



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 12, 2026 – 02:51 PM UTC

PDB ID : 5K8P / pdb_00005k8p
Title : Zn²⁺/Tetrahedral intermediate-bound R289A 5-nitroanthranilate aminohydrolase
Authors : Kalyoncu, S.
Deposited on : 2016-05-30
Resolution : 2.20 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

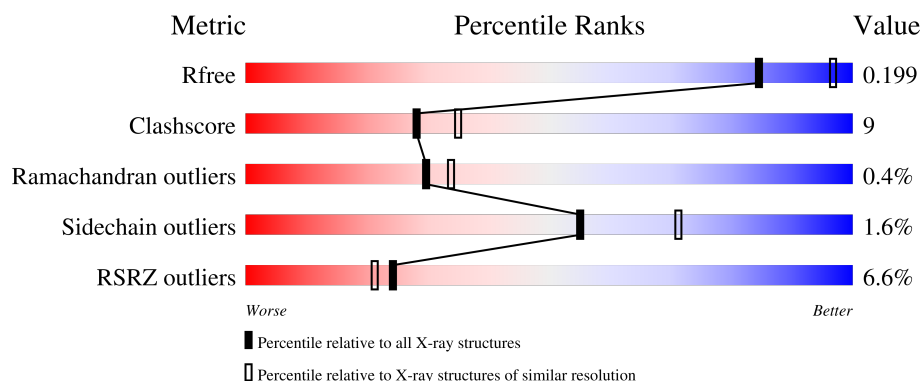
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.20 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	6164 (2.20-2.20)
Clashscore	190562	6851 (2.20-2.20)
Ramachandran outliers	187476	6768 (2.20-2.20)
Sidechain outliers	187428	6769 (2.20-2.20)
RSRZ outliers	180081	6166 (2.20-2.20)

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	425	8% 81% 16% ..
1	B	425	6% 85% 13% ..
1	C	425	6% 82% 16% ..
1	D	425	8% 83% 17%
1	E	425	4% 88% 11%

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Mol	Chain	Length	Quality of chain
1	F	425	
1	G	425	
1	H	425	

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 27782 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 5-nitroanthranilic acid aminohydrolase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	421	Total	C	N	O	S	0	0	0
			3229	2043	559	608	19			
1	B	421	Total	C	N	O	S	0	0	0
			3229	2043	559	608	19			
1	C	422	Total	C	N	O	S	0	0	0
			3235	2046	560	610	19			
1	D	425	Total	C	N	O	S	0	0	0
			3252	2056	563	613	20			
1	E	423	Total	C	N	O	S	0	0	0
			3239	2048	561	611	19			
1	F	425	Total	C	N	O	S	0	0	0
			3252	2056	563	613	20			
1	G	421	Total	C	N	O	S	0	0	0
			3229	2043	559	608	19			
1	H	422	Total	C	N	O	S	0	0	0
			3235	2046	560	610	19			

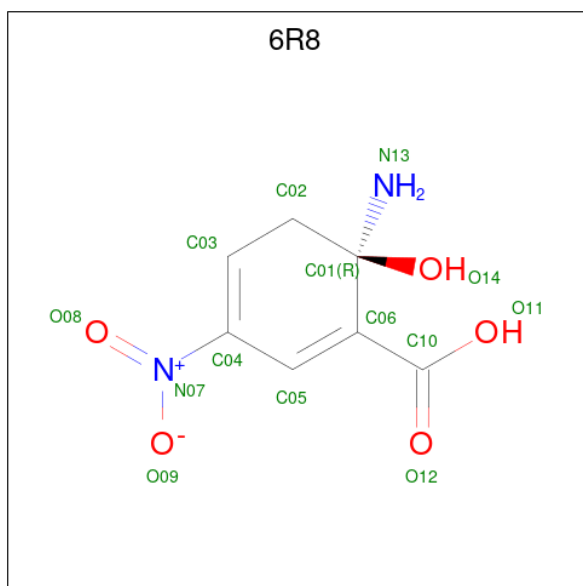
There are 8 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	289	ALA	ARG	engineered mutation	UNP D3WZ85
B	289	ALA	ARG	engineered mutation	UNP D3WZ85
C	289	ALA	ARG	engineered mutation	UNP D3WZ85
D	289	ALA	ARG	engineered mutation	UNP D3WZ85
E	289	ALA	ARG	engineered mutation	UNP D3WZ85
F	289	ALA	ARG	engineered mutation	UNP D3WZ85
G	289	ALA	ARG	engineered mutation	UNP D3WZ85
H	289	ALA	ARG	engineered mutation	UNP D3WZ85

