein



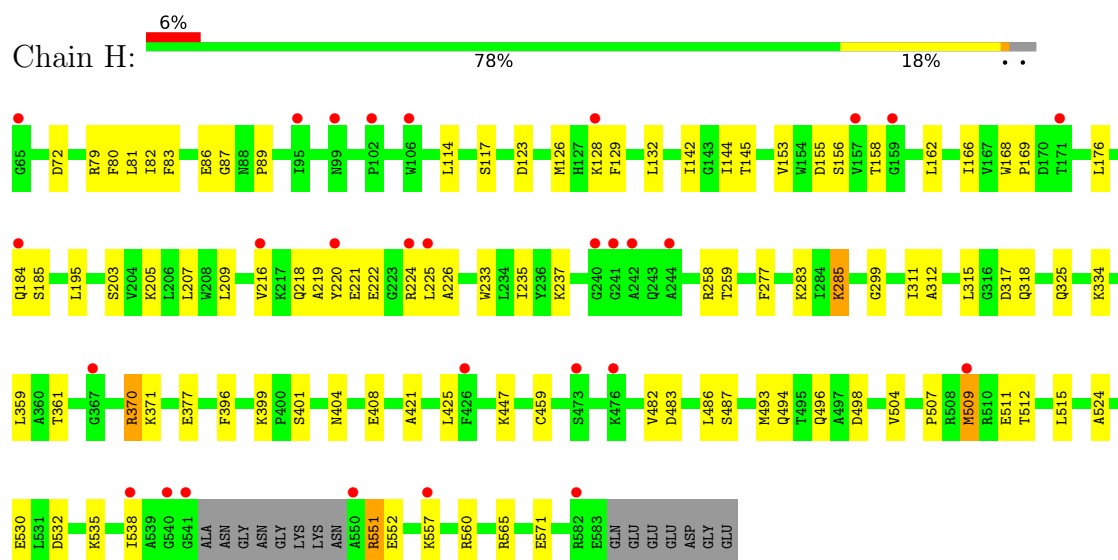
• Molecule 1: Glycerol kinase-like protein



• Molecule 1: Glycerol kinase-like protein



• Molecule 1: Glycerol kinase-like protein



4 Data and refinement statistics

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α , β , γ	61.38Å 112.82Å 179.54Å 85.77° 90.04° 85.45°	Depositor
Resolution (Å)	23.01 – 2.02 23.01 – 2.02	Depositor EDS
% Data completeness (in resolution range)	97.3 (23.01-2.02) 97.7 (23.01-2.02)	Depositor EDS
R_{merge}	0.22	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	0.96 (at 2.01Å)	Xtriage
Refinement program	PHENIX 1.17.1 _3660	Depositor
R, R_{free}	0.205 , 0.240 0.206 , 0.238	Depositor DCC
R_{free} test set	3228 reflections (1.05%)	wwPDB-VP
Wilson B-factor (Å ²)	36.8	Xtriage
Anisotropy	0.218	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.45 , 63.0	EDS
L-test for twinning ²	$\langle L \rangle = 0.46$, $\langle L^2 \rangle = 0.29$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	63968	wwPDB-VP
Average B, all atoms (Å ²)	57.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.81% 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: PO4, GOL

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	0.49	3/4018 (0.1%)	0.71	13/5445 (0.2%)
1	B	0.58	5/3990 (0.1%)	0.67	8/5407 (0.1%)
1	C	0.40	2/3976 (0.1%)	0.61	11/5390 (0.2%)
1	D	0.38	2/3975 (0.1%)	0.53	3/5388 (0.1%)
1	E	0.45	5/3984 (0.1%)	0.61	8/5400 (0.1%)
1	F	0.46	6/3992 (0.2%)	0.61	14/5411 (0.3%)
1	G	0.38	3/3992 (0.1%)	0.60	8/5411 (0.1%)
1	H	0.42	3/3984 (0.1%)	0.61	7/5400 (0.1%)
All	All	0.45	29/31911 (0.1%)	0.62	72/43252 (0.2%)

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	B	0	2
1	E	0	1
All	All	0	3

All (29) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	D	246	ARG	C-N	15.72	1.54	1.33
1	B	246	ARG	C-N	15.08	1.53	1.33
1	F	246	ARG	C-N	14.54	1.53	1.33
1	A	246	ARG	C-N	14.52	1.53	1.33
1	B	286	LEU	C-N	13.83	1.51	1.33
1	H	371	LYS	C-N	13.59	1.51	1.33
1	B	399	LYS	CE-NZ	-12.03	1.13	1.49
1	A	399	LYS	CE-NZ	-10.06	1.19	1.49

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	E	300	LYS	CD-CE	-10.01	1.22	1.52
1	A	582	ARG	CZ-NH1	9.82	1.46	1.32
1	C	551	ARG	CG-CD	-8.35	1.27	1.52
1	G	285	LYS	CB-CG	-8.09	1.28	1.52
1	B	399	LYS	CD-CE	-7.30	1.30	1.52
1	E	300	LYS	CE-NZ	-7.16	1.27	1.49
1	G	285	LYS	CG-CD	-7.13	1.31	1.52
1	E	510	ARG	CG-CD	6.77	1.72	1.52
1	C	551	ARG	CZ-NH1	6.56	1.42	1.32
1	H	487	SER	C-O	-6.47	1.15	1.24
1	B	283	LYS	CB-CG	-6.09	1.34	1.52
1	E	218	GLN	C-O	-5.95	1.17	1.24
1	F	222	GLU	CB-CG	5.92	1.70	1.52
1	F	300	LYS	CB-CG	-5.85	1.34	1.52
1	F	222	GLU	CA-CB	5.65	1.62	1.53
1	E	132	LEU	C-O	-5.54	1.16	1.24
1	D	552	GLU	C-O	-5.52	1.16	1.24
1	H	552	GLU	C-O	-5.51	1.15	1.23
1	G	92	SER	C-O	-5.39	1.17	1.23
1	F	224	ARG	NE-CZ	5.26	1.38	1.33
1	F	222	GLU	CD-OE2	5.20	1.35	1.25

All (72) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	G	285	LYS	CG-CD-CE	11.34	137.39	111.30
1	A	399	LYS	CA-CB-CG	11.25	136.60	114.10
1	A	582	ARG	NE-CZ-NH1	11.15	132.65	121.50
1	A	510	ARG	CA-CB-CG	9.97	134.04	114.10
1	E	510	ARG	CB-CG-CD	9.43	132.98	111.30
1	F	222	GLU	CB-CG-CD	9.17	128.19	112.60
1	A	582	ARG	NE-CZ-NH2	-9.02	111.09	119.20
1	B	272	LYS	CA-CB-CG	-8.79	96.52	114.10
1	D	246	ARG	CA-C-N	8.46	128.22	119.76
1	D	246	ARG	C-N-CA	8.46	128.22	119.76
1	F	218	GLN	CA-CB-CG	8.38	130.85	114.10
1	H	128	LYS	CB-CG-CD	8.10	129.93	111.30
1	F	582	ARG	CB-CG-CD	-8.08	92.72	111.30
1	A	399	LYS	CB-CG-CD	-8.01	92.87	111.30
1	B	272	LYS	CG-CD-CE	7.97	129.64	111.30
1	B	246	ARG	CA-C-N	7.79	127.78	119.76
1	B	246	ARG	C-N-CA	7.79	127.78	119.76

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	411	LEU	CB-CG-CD1	7.78	134.04	110.70
1	B	286	LEU	CA-C-N	7.75	127.51	119.76
1	B	286	LEU	C-N-CA	7.75	127.51	119.76
1	A	246	ARG	CA-C-N	7.72	127.73	119.78
1	A	246	ARG	C-N-CA	7.72	127.73	119.78
1	C	521	ALA	CA-C-N	7.36	128.14	119.98
1	C	521	ALA	C-N-CA	7.36	128.14	119.98
1	H	371	LYS	CA-C-N	7.24	127.23	119.78
1	H	371	LYS	C-N-CA	7.24	127.23	119.78
1	F	246	ARG	CA-C-N	7.01	127.00	119.78
1	F	246	ARG	C-N-CA	7.01	127.00	119.78
1	A	127	HIS	CA-C-N	-6.72	110.74	120.29
1	A	127	HIS	C-N-CA	-6.72	110.74	120.29
1	F	582	ARG	CA-CB-CG	6.69	127.48	114.10
1	G	272	LYS	CD-CE-NZ	-6.47	91.18	111.90
1	E	240	GLY	N-CA-C	-6.45	103.28	111.72
1	E	300	LYS	CB-CG-CD	6.39	126.01	111.30
1	E	561	LYS	CG-CD-CE	-6.37	96.66	111.30
1	C	527	VAL	CA-C-N	6.30	132.40	122.94
1	C	527	VAL	C-N-CA	6.30	132.40	122.94
1	E	561	LYS	CB-CG-CD	6.23	125.62	111.30
1	G	241	GLY	CA-C-N	6.20	133.37	121.54
1	G	241	GLY	C-N-CA	6.20	133.37	121.54
1	C	411	LEU	CB-CG-CD2	-6.11	92.36	110.70
1	H	509	MET	CA-CB-CG	-6.10	101.90	114.10
1	C	241	GLY	CA-C-O	-5.78	116.33	121.41
1	E	368	ARG	CB-CG-CD	5.72	124.45	111.30
1	C	526	GLY	CA-C-N	5.71	128.29	120.46
1	C	526	GLY	C-N-CA	5.71	128.29	120.46
1	F	222	GLU	CG-CD-OE2	-5.71	105.27	118.40
1	C	184	GLN	CB-CA-C	5.68	118.91	109.53
1	E	510	ARG	CA-CB-CG	5.64	125.39	114.10
1	A	582	ARG	CG-CD-NE	5.63	124.38	112.00
1	B	399	LYS	CD-CE-NZ	5.58	129.76	111.90
1	H	401	SER	N-CA-CB	5.55	118.28	110.12
1	F	217	LYS	CA-C-N	-5.47	112.52	120.29
1	F	217	LYS	C-N-CA	-5.47	112.52	120.29
1	F	399	LYS	CA-CB-CG	5.41	124.93	114.10
1	F	218	GLN	N-CA-CB	5.39	118.13	110.16
1	E	218	GLN	N-CA-C	-5.38	105.33	111.14
1	G	245	GLU	N-CA-C	-5.33	101.76	109.59
1	H	285	LYS	CA-CB-CG	5.29	124.68	114.10

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	245	GLU	N-CA-C	-5.25	102.51	110.28
1	F	222	GLU	OE1-CD-OE2	5.23	135.46	122.90
1	A	510	ARG	CB-CG-CD	-5.22	99.29	111.30
1	A	283	LYS	CB-CA-C	5.17	117.41	109.03
1	D	561	LYS	CA-CB-CG	5.16	124.42	114.10
1	C	527	VAL	O-C-N	5.13	126.85	121.87
1	F	224	ARG	CD-NE-CZ	5.09	131.53	124.40
1	G	181	LYS	CG-CD-CE	5.05	122.91	111.30
1	G	127	HIS	N-CA-CB	-5.03	102.77	110.07
1	H	565	ARG	N-CA-C	-5.03	105.69	111.07
1	F	240	GLY	N-CA-C	-5.02	106.66	112.29
1	B	557	LYS	CB-CG-CD	-5.01	99.77	111.30
1	G	181	LYS	CA-CB-CG	5.01	124.12	114.10

There are no chirality outliers.

All (3) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	B	539	ALA	Peptide
1	B	540	GLY	Peptide
1	E	510	ARG	Sidechain

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	3927	3890	3881	40	0
1	B	3905	3868	3868	45	1
1	C	3894	3854	3854	57	0
1	D	3893	3852	3852	51	0
1	E	3902	3860	3860	51	0
1	F	3910	3866	3866	44	0
1	G	3910	3867	3866	44	1
1	H	3902	3860	3860	78	0
2	A	5	0	0	2	0
2	B	5	0	0	0	0
2	C	5	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	D	5	0	0	1	0
2	E	5	0	0	0	0
2	F	5	0	0	0	0
3	A	6	3	8	1	0
3	B	6	3	8	1	0
3	C	6	3	8	0	0
3	D	6	3	8	0	0
3	E	6	3	8	0	0
3	F	6	3	8	0	0
3	G	6	3	8	0	0
3	H	6	3	8	0	0
4	A	192	0	0	7	0
4	B	276	0	0	6	0
4	C	243	0	0	9	0
4	D	208	0	0	7	0
4	E	220	0	0	9	0
4	F	234	0	0	7	0
4	G	186	0	0	3	0
4	H	147	0	0	7	0
All	All	33027	30941	30971	406	1

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.

All (406) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:221:GLU:OE1	1:B:283:LYS:NZ	1.94	1.01
1:D:183:ARG:NH2	1:D:276:PHE:O	1.95	0.98
1:B:221:GLU:HA	1:B:283:LYS:HE2	1.49	0.95
1:H:482:VAL:HG11	1:H:493:MET:HE1	1.47	0.94
1:A:119:GLN:OE1	4:A:701:HOH:O	1.86	0.93
1:H:482:VAL:HG21	1:H:493:MET:HE2	1.49	0.93
1:D:583:GLU:OE2	4:D:701:HOH:O	1.93	0.86
1:D:482:VAL:HG11	1:D:493:MET:HE2	1.58	0.85
1:C:509:MET:HE1	1:C:511:GLU:HB2	1.60	0.84
1:H:216:VAL:HG13	1:H:225:LEU:HD11	1.60	0.83
1:B:571:GLU:OE2	4:B:701:HOH:O	2.01	0.79
1:E:107:HIS:ND1	4:E:704:HOH:O	2.15	0.79
1:A:536:GLU:OE2	4:A:702:HOH:O	2.01	0.79
1:H:216:VAL:HG13	1:H:225:LEU:CD1	2.14	0.78