- Molecule 2 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	1	Total	Zn	0	0
			1	1		
2	B	1	Total	Zn	0	0
			1	1		
2	C	1	Total	Zn	0	0
			1	1		
2	D	1	Total	Zn	0	0
			1	1		
2	E	1	Total	Zn	0	0
			1	1		
2	F	1	Total	Zn	0	0
			1	1		
2	G	1	Total	Zn	0	0
			1	1		
2	H	1	Total	Zn	0	0
			1	1		

- Molecule 3 is (6 {R})-6-azanyl-3-nitro-6-oxidanyl-cyclohexa-1,3-diene-1-carboxylic acid (CCD ID: 6R8) (formula: C₇H₈N₂O₅).



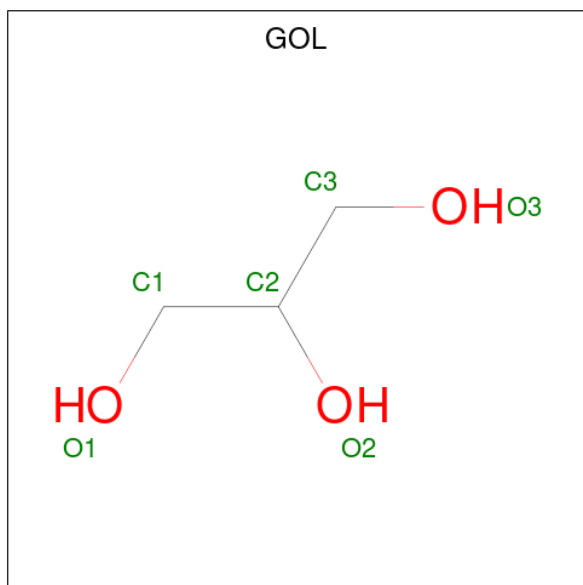
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	A	1	Total	C	N	O	0	0
			14	7	2	5		
3	B	1	Total	C	N	O	0	0
			14	7	2	5		
3	C	1	Total	C	N	O	0	0
			14	7	2	5		

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Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	E	1	Total	C	N	O	0	0
			14	7	2	5		
3	G	1	Total	C	N	O	0	0
			14	7	2	5		
3	H	1	Total	C	N	O	0	0
			14	7	2	5		

- Molecule 4 is GLYCEROL (CCD ID: GOL) (formula: $C_3H_8O_3$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	A	1	Total	C	O	0	0
			6	3	3		
4	B	1	Total	C	O	0	0
			6	3	3		
4	C	1	Total	C	O	0	0
			6	3	3		
4	D	1	Total	C	O	0	0
			6	3	3		
4	E	1	Total	C	O	0	0
			6	3	3		
4	F	1	Total	C	O	0	0
			6	3	3		
4	G	1	Total	C	O	0	0
			6	3	3		
4	H	1	Total	C	O	0	0
			6	3	3		