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:207:LEU:HD13	1:E:277:PHE:O	1.86	0.75
1:E:490:ASP:OD2	4:E:701:HOH:O	2.05	0.75
1:D:184:GLN:O	1:D:185:SER:OG	2.05	0.75
1:B:258:ARG:HH11	1:B:361:THR:HG21	1.51	0.74
1:C:370:ARG:NH1	4:C:703:HOH:O	2.18	0.74
1:H:226:ALA:HA	1:H:285:LYS:HB2	1.69	0.74
1:F:575:GLU:OE1	4:F:701:HOH:O	2.04	0.74
1:A:113:GLU:OE2	4:A:703:HOH:O	2.06	0.73
1:C:399:LYS:HE2	1:C:400:PRO:HD2	1.70	0.73
1:F:258:ARG:HH11	1:F:361:THR:HG21	1.53	0.73
1:F:236:TYR:O	1:F:240:GLY:O	2.06	0.73
1:H:493:MET:CE	1:H:504:VAL:HG11	2.19	0.72
1:E:65:GLY:N	4:E:706:HOH:O	2.22	0.72
1:E:232:SER:OG	1:E:250:VAL:O	2.06	0.72
1:C:483:ASP:OD1	4:C:701:HOH:O	2.08	0.71
1:H:482:VAL:HG11	1:H:493:MET:CE	2.20	0.71
1:D:551:ARG:NH1	4:D:704:HOH:O	2.23	0.71
1:E:246:ARG:HH22	1:E:299:GLY:HA2	1.56	0.70
1:G:258:ARG:HH11	1:G:361:THR:HG21	1.56	0.70
1:B:280:ASP:HB3	1:B:283:LYS:HB2	1.74	0.70
1:F:443:GLN:NE2	4:F:702:HOH:O	2.25	0.70
1:G:258:ARG:NH1	1:G:361:THR:HG21	2.06	0.69
1:C:240:GLY:O	1:C:244:ALA:HB2	1.92	0.69
1:B:155:ASP:OD2	1:B:224:ARG:NH1	2.26	0.69
1:B:280:ASP:OD1	4:B:702:HOH:O	2.10	0.69
1:H:86:GLU:OE2	4:H:702:HOH:O	2.10	0.69
1:D:509:MET:HE1	1:D:511:GLU:HB2	1.74	0.69
1:H:83:PHE:HE1	1:H:509:MET:CE	2.05	0.69
1:H:493:MET:HE3	1:H:504:VAL:HG11	1.75	0.68
1:E:246:ARG:NH2	1:E:299:GLY:HA2	2.09	0.68
1:B:482:VAL:HG21	1:B:493:MET:SD	2.33	0.68
1:H:299:GLY:O	4:H:701:HOH:O	2.10	0.68
1:E:106:TRP:O	4:E:703:HOH:O	2.12	0.68
1:B:258:ARG:NH1	1:B:361:THR:HG21	2.09	0.67
1:F:222:GLU:CB	1:F:224:ARG:NH1	2.57	0.67
1:E:350:GLU:OE2	4:E:702:HOH:O	2.12	0.67
1:B:343:LEU:HD21	1:B:462:THR:HG23	1.76	0.67
1:H:532:ASP:OD2	4:H:703:HOH:O	2.12	0.66
1:B:477:LEU:HG	1:B:502:ILE:HD13	1.77	0.66
1:A:483:ASP:OD1	4:A:704:HOH:O	2.13	0.65
1:C:132:LEU:HD22	1:H:132:LEU:HD22	1.78	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:483:ASP:OD1	4:G:701:HOH:O	2.14	0.65
1:C:268:GLN:NE2	4:C:706:HOH:O	2.29	0.65
1:C:412:ASP:OD1	4:C:702:HOH:O	2.14	0.65
1:D:343:LEU:HD21	1:D:462:THR:HG23	1.79	0.65
1:H:258:ARG:HH11	1:H:361:THR:HG21	1.62	0.65
1:F:515:LEU:HD21	1:F:538:ILE:HD12	1.78	0.64
1:G:222:GLU:OE1	1:G:224:ARG:NH1	2.30	0.64
1:F:258:ARG:NH1	1:F:361:THR:HG21	2.13	0.64
1:E:240:GLY:O	4:E:705:HOH:O	2.16	0.63
1:D:107:HIS:ND1	4:D:709:HOH:O	2.30	0.63
1:A:200:TYR:CD1	2:A:601:PO4:O2	2.52	0.63
1:C:155:ASP:HB2	1:C:162:LEU:HD21	1.81	0.62
1:H:399:LYS:NZ	4:H:712:HOH:O	2.33	0.62
1:H:123:ASP:OD1	4:H:704:HOH:O	2.16	0.61
1:A:200:TYR:CG	2:A:601:PO4:O2	2.54	0.61
1:F:222:GLU:HB2	1:F:224:ARG:NH1	2.15	0.61
1:G:270:ASP:OD1	1:G:272:LYS:HB2	2.01	0.61
1:G:214:ASP:N	4:G:707:HOH:O	2.32	0.61
1:E:183:ARG:NH2	1:E:276:PHE:O	2.34	0.61
1:H:498:ASP:O	1:H:560:ARG:NH1	2.33	0.60
1:C:538:ILE:O	1:C:538:ILE:HG22	2.00	0.60
1:H:258:ARG:NH1	1:H:361:THR:HG21	2.17	0.59
1:B:325:GLN:HG2	1:B:512:THR:HG21	1.82	0.59
1:D:582:ARG:NH2	4:D:713:HOH:O	2.34	0.59
1:H:509:MET:SD	1:H:511:GLU:N	2.75	0.59
1:A:128:LYS:O	1:A:129:PHE:C	2.44	0.59
1:C:72:ASP:HB3	1:C:79:ARG:HG2	1.85	0.59
1:H:155:ASP:CG	1:H:158:THR:HG23	2.28	0.58
1:F:218:GLN:NE2	1:F:222:GLU:OE2	2.36	0.58
1:A:438:LEU:HD23	1:A:441:ILE:HD11	1.86	0.58
1:G:443:GLN:OE1	4:G:702:HOH:O	2.16	0.58
1:B:438:LEU:HD23	1:B:441:ILE:HD11	1.85	0.58
1:C:438:LEU:HD23	1:C:441:ILE:HD11	1.86	0.58
1:G:259:THR:O	1:G:260:MET:HB2	2.02	0.58
1:A:575:GLU:O	1:A:578:ARG:HG2	2.04	0.58
1:C:132:LEU:CD2	1:H:132:LEU:HD22	2.33	0.58
1:F:72:ASP:HB3	1:F:79:ARG:HG2	1.87	0.57
1:H:184:GLN:O	1:H:185:SER:HB2	2.04	0.57
1:E:515:LEU:HD21	1:E:538:ILE:HD13	1.87	0.57
1:A:214:ASP:O	1:A:218:GLN:HB2	2.05	0.57
1:B:398:PRO:HD2	1:B:402:GLU:OE1	2.05	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:494:GLN:HG2	1:H:557:LYS:HZ1	1.70	0.56
1:C:89:PRO:HD3	1:C:509:MET:HE3	1.88	0.56
1:C:259:THR:O	1:C:260:MET:HB2	2.04	0.56
1:H:571:GLU:OE2	4:H:705:HOH:O	2.17	0.56
1:D:575:GLU:O	1:D:578:ARG:HG2	2.06	0.56
1:B:502:ILE:HG13	1:B:503:PRO:HD2	1.87	0.56
1:E:443:GLN:NE2	4:E:711:HOH:O	2.29	0.56
1:A:81:LEU:HD21	1:A:511:GLU:HG3	1.88	0.56
1:B:355:LYS:NZ	4:B:708:HOH:O	2.34	0.55
1:D:176:LEU:HD23	1:D:176:LEU:O	2.07	0.55
1:E:259:THR:O	1:E:260:MET:HB2	2.07	0.55
1:E:482:VAL:HG21	1:E:493:MET:SD	2.47	0.55
1:A:80:PHE:C	1:A:81:LEU:HD12	2.31	0.55
1:A:447:LYS:NZ	4:A:714:HOH:O	2.39	0.55
1:E:575:GLU:O	1:E:578:ARG:HG2	2.07	0.55
1:E:582:ARG:O	1:E:583:GLU:CD	2.50	0.55