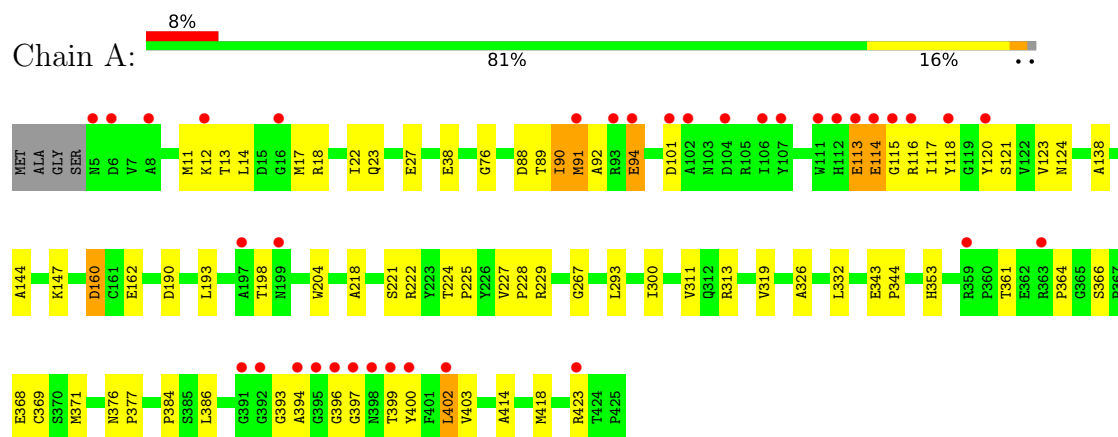
- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	175	Total 175	O 175	0	0
5	B	249	Total 249	O 249	0	0
5	C	251	Total 251	O 251	0	0
5	D	235	Total 235	O 235	0	0
5	E	225	Total 225	O 225	0	0
5	F	233	Total 233	O 233	0	0
5	G	179	Total 179	O 179	0	0
5	H	195	Total 195	O 195	0	0

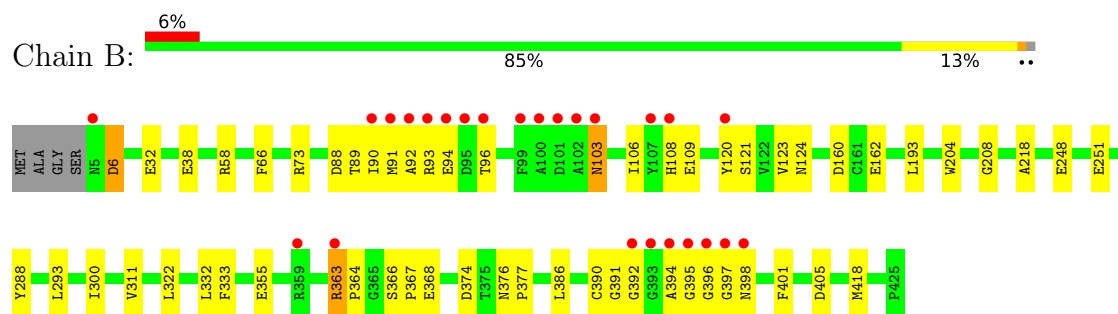
3 Residue-property plots

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.

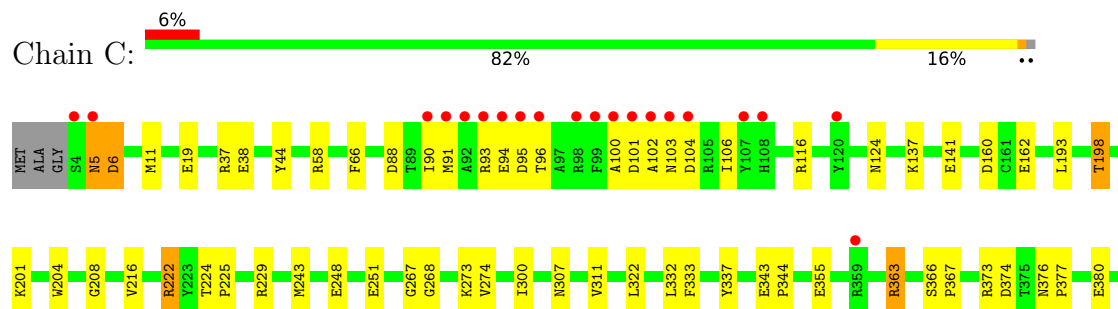
- Molecule 1: 5-nitroanthranilic acid aminohydrolase

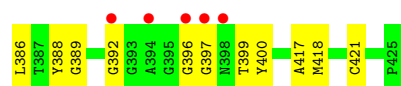


- Molecule 1: 5-nitroanthranilic acid aminohydrolase

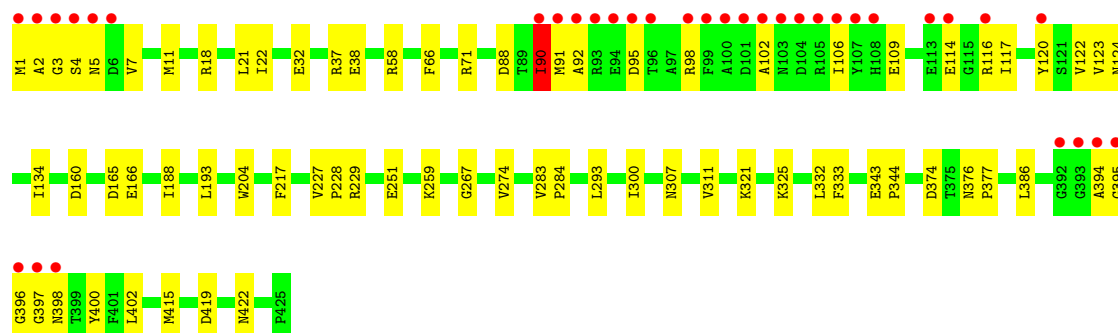
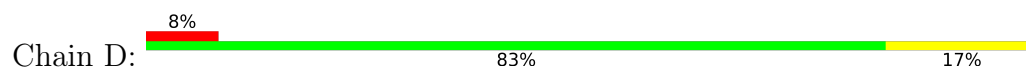


- Molecule 1: 5-nitroanthranilic acid aminohydrolase

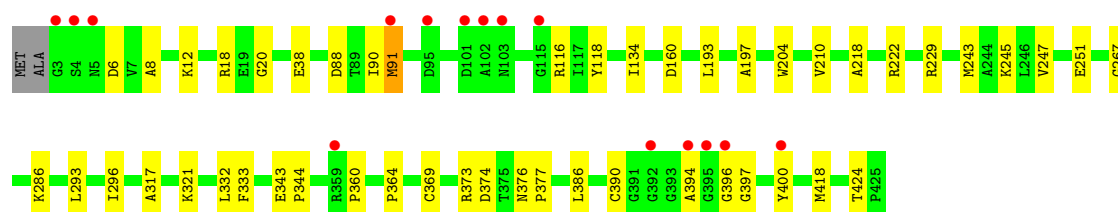
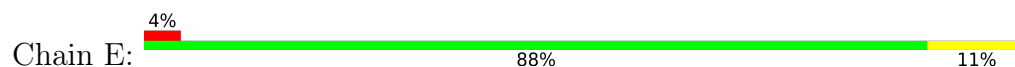




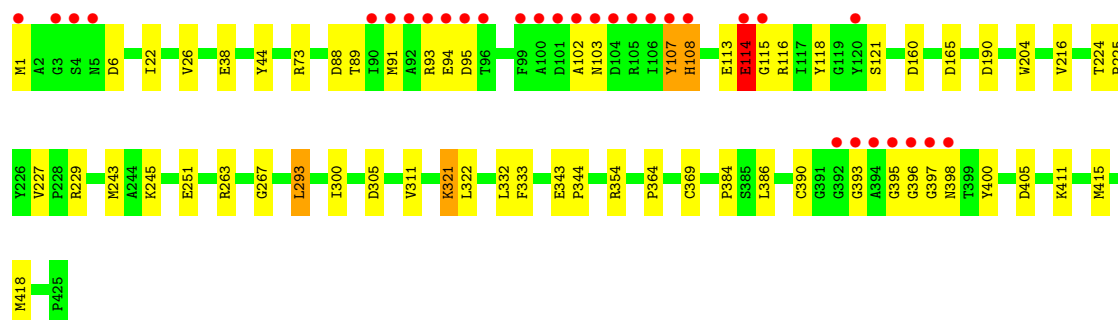
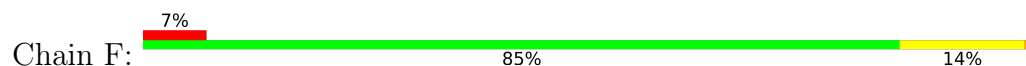
- Molecule 1: 5-nitroanthranilic acid aminohydrolase