1:C:515:LEU:HD21	1:C:538:ILE:HD13	1.89	0.55
1:D:82:ILE:HD12	1:D:91:ALA:HB3	1.89	0.55
1:A:343:LEU:HD21	1:A:462:THR:HG23	1.88	0.54
1:D:81:LEU:HD23	1:D:89:PRO:HB3	1.89	0.54
1:G:532:ASP:O	1:G:536:GLU:HG2	2.07	0.54
1:H:89:PRO:HD3	1:H:509:MET:HE2	1.89	0.54
1:B:184:GLN:HA	1:B:184:GLN:OE1	2.07	0.54
1:A:530:GLU:HG2	1:A:533:HIS:H	1.73	0.54
1:C:213:VAL:HB	1:C:216:VAL:HG22	1.89	0.54
1:D:72:ASP:HB3	1:D:79:ARG:HG2	1.90	0.54
1:C:535:LYS:CE	4:C:742:HOH:O	2.55	0.54
1:E:184:GLN:O	1:E:185:SER:HB2	2.08	0.54
1:B:484:GLY:HA2	1:B:510:ARG:HH12	1.73	0.54
1:E:151:THR:HG23	1:E:227:PHE:CE1	2.42	0.54
1:H:219:ALA:O	1:H:224:ARG:N	2.40	0.54
1:B:246:ARG:O	1:B:246:ARG:HG2	2.08	0.53
1:F:259:THR:O	1:F:260:MET:HB2	2.09	0.53
1:C:177:VAL:HG12	1:C:181:LYS:HD2	1.90	0.53
1:D:89:PRO:HD3	1:D:509:MET:HE3	1.90	0.53
1:C:529:ARG:HH21	1:C:529:ARG:HG3	1.74	0.53
1:A:317:ASP:OD1	1:A:318:GLN:N	2.41	0.53
1:C:535:LYS:HE3	4:C:742:HOH:O	2.08	0.53
1:E:192:LEU:HD11	1:E:272:LYS:HD3	1.91	0.53
1:E:343:LEU:HD21	1:E:462:THR:HG23	1.90	0.53
1:B:443:GLN:OE1	4:B:703:HOH:O	2.18	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:210:ILE:O	1:C:217:LYS:HD2	2.09	0.52
1:E:73:GLN:HG3	1:E:234:LEU:HD11	1.91	0.52
1:F:529:ARG:HD3	1:G:370:ARG:HH21	1.74	0.52
1:H:221:GLU:HA	1:H:283:LYS:HD3	1.91	0.52
1:A:471:LYS:NZ	4:A:718:HOH:O	2.42	0.52
1:D:207:LEU:HD13	1:D:277:PHE:O	2.09	0.52
1:F:87:GLY:HA3	1:F:538:ILE:HD13	1.92	0.52
1:F:447:LYS:NZ	4:F:711:HOH:O	2.42	0.52
1:C:399:LYS:HG2	1:C:400:PRO:HD2	1.92	0.52
1:F:244:ALA:O	1:F:247:PRO:HD3	2.10	0.52
1:H:166:ILE:HD11	1:H:209:LEU:HD21	1.92	0.52
1:D:187:ASP:O	4:D:702:HOH:O	2.18	0.52
1:F:502:ILE:HG13	1:F:503:PRO:HD2	1.91	0.52
1:H:325:GLN:HG2	1:H:512:THR:HG21	1.92	0.52
1:A:222:GLU:OE2	1:A:224:ARG:NE	2.34	0.51
1:E:72:ASP:HB3	1:E:79:ARG:CG	2.40	0.51
1:H:168:TRP:CG	1:H:169:PRO:HD3	2.46	0.51
1:G:575:GLU:O	1:G:578:ARG:HG2	2.11	0.51
1:D:406:LEU:HA	1:D:409:SER:OG	2.11	0.51
1:G:243:GLN:HG3	1:G:243:GLN:O	2.11	0.51
1:G:505:ASP:OD1	1:G:553:VAL:HG22	2.10	0.51
1:H:176:LEU:HD21	1:H:207:LEU:HD22	1.92	0.51
1:B:72:ASP:HB3	1:B:79:ARG:HG2	1.93	0.51
1:C:502:ILE:HG13	1:C:503:PRO:HD2	1.93	0.51
1:D:200:TYR:CD1	2:D:601:PO4:O1	2.63	0.51
1:D:280:ASP:HB3	1:D:283:LYS:HB2	1.93	0.51
1:C:508:ARG:NE	1:C:552:GLU:OE1	2.44	0.50
1:A:150:THR:HG23	1:A:167:VAL:HA	1.92	0.50
1:E:438:LEU:HD23	1:E:441:ILE:HD11	1.94	0.50
1:G:370:ARG:HH11	1:G:370:ARG:HG2	1.76	0.50
1:C:168:TRP:CG	1:C:169:PRO:HD3	2.47	0.50
1:G:155:ASP:OD1	1:G:157:VAL:HG12	2.12	0.50
1:B:176:LEU:HD23	1:B:180:LEU:HG	1.93	0.49
1:A:155:ASP:OD1	1:A:157:VAL:N	2.44	0.49
1:B:221:GLU:HA	1:B:283:LYS:CE	2.33	0.49
1:E:183:ARG:HG2	1:E:184:GLN:O	2.13	0.49
1:H:155:ASP:HB2	1:H:162:LEU:HD21	1.95	0.49
1:H:494:GLN:HG2	1:H:557:LYS:NZ	2.28	0.49
1:C:180:LEU:O	1:C:183:ARG:HB2	2.13	0.49
1:D:502:ILE:HG13	1:D:503:PRO:HD2	1.95	0.49
1:F:168:TRP:CG	1:F:169:PRO:HD3	2.48	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:128:LYS:HD2	1:C:128:LYS:O	2.13	0.49
1:E:168:TRP:CG	1:E:169:PRO:HD3	2.48	0.48
1:D:145:THR:OG1	1:D:317:ASP:HA	2.14	0.48
1:D:240:GLY:O	1:D:244:ALA:HB2	2.14	0.48
1:A:168:TRP:CG	1:A:169:PRO:HD3	2.49	0.48
1:C:404:ASN:ND2	4:C:717:HOH:O	2.47	0.48
1:E:318:GLN:OE1	1:E:334:LYS:NZ	2.46	0.48
1:F:79:ARG:NE	4:F:713:HOH:O	2.43	0.48
1:G:168:TRP:CG	1:G:169:PRO:HD3	2.49	0.48
1:D:81:LEU:HD21	1:D:511:GLU:HG3	1.95	0.48
1:D:184:GLN:HG2	1:D:185:SER:N	2.27	0.48
1:A:530:GLU:O	1:A:534:VAL:HG23	2.14	0.48
1:H:207:LEU:HD12	1:H:277:PHE:O	2.14	0.48
1:A:155:ASP:HB3	1:A:158:THR:OG1	2.14	0.48
1:G:575:GLU:OE2	1:G:578:ARG:HD3	2.13	0.48
1:B:176:LEU:HD23	1:B:176:LEU:O	2.14	0.47
1:E:97:PHE:CD1	1:E:97:PHE:C	2.92	0.47
1:G:325:GLN:HG2	1:G:512:THR:HG21	1.96	0.47
1:C:222:GLU:OE2	1:C:224:ARG:NH1	2.47	0.47
1:E:151:THR:HG23	1:E:227:PHE:HE1	1.79	0.47
1:E:201:PRO:HB3	1:E:260:MET:HG3	1.96	0.47
1:F:268:GLN:NE2	4:F:707:HOH:O	2.34	0.47
1:H:515:LEU:HD21	1:H:538:ILE:HD12	1.97	0.47
1:B:168:TRP:CG	1:B:169:PRO:HD3	2.49	0.47
1:D:168:TRP:CG	1:D:169:PRO:HD3	2.50	0.47
1:F:81:LEU:HD21	1:F:511:GLU:HG3	1.96	0.47
1:D:201:PRO:HB3	1:D:260:MET:HG3	1.96	0.47
1:E:81:LEU:HD13	1:E:514:ALA:CB	2.44	0.47
1:H:220:TYR:O	1:H:283:LYS:HG2	2.14	0.47
1:D:221:GLU:OE1	1:D:283:LYS:NZ	2.47	0.47
1:F:81:LEU:CD2	1:F:511:GLU:HG3	2.44	0.47
1:A:399:LYS:HB2	1:A:402:GLU:HG3	1.96	0.47
1:E:176:LEU:O	1:E:176:LEU:HD23	2.15	0.47
1:G:265:ARG:HG3	1:G:265:ARG:HH11	1.80	0.47
1:H:203:SER:HB3	1:H:259:THR:O	2.15	0.47
1:C:408:GLU:OE2	4:C:704:HOH:O	2.20	0.46
1:C:552:GLU:OE1	4:C:705:HOH:O	2.21	0.46
1:E:270:ASP:HB3	1:E:273:LEU:HD12	1.96	0.46
1:G:300:LYS:HB3	1:G:309:VAL:O	2.15	0.46
1:H:83:PHE:CE1	1:H:509:MET:HE1	2.50	0.46
1:D:477:LEU:HG	1:D:502:ILE:HD13	1.96	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:166:ILE:HG22	1:B:205:LYS:HE3	1.97	0.46
1:G:391:MET:HG3	1:G:403:ILE:HG13	1.97	0.46
1:H:72:ASP:HB3	1:H:79:ARG:HG2	1.97	0.46
1:A:184:GLN:O	1:A:185:SER:HB2	2.15	0.46
1:A:404:ASN:O	1:A:408:GLU:HG3	2.16	0.46
1:C:82:ILE:HD11	1:C:126:MET:SD	2.55	0.46
1:C:176:LEU:CD2	1:C:180:LEU:HD11	2.46	0.46
1:H:129:PHE:HA	1:H:132:LEU:HD12	1.98	0.46
1:D:145:THR:HA	1:D:315:LEU:O	2.15	0.46
1:B:201:PRO:O	1:B:204:VAL:HG22	2.16	0.46
1:C:126:MET:HE1	1:C:139:ILE:HD11	1.98	0.46
1:A:107:HIS:CD2	1:A:167:VAL:HG21	2.51	0.46
1:F:222:GLU:OE1	1:F:224:ARG:NH1	2.47	0.46
1:G:233:TRP:CH2	1:G:237:LYS:HE2	2.51	0.46
1:C:325:GLN:HG2	1:C:512:THR:HG21	1.98	0.46
1:A:109:GLN:HG3	1:A:167:VAL:CG2	2.47	0.45
1:B:337:TYR:CZ	1:B:493:MET:HE1	2.51	0.45
1:D:173:THR:O	1:D:177:VAL:HG23	2.15	0.45
1:H:114:LEU:O	1:H:117:SER:OG	2.34	0.45
1:H:318:GLN:OE1	1:H:334:LYS:NZ	2.47	0.45
1:A:534:VAL:O	1:A:538:ILE:HG12	2.16	0.45
1:D:529:ARG:HB2	1:D:530:GLU:OE2	2.16	0.45
1:F:529:ARG:HD3	1:G:370:ARG:NH2	2.31	0.45
1:B:502:ILE:HG13	1:B:503:PRO:CD	2.46	0.45
1:F:73:GLN:HG3	1:F:234:LEU:HD11	1.98	0.45
1:A:226:ALA:HA	1:A:285:LYS:HB2	1.99	0.45
1:B:218:GLN:NE2	1:B:222:GLU:OE1	2.46	0.45
1:B:220:TYR:CZ	1:B:283:LYS:HD3	2.51	0.45
1:F:119:GLN:NE2	4:F:721:HOH:O	2.48	0.45
1:H:145:THR:HA	1:H:315:LEU:O	2.16	0.45
1:E:176:LEU:HD21	1:E:207:LEU:HD23	1.98	0.45
1:E:368:ARG:N	4:E:719:HOH:O	2.42	0.45
1:G:176:LEU:HD21	1:G:207:LEU:HD23	1.98	0.45
1:B:569:LYS:HD2	1:B:569:LYS:HA	1.85	0.45
1:C:168:TRP:HA	1:C:205:LYS:HE2	1.99	0.45
1:G:167:VAL:HG12	1:G:169:PRO:HD3	1.97	0.45
1:G:334:LYS:HD2	1:G:334:LYS:C	2.41	0.45
1:H:483:ASP:OD1	4:H:706:HOH:O	2.20	0.45
1:H:551:ARG:HH11	1:H:551:ARG:HB3	1.80	0.45
1:D:487:SER:HA	1:D:493:MET:SD	2.56	0.45
1:H:225:LEU:O	1:H:285:LYS:HB2	2.17	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:317:ASP:OD1	1:G:318:GLN:N	2.50	0.45
1:H:233:TRP:CH2	1:H:237:LYS:HE2	2.52	0.45
1:C:572:GLN:OE1	1:C:576:MET:HE2	2.17	0.44
1:D:530:GLU:HG2	1:D:533:HIS:H	1.82	0.44
1:H:216:VAL:HG13	1:H:225:LEU:HD13	1.97	0.44
1:H:482:VAL:HG21	1:H:493:MET:CE	2.35	0.44
1:A:79:ARG:HD3	1:A:94:GLN:OE1	2.17	0.44
1:D:408:GLU:HG3	1:D:491:LEU:HD22	1.99	0.44
1:F:300:LYS:HB3	1:F:310:PRO:HA	1.98	0.44
1:H:87:GLY:HA3	1:H:538:ILE:HD13	1.98	0.44
1:H:153:VAL:HG21	1:H:209:LEU:HD13	1.99	0.44
1:B:553:VAL:HG11	1:B:555:TYR:CZ	2.52	0.44
1:E:207:LEU:CD1	1:E:277:PHE:O	2.62	0.44
1:H:509:MET:SD	1:H:509:MET:C	3.01	0.44
1:C:176:LEU:HD23	1:C:180:LEU:CD1	2.47	0.44
1:D:218:GLN:O	1:D:222:GLU:HB2	2.18	0.44
1:A:318:GLN:OE1	1:A:334:LYS:NZ	2.48	0.44
1:E:97:PHE:HB2	1:E:113:GLU:CG	2.48	0.44
1:E:345:TYR:HB2	1:E:469:MET:SD	2.58	0.44
1:E:145:THR:OG1	1:E:317:ASP:HA	2.18	0.44
1:E:312:ALA:HB1	1:E:524:ALA:HB3	1.99	0.44
1:A:145:THR:HA	1:A:315:LEU:O	2.18	0.44
1:A:494:GLN:NE2	4:A:717:HOH:O	2.42	0.43
1:B:510:ARG:NH2	4:B:734:HOH:O	2.52	0.43
1:D:97:PHE:HB2	1:D:113:GLU:HG3	2.00	0.43
1:D:177:VAL:HG12	1:D:181:LYS:HD2	1.99	0.43
1:D:560:ARG:HA	1:D:560:ARG:NE	2.33	0.43
1:A:149:GLU:OE1	3:A:602:GOL:O1	2.33	0.43
1:C:144:ILE:O	1:C:314:CYS:HA	2.18	0.43
1:D:73:GLN:HG3	1:D:234:LEU:HD11	2.00	0.43
1:G:151:THR:HG23	1:G:227:PHE:CE1	2.53	0.43
1:B:155:ASP:HB3	1:B:158:THR:OG1	2.19	0.43
1:B:298:PHE:HB2	1:B:311:ILE:O	2.18	0.43
1:G:144:ILE:HD12	1:G:235:ILE:HG13	2.00	0.43
1:B:211:GLN:OE1	4:B:704:HOH:O	2.21	0.43
1:C:113:GLU:O	1:C:117:SER:HB2	2.18	0.43
1:G:124:GLY:O	1:G:127:HIS:HB2	2.18	0.43
1:E:252:ASP:OD2	1:E:254:THR:OG1	2.28	0.43
1:G:494:GLN:NE2	1:G:557:LYS:HG2	2.32	0.43
1:B:149:GLU:OE1	3:B:602:GOL:O1	2.30	0.43
1:E:152:VAL:HG22	1:E:165:ALA:HB2	2.00	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:478:GLU:OE2	4:D:703:HOH:O	2.21	0.43
1:F:502:ILE:HG13	1:F:503:PRO:CD	2.48	0.43
1:F:222:GLU:HB3	1:F:224:ARG:NH1	2.32	0.43
1:F:166:ILE:HD11	1:F:209:LEU:HD21	2.00	0.43
1:F:257:SER:HA	1:F:262:MET:HE2	2.01	0.43
1:F:317:ASP:OD1	1:F:318:GLN:N	2.51	0.43