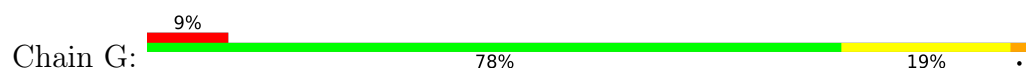
- Molecule 1: 5-nitroanthranilic acid aminohydrolase

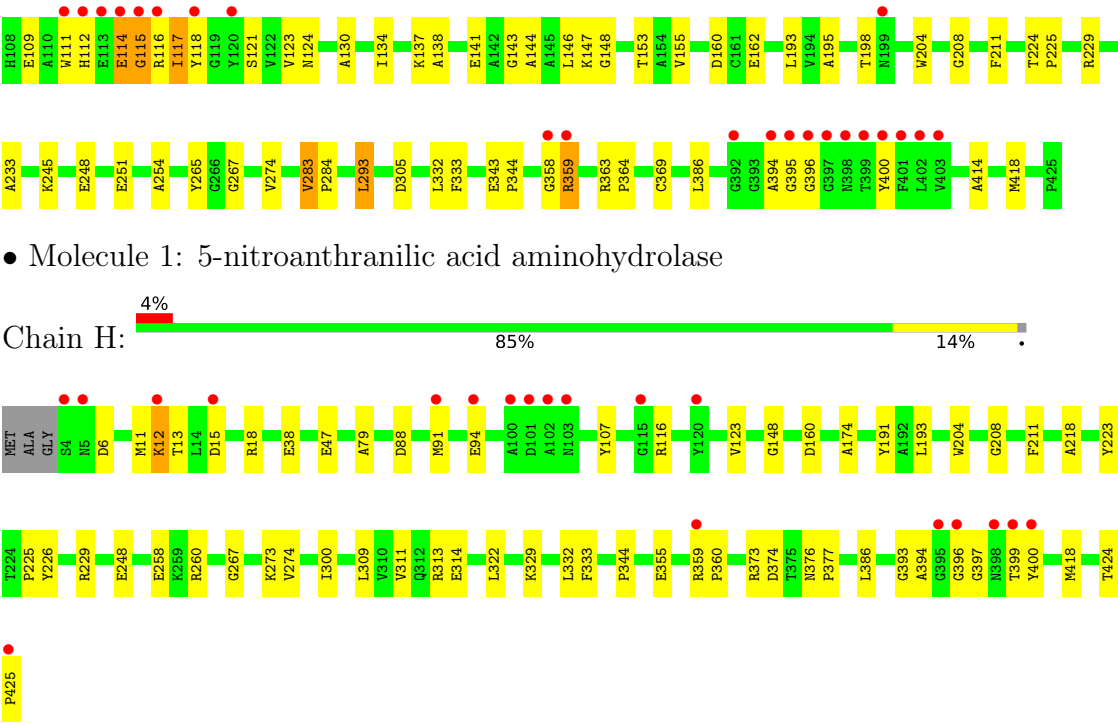


- Molecule 1: 5-nitroanthranilic acid aminohydrolase

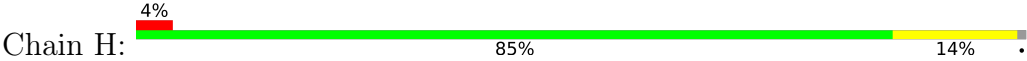


- Molecule 1: 5-nitroanthranilic acid aminohydrolase





● Molecule 1: 5-nitroanthranilic acid aminohydrolase



4 Data and refinement statistics

Property	Value	Source
Space group	C 2 2 21	Depositor
Cell constants a, b, c, α , β , γ	185.88Å 247.63Å 247.87Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	37.16 – 2.20 37.16 – 2.20	Depositor EDS
% Data completeness (in resolution range)	60.3 (37.16-2.20) 94.0 (37.16-2.20)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.14 (at 2.20Å)	Xtriage
Refinement program	PHENIX 1.9_1692	Depositor
R, R_{free}	0.174 , 0.204 0.172 , 0.199	Depositor DCC
R_{free} test set	2000 reflections (0.70%)	wwPDB-VP
Wilson B-factor (Å ²)	28.8	Xtriage
Anisotropy	0.005	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 34.5	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	27782	wwPDB-VP
Average B, all atoms (Å ²)	32.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 12.31% 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: ZN, 6R8, 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	0.56	0/3303	0.81	4/4484 (0.1%)
1	B	0.60	0/3303	0.78	1/4484 (0.0%)
1	C	0.61	0/3309	0.80	3/4492 (0.1%)
1	D	0.59	0/3326	0.80	2/4514 (0.0%)
1	E	0.60	0/3313	0.80	0/4497
1	F	0.58	0/3326	0.80	1/4514 (0.0%)
1	G	0.57	0/3303	0.83	8/4484 (0.2%)
1	H	0.59	0/3309	0.78	2/4492 (0.0%)
All	All	0.59	0/26492	0.80	21/35961 (0.1%)

There are no bond length outliers.