1:H:82:ILE:HD11	1:H:126:MET:SD	2.58	0.43
1:H:144:ILE:HD12	1:H:235:ILE:HG12	2.01	0.43
1:B:345:TYR:HB2	1:B:469:MET:SD	2.59	0.43
1:E:145:THR:HA	1:E:315:LEU:O	2.19	0.43
1:C:178:ARG:HG2	1:C:178:ARG:HH11	1.84	0.42
1:H:145:THR:OG1	1:H:317:ASP:HA	2.18	0.42
1:A:145:THR:OG1	1:A:317:ASP:HA	2.18	0.42
1:F:456:GLU:HB3	1:F:460:TYR:CE2	2.55	0.42
1:B:341:CYS:HB2	1:B:380:ILE:HB	2.02	0.42
1:F:111:PRO:HG2	1:F:161:PRO:HB3	2.01	0.42
1:G:267:LEU:HD11	1:G:372:PRO:HG2	2.00	0.42
1:H:218:GLN:O	1:H:222:GLU:HB2	2.19	0.42
1:B:281:ARG:C	1:B:283:LYS:H	2.27	0.42
1:E:72:ASP:HB3	1:E:79:ARG:HG2	2.01	0.42
1:E:387:ILE:HD11	1:E:455:LEU:CD2	2.49	0.42
1:E:391:MET:HG3	1:E:403:ILE:HG13	2.00	0.42
1:G:176:LEU:O	1:G:180:LEU:HG	2.19	0.42
1:C:446:THR:H	1:C:449:HIS:HD2	1.68	0.42
1:G:345:TYR:HB2	1:G:469:MET:SD	2.60	0.42
1:A:201:PRO:HB3	1:A:260:MET:HG3	2.02	0.42
1:C:317:ASP:OD1	1:C:318:GLN:N	2.53	0.42
1:C:343:LEU:HD21	1:C:462:THR:HG23	2.01	0.42
1:E:443:GLN:NE2	4:E:732:HOH:O	2.52	0.42
1:F:370:ARG:NH1	4:F:725:HOH:O	2.53	0.42
1:G:122:ILE:O	1:G:126:MET:HG2	2.20	0.42
1:B:167:VAL:HG12	1:B:169:PRO:HD3	2.01	0.42
1:C:89:PRO:HG3	1:C:509:MET:HE3	2.02	0.42
1:C:334:LYS:HD2	1:C:334:LYS:C	2.44	0.42
1:F:318:GLN:OE1	1:F:334:LYS:NZ	2.46	0.42
1:F:220:TYR:O	1:F:283:LYS:HG2	2.18	0.42
1:G:292:SER:N	1:G:365:ASP:O	2.52	0.42
1:H:219:ALA:HB3	1:H:225:LEU:HD13	2.02	0.42
1:D:259:THR:O	1:D:260:MET:HB2	2.19	0.42
1:H:370:ARG:HA	1:H:370:ARG:HD2	1.67	0.42
1:H:486:LEU:HD23	1:H:486:LEU:HA	1.86	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:156:SER:HB2	1:C:224:ARG:O	2.20	0.41
1:C:530:GLU:HG2	1:C:533:HIS:H	1.84	0.41
1:D:259:THR:O	1:D:260:MET:CB	2.68	0.41
1:F:86:GLU:N	1:F:86:GLU:CD	2.78	0.41
1:G:72:ASP:HB3	1:G:79:ARG:HG2	2.02	0.41
1:H:142:ILE:HD11	1:H:311:ILE:HG12	2.00	0.41
1:H:396:PHE:HA	1:H:447:LYS:HE2	2.01	0.41
1:H:482:VAL:O	1:H:507:PRO:HD2	2.19	0.41
1:A:176:LEU:HD21	1:A:207:LEU:HD23	2.03	0.41
1:D:505:ASP:OD1	1:D:553:VAL:HG22	2.20	0.41
1:F:177:VAL:HG12	1:F:181:LYS:HD2	2.02	0.41
1:G:157:VAL:HG13	1:G:158:THR:HG23	2.02	0.41
1:H:195:LEU:HD23	1:H:359:LEU:HB3	2.02	0.41
1:H:222:GLU:OE1	1:H:224:ARG:HD2	2.19	0.41
1:H:312:ALA:HB1	1:H:524:ALA:HB3	2.02	0.41
1:A:325:GLN:HG2	1:A:512:THR:HG21	2.02	0.41
1:G:387:ILE:HD11	1:G:455:LEU:HD23	2.02	0.41
1:H:535:LYS:HE3	1:H:535:LYS:HB3	1.78	0.41
1:C:178:ARG:HG2	1:C:178:ARG:NH1	2.34	0.41
1:C:318:GLN:OE1	1:C:334:LYS:NZ	2.47	0.41
1:E:259:THR:O	1:E:260:MET:CB	2.69	0.41
1:F:259:THR:O	1:F:260:MET:CB	2.68	0.41
1:A:203:SER:HB3	1:A:259:THR:O	2.21	0.41
1:C:345:TYR:HB2	1:C:469:MET:SD	2.60	0.41
1:F:144:ILE:O	1:F:314:CYS:HA	2.21	0.41
1:G:145:THR:OG1	1:G:317:ASP:HA	2.20	0.41
1:H:83:PHE:CE1	1:H:509:MET:CE	2.93	0.41
1:H:207:LEU:CD1	1:H:277:PHE:O	2.69	0.41
1:H:216:VAL:HG12	1:H:225:LEU:HD22	2.03	0.41
1:B:145:THR:HA	1:B:315:LEU:O	2.20	0.41
1:D:200:TYR:HB2	1:D:201:PRO:HD3	2.02	0.41
1:D:317:ASP:OD1	1:D:318:GLN:N	2.53	0.41
1:H:459:CYS:HA	1:H:496:GLN:OE1	2.21	0.41
1:F:203:SER:HB3	1:F:259:THR:O	2.20	0.41
1:H:494:GLN:CD	1:H:557:LYS:NZ	2.78	0.41
1:B:144:ILE:O	1:B:314:CYS:HA	2.21	0.41
1:E:262:MET:HE3	1:E:267:LEU:HA	2.02	0.41
1:G:72:ASP:HB3	1:G:79:ARG:CG	2.51	0.41
1:H:220:TYR:O	1:H:283:LYS:CG	2.68	0.41
1:H:404:ASN:O	1:H:408:GLU:HG3	2.21	0.41
1:C:176:LEU:HD21	1:C:207:LEU:HD23	2.03	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:553:VAL:HG11	1:C:555:TYR:CZ	2.55	0.41
1:D:337:TYR:CZ	1:D:493:MET:HE1	2.56	0.41
1:D:421:ALA:HB2	1:D:425:LEU:HG	2.02	0.41
1:D:476:LYS:HB3	1:D:476:LYS:HE3	1.81	0.41
1:F:553:VAL:HG11	1:F:555:TYR:CZ	2.56	0.41
1:H:80:PHE:C	1:H:81:LEU:HD12	2.46	0.41
1:H:421:ALA:HB2	1:H:425:LEU:HG	2.02	0.41
1:C:298:PHE:HB2	1:C:311:ILE:O	2.20	0.41
1:D:240:GLY:O	1:D:244:ALA:CB	2.69	0.41
1:B:157:VAL:HG23	1:B:158:THR:N	2.36	0.40
1:C:73:GLN:HG3	1:C:234:LEU:HD11	2.02	0.40
1:C:259:THR:O	1:C:260:MET:CB	2.69	0.40
1:F:343:LEU:HD21	1:F:462:THR:HG23	2.03	0.40
1:G:515:LEU:HD21	1:G:538:ILE:HD13	2.04	0.40
1:D:471:LYS:NZ	4:D:711:HOH:O	2.33	0.40
1:E:155:ASP:CG	1:E:224:ARG:HE	2.30	0.40
1:F:404:ASN:HD21	1:F:489:SER:HB2	1.86	0.40
1:G:366:PHE:CE2	1:G:531:LEU:HD21	2.57	0.40
1:H:166:ILE:HG22	1:H:205:LYS:HE3	2.02	0.40
1:H:258:ARG:NH1	1:H:377:GLU:OE1	2.50	0.40
1:E:582:ARG:HH21	1:E:582:ARG:HD3	1.64	0.40
1:G:456:GLU:HB3	1:G:460:TYR:CE2	2.57	0.40
1:H:156:SER:HB2	1:H:285:LYS:HG3	2.03	0.40

All (1) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:280:ASP:OD2	1:G:184:GLN:NE2[1_455]	2.03	0.17

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	510/526 (97%)	495 (97%)	14 (3%)	1 (0%)	43	40
1	B	507/526 (96%)	493 (97%)	13 (3%)	1 (0%)	43	40
1	C	505/526 (96%)	490 (97%)	15 (3%)	0	100	100
1	D	505/526 (96%)	492 (97%)	13 (3%)	0	100	100
1	E	507/526 (96%)	495 (98%)	12 (2%)	0	100	100
1	F	508/526 (97%)	495 (97%)	13 (3%)	0	100	100
1	G	508/526 (97%)	492 (97%)	15 (3%)	1 (0%)	43	40
1	H	507/526 (96%)	490 (97%)	17 (3%)	0	100	100
All	All	4057/4208 (96%)	3942 (97%)	112 (3%)	3 (0%)	48	45

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	241	GLY
1	G	241	GLY
1	B	245	GLU

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	413/420 (98%)	411 (100%)	2 (0%)	81	81
1	B	410/420 (98%)	409 (100%)	1 (0%)	87	88
1	C	409/420 (97%)	409 (100%)	0	100	100
1	D	409/420 (97%)	408 (100%)	1 (0%)	87	88
1	E	409/420 (97%)	406 (99%)	3 (1%)	76	77
1	F	410/420 (98%)	410 (100%)	0	100	100
1	G	410/420 (98%)	407 (99%)	3 (1%)	76	77
1	H	409/420 (97%)	406 (99%)	3 (1%)	76	77
All	All	3279/3360 (98%)	3266 (100%)	13 (0%)	84	84

All (13) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	560	ARG
1	A	561	LYS
1	B	530	GLU
1	D	493	MET
1	E	218	GLN
1	E	399	LYS
1	E	401	SER
1	G	92	SER
1	G	370	ARG
1	G	510	ARG
1	H	370	ARG
1	H	530	GLU
1	H	551	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (12) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	212	ASN
1	A	461	GLN
1	A	494	GLN
1	B	282	ASN
1	B	449	HIS
1	E	212	ASN
1	E	218	GLN
1	F	212	ASN
1	F	549	ASN
1	G	212	ASN
1	H	212	ASN
1	H	572	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 [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

14 ligands are modelled in this entry.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
3	GOL	H	601	-	5,5,5	0.97	0	5,5,5	1.18	1 (20%)
3	GOL	C	602	-	5,5,5	0.80	0	5,5,5	1.15	1 (20%)
2	PO4	F	601	-	4,4,4	1.94	1 (25%)	6,6,6	0.43	0
3	GOL	F	602	-	5,5,5	0.81	0	5,5,5	1.18	1 (20%)
2	PO4	B	601	-	4,4,4	1.85	1 (25%)	6,6,6	0.71	0
3	GOL	G	601	-	5,5,5	0.93	0	5,5,5	1.12	1 (20%)
3	GOL	A	602	-	5,5,5	0.89	0	5,5,5	1.16	1 (20%)
2	PO4	E	601	-	4,4,4	1.46	1 (25%)	6,6,6	0.79	0
3	GOL	D	602	-	5,5,5	0.66	0	5,5,5	1.15	1 (20%)
2	PO4	C	601	-	4,4,4	0.99	0	6,6,6	0.56	0
2	PO4	A	601	-	4,4,4	1.63	1 (25%)	6,6,6	0.50	0
2	PO4	D	601	-	4,4,4	0.95	0	6,6,6	0.61	0
3	GOL	E	602	-	5,5,5	0.26	0	5,5,5	0.30	0
3	GOL	B	602	-	5,5,5	0.70	0	5,5,5	1.15	1 (20%)

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	GOL	H	601	-	-	3/4/4/4	-
3	GOL	C	602	-	-	0/4/4/4	-
3	GOL	F	602	-	-	0/4/4/4	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	GOL	G	601	-	-	0/4/4/4	-
3	GOL	A	602	-	-	0/4/4/4	-
3	GOL	D	602	-	-	1/4/4/4	-
3	GOL	E	602	-	-	0/4/4/4	-
3	GOL	B	602	-	-	0/4/4/4	-

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	601	PO4	P-O4	-3.29	1.45	1.54
2	F	601	PO4	P-O3	-2.46	1.47	1.54
2	A	601	PO4	P-O2	-2.11	1.48	1.54
2	E	601	PO4	P-O2	-2.05	1.48	1.54

All (7) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	D	602	GOL	C3-C2-C1	-2.28	103.42	111.80
3	H	601	GOL	C3-C2-C1	-2.27	103.47	111.80
3	F	602	GOL	C3-C2-C1	-2.24	103.59	111.80
3	B	602	GOL	C3-C2-C1	-2.22	103.67	111.80
3	A	602	GOL	C3-C2-C1	-2.21	103.68	111.80
3	C	602	GOL	C3-C2-C1	-2.18	103.80	111.80
3	G	601	GOL	C3-C2-C1	-2.09	104.15	111.80

There are no chirality outliers.