All (21) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	G	115	GLY	N-CA-C	-8.48	102.09	116.01
1	D	90	ILE	N-CA-C	7.50	117.56	110.74
1	C	392	GLY	N-CA-C	-6.25	104.08	112.14
1	H	208	GLY	N-CA-C	-6.09	103.90	112.60
1	G	6	ASP	N-CA-C	-6.07	104.97	112.38
1	A	198	THR	N-CA-C	-6.06	100.97	110.36
1	G	208	GLY	N-CA-C	-5.97	104.06	112.60
1	A	198	THR	CA-C-N	-5.70	114.14	122.06
1	A	198	THR	C-N-CA	-5.70	114.14	122.06
1	A	90	ILE	N-CA-C	5.58	116.23	110.82
1	D	165	ASP	CB-CA-C	-5.53	110.18	116.54
1	G	283	VAL	CA-C-N	5.53	125.36	119.28
1	G	283	VAL	C-N-CA	5.53	125.36	119.28
1	H	13	THR	N-CA-C	-5.51	105.68	112.90
1	G	198	THR	N-CA-C	-5.31	102.13	110.36
1	C	6	ASP	N-CA-C	-5.30	105.50	111.28

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	G	198	THR	CA-C-N	-5.15	114.91	122.06
1	G	198	THR	C-N-CA	-5.15	114.91	122.06
1	B	208	GLY	N-CA-C	-5.03	105.41	112.60
1	C	208	GLY	N-CA-C	-5.02	104.88	112.41
1	F	165	ASP	CB-CA-C	-5.01	110.78	116.54

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	3229	0	3157	62	0
1	B	3229	0	3157	44	0
1	C	3235	0	3162	61	0
1	D	3252	0	3182	69	0
1	E	3239	0	3165	43	0
1	F	3252	0	3182	61	0
1	G	3229	0	3157	89	0
1	H	3235	0	3162	50	0
2	A	1	0	0	0	0
2	B	1	0	0	0	0
2	C	1	0	0	0	0
2	D	1	0	0	0	0
2	E	1	0	0	0	0
2	F	1	0	0	0	0
2	G	1	0	0	0	0
2	H	1	0	0	0	0
3	A	14	0	0	2	0
3	B	14	0	0	0	0
3	C	14	0	0	1	0
3	E	14	0	0	0	0
3	G	14	0	0	0	0
3	H	14	0	0	1	0
4	A	6	0	8	0	0
4	B	6	0	8	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	C	6	0	8	1	0
4	D	6	0	8	1	0
4	E	6	0	8	0	0
4	F	6	0	8	1	0
4	G	6	0	8	0	0
4	H	6	0	8	0	0
5	A	175	0	0	1	0
5	B	249	0	0	3	0
5	C	251	0	0	2	0
5	D	235	0	0	8	0
5	E	225	0	0	5	0
5	F	233	0	0	7	1
5	G	179	0	0	7	1
5	H	195	0	0	4	0
All	All	27782	0	25388	457	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 9.