All (4) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	H	601	GOL	O1-C1-C2-C3
3	H	601	GOL	O1-C1-C2-O2
3	H	601	GOL	O2-C2-C3-O3
3	D	602	GOL	O2-C2-C3-O3

There are no ring outliers.

4 monomers are involved in 5 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	602	GOL	1	0
2	A	601	PO4	2	0
2	D	601	PO4	1	0

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Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	B	602	GOL	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	510/526 (96%)	0.17	16 (3%)	51	51	19, 51, 88, 119	3 (0%)
1	B	510/526 (96%)	-0.00	10 (1%)	65	65	23, 45, 86, 115	1 (0%)
1	C	509/526 (96%)	0.13	15 (2%)	53	53	30, 50, 89, 155	0
1	D	509/526 (96%)	0.15	16 (3%)	51	51	25, 49, 90, 135	0
1	E	511/526 (97%)	0.17	17 (3%)	49	48	26, 51, 98, 136	0
1	F	512/526 (97%)	0.10	14 (2%)	56	56	29, 49, 89, 168	0
1	G	512/526 (97%)	0.27	20 (3%)	43	43	33, 56, 93, 167	0
1	H	511/526 (97%)	0.42	29 (5%)	29	28	34, 60, 105, 194	0
All	All	4084/4208 (97%)	0.17	137 (3%)	48	47	19, 52, 93, 194	4 (0%)

All (137) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	469	MET	6.0
1	H	550	ALA	5.8
1	G	550	ALA	5.7
1	D	459	CYS	5.2
1	C	242	ALA	5.0
1	B	241	GLY	4.9
1	E	550	ALA	4.6
1	H	541	GLY	4.3
1	G	541	GLY	4.2
1	F	541	GLY	4.1
1	B	539	ALA	4.0
1	D	162	LEU	3.9
1	E	240	GLY	3.7
1	F	550	ALA	3.7
1	A	65	GLY	3.7
1	F	65	GLY	3.7

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Mol	Chain	Res	Type	RSRZ
1	A	550	ALA	3.6
1	H	216	VAL	3.6
1	C	550	ALA	3.6
1	B	555	TYR	3.6
1	H	367	GLY	3.5
1	C	241	GLY	3.5
1	E	541	GLY	3.5
1	H	157	VAL	3.5
1	A	171	THR	3.4
1	C	539	ALA	3.4
1	H	184	GLN	3.4
1	E	540	GLY	3.4
1	H	171	THR	3.3
1	H	240	GLY	3.3
1	G	242	ALA	3.3
1	H	538	ILE	3.3
1	G	368	ARG	3.3
1	H	540	GLY	3.3
1	A	127	HIS	3.2
1	G	127	HIS	3.2
1	H	582	ARG	3.2
1	E	213	VAL	3.2
1	G	157	VAL	3.2
1	A	540	GLY	3.0
1	F	538	ILE	3.0
1	C	240	GLY	3.0
1	C	184	GLN	3.0
1	G	582	ARG	3.0
1	D	65	GLY	3.0
1	F	171	THR	2.9
1	C	65	GLY	2.9
1	G	540	GLY	2.8
1	H	65	GLY	2.8
1	G	510	ARG	2.8
1	D	240	GLY	2.8
1	E	510	ARG	2.8
1	A	582	ARG	2.7
1	D	242	ALA	2.7
1	A	244	ALA	2.7
1	A	225	LEU	2.7
1	E	186	ALA	2.6
1	E	242	ALA	2.6

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Mol	Chain	Res	Type	RSRZ
1	C	156	SER	2.6
1	F	540	GLY	2.6
1	H	241	GLY	2.6
1	G	184	GLN	2.6
1	B	541	GLY	2.6
1	G	159	GLY	2.6
1	B	582	ARG	2.6
1	D	241	GLY	2.6
1	E	278	GLY	2.6
1	F	582	ARG	2.6
1	G	563	ALA	2.6
1	A	128	LYS	2.5
1	B	244	ALA	2.5
1	H	242	ALA	2.5
1	A	370[A]	ARG	2.5
1	H	557	LYS	2.5
1	H	102	PRO	2.4
1	D	539	ALA	2.4
1	H	224	ARG	2.4
1	E	214	ASP	2.4
1	C	66	SER	2.4
1	H	220	TYR	2.4
1	H	106	TRP	2.4
1	E	368	ARG	2.4
1	H	128	LYS	2.4
1	F	242	ALA	2.4
1	F	162	LEU	2.4
1	D	559	ASP	2.4
1	E	246	ARG	2.4
1	D	540	GLY	2.3
1	E	223	GLY	2.3
1	A	368	ARG	2.3
1	C	157	VAL	2.3
1	A	539	ALA	2.3
1	C	476	LYS	2.3
1	G	216	VAL	2.3
1	A	530	GLU	2.3
1	A	210	ILE	2.3
1	E	157	VAL	2.3
1	H	244	ALA	2.3
1	D	583	GLU	2.2
1	G	564	GLU	2.2

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Mol	Chain	Res	Type	RSRZ
1	G	551	ARG	2.2
1	C	182	ALA	2.2
1	F	245	GLU	2.2
1	C	216	VAL	2.2
1	G	219	ALA	2.2
1	H	225	LEU	2.2
1	D	280	ASP	2.2
1	G	241	GLY	2.2
1	C	551	ARG	2.2
1	H	473	SER	2.2
1	C	538	ILE	2.1
1	F	222	GLU	2.1
1	G	536	GLU	2.1
1	D	218	GLN	2.1
1	F	241	GLY	2.1
1	E	551	ARG	2.1
1	B	557	LYS	2.1
1	H	99	ASN	2.1
1	E	218	GLN	2.1
1	D	97	PHE	2.1
1	H	426	PHE	2.1
1	G	244	ALA	2.1
1	A	473	SER	2.1
1	E	243	GLN	2.1
1	B	538	ILE	2.1
1	H	509	MET	2.1
1	H	159	GLY	2.1
1	B	510	ARG	2.0
1	H	95	ILE	2.0
1	D	157	VAL	2.0
1	G	583	GLU	2.0
1	D	156	SER	2.0
1	F	539	ALA	2.0
1	H	476	LYS	2.0
1	D	247	PRO	2.0
1	A	240	GLY	2.0
1	F	240	GLY	2.0

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

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

6.3 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

6.4 Ligands [i](#)

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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
2	PO4	E	601	5/5	0.79	0.17	56,60,67,67	5
2	PO4	A	601	5/5	0.81	0.18	57,60,66,68	5
2	PO4	C	601	5/5	0.82	0.20	54,59,64,68	5
2	PO4	F	601	5/5	0.83	0.17	47,51,58,58	5
2	PO4	B	601	5/5	0.87	0.16	55,57,65,66	5
2	PO4	D	601	5/5	0.87	0.16	53,56,65,69	5
3	GOL	H	601	6/6	0.95	0.11	32,37,45,45	0
3	GOL	A	602	6/6	0.96	0.06	30,34,41,41	0
3	GOL	E	602	6/6	0.97	0.05	32,33,42,46	0
3	GOL	F	602	6/6	0.97	0.05	30,31,39,39	0
3	GOL	G	601	6/6	0.97	0.05	32,34,40,41	0
3	GOL	C	602	6/6	0.97	0.06	23,26,31,33	0
3	GOL	B	602	6/6	0.98	0.04	22,26,31,31	0
3	GOL	D	602	6/6	0.98	0.04	24,29,34,34	0

6.5 Other polymers [i](#)

There are no such residues in this entry.