All (457) 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:G:49:MET:HE2	1:G:56:PRO:HB3	1.24	1.15
1:H:373:ARG:NH1	3:H:502:6R8:O11	1.90	1.03
1:C:91:MET:HE2	1:C:103:ASN:HD21	1.23	1.00
1:G:49:MET:HE1	1:G:70:GLY:HA3	1.44	0.98
1:E:38:GLU:HG2	1:E:88:ASP:HB3	1.46	0.97
1:A:116:ARG:HD2	1:A:400:TYR:CD2	2.10	0.87
1:D:2:ALA:HB2	1:D:419:ASP:HB2	1.55	0.87
1:C:91:MET:HE3	1:C:95:ASP:HB2	1.56	0.87
1:G:229:ARG:NH1	1:H:274:VAL:O	2.09	0.86
1:G:395:GLY:H	1:G:396:GLY:HA3	1.40	0.85
1:G:11:MET:HE2	1:G:11:MET:HA	1.57	0.85
1:F:91:MET:HG2	1:F:107:TYR:CE1	2.12	0.84
1:H:38:GLU:HG2	1:H:88:ASP:HB3	1.57	0.84
1:C:363:ARG:HH21	1:C:363:ARG:HG3	1.43	0.83
1:C:91:MET:HE2	1:C:103:ASN:ND2	1.93	0.83
1:D:32:GLU:OE2	1:D:37:ARG:NH2	2.11	0.82
1:G:22:ILE:HG23	1:G:117:ILE:HD11	1.62	0.81
1:H:12:LYS:NZ	1:H:15:ASP:HB3	1.96	0.81
1:D:91:MET:HE1	1:D:102:ALA:HB1	1.65	0.79

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:71:ARG:NH2	5:D:601:HOH:O	1.93	0.78
1:G:49:MET:HE1	1:G:70:GLY:CA	2.13	0.78
1:G:123:VAL:HG11	1:G:394:ALA:HB2	1.66	0.77
1:C:91:MET:CE	1:C:103:ASN:HD21	1.98	0.77
1:A:113:GLU:HG3	1:A:118:TYR:CE2	2.20	0.77
1:C:198:THR:HG23	1:C:201:LYS:H	1.50	0.77
1:B:91:MET:HE2	1:B:103:ASN:H	1.50	0.76
1:G:49:MET:CE	1:G:70:GLY:HA3	2.16	0.76
1:F:93:ARG:HH11	1:F:108:HIS:HD2	1.34	0.76
1:C:198:THR:HG22	1:C:389:GLY:H	1.49	0.75
1:G:116:ARG:HD3	1:G:400:TYR:HB2	1.68	0.75
1:H:329:LYS:NZ	5:H:601:HOH:O	2.18	0.75
1:G:38:GLU:HG2	1:G:88:ASP:HB3	1.68	0.75
1:G:114:GLU:CD	1:G:116:ARG:HB2	2.12	0.74
1:G:114:GLU:OE2	1:G:116:ARG:HB2	1.87	0.74
1:G:414:ALA:O	1:G:418:MET:HG3	1.89	0.73
1:C:38:GLU:HG2	1:C:88:ASP:HB3	1.70	0.72
1:G:111:TRP:O	5:G:601:HOH:O	2.08	0.71
1:G:364:PRO:HG2	1:G:369:CYS:SG	2.30	0.71
1:A:393:GLY:O	1:A:397:GLY:HA2	1.91	0.71
1:A:364:PRO:HG2	1:A:369:CYS:SG	2.31	0.71
1:C:106:ILE:HD11	1:C:399:THR:HG23	1.73	0.70
1:B:38:GLU:HG2	1:B:88:ASP:HB3	1.74	0.70
1:F:114:GLU:HG2	1:F:115:GLY:H	1.57	0.69
1:A:90:ILE:HB	1:A:91:MET:HE2	1.74	0.69
1:E:321:LYS:HD3	1:E:321:LYS:N	2.06	0.69
1:F:93:ARG:HH11	1:F:108:HIS:CD2	2.11	0.69
1:F:38:GLU:HG2	1:F:88:ASP:HB3	1.74	0.68
1:G:116:ARG:HD3	1:G:400:TYR:CD2	2.27	0.68
1:H:12:LYS:HZ1	1:H:15:ASP:HB3	1.58	0.68
1:G:49:MET:HE2	1:G:56:PRO:CB	2.14	0.68
1:D:71:ARG:NH1	5:D:603:HOH:O	2.23	0.67
1:G:22:ILE:HG23	1:G:117:ILE:CD1	2.24	0.66
1:B:6:ASP:HB3	1:B:418:MET:CE	2.24	0.66
1:D:398:ASN:ND2	1:D:400:TYR:O	2.28	0.66
1:G:90:ILE:HB	1:G:91:MET:HE2	1.78	0.65
1:C:229:ARG:HH22	1:F:251:GLU:CD	2.03	0.65
1:F:1:MET:O	5:F:601:HOH:O	2.15	0.65
1:C:198:THR:HG21	1:C:388:TYR:HA	1.77	0.65
1:G:22:ILE:O	1:G:26:VAL:HG23	1.97	0.65
1:F:116:ARG:HD3	1:F:400:TYR:CD2	2.32	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:293:LEU:HD12	1:F:293:LEU:H	1.61	0.64
1:A:38:GLU:CG	1:A:88:ASP:HB3	2.28	0.64
1:G:38:GLU:CG	1:G:88:ASP:HB3	2.28	0.64
1:G:123:VAL:CG1	1:G:394:ALA:HB2	2.26	0.64
1:E:364:PRO:HG2	1:E:369:CYS:SG	2.37	0.64
1:H:394:ALA:O	1:H:397:GLY:HA3	1.98	0.64
1:A:144:ALA:HB1	1:A:418:MET:HE3	1.80	0.64
1:E:38:GLU:CG	1:E:88:ASP:HB3	2.26	0.64
1:F:393:GLY:O	1:F:397:GLY:HA2	1.98	0.63
1:B:123:VAL:HG12	1:B:394:ALA:HB2	1.80	0.63
1:G:90:ILE:HD11	1:G:124:ASN:HD22	1.64	0.63
1:D:22:ILE:HG23	1:D:117:ILE:HD11	1.79	0.62
1:H:18:ARG:HD3	5:H:604:HOH:O	1.98	0.62
1:A:38:GLU:HG2	1:A:88:ASP:HB3	1.79	0.62
1:D:91:MET:HE1	1:D:102:ALA:CB	2.29	0.62
1:F:293:LEU:HD12	1:F:293:LEU:N	2.15	0.62
1:C:332:LEU:HG	1:C:333:PHE:N	2.14	0.62
1:E:90:ILE:HB	1:E:91:MET:HE2	1.82	0.62
1:F:411:LYS:NZ	5:F:606:HOH:O	2.33	0.61
1:H:38:GLU:CG	1:H:88:ASP:HB3	2.26	0.61
1:E:6:ASP:HB3	1:E:418:MET:CE	2.30	0.61
1:A:11:MET:HA	1:A:11:MET:HE2	1.81	0.61
1:A:414:ALA:O	1:A:418:MET:HG3	2.00	0.61
1:F:103:ASN:N	1:F:107:TYR:HE2	1.99	0.61
1:A:113:GLU:HG3	1:A:118:TYR:HE2	1.63	0.61
1:B:363:ARG:HD2	1:B:364:PRO:HD2	1.82	0.61
1:G:6:ASP:N	5:G:603:HOH:O	2.31	0.61
1:C:251:GLU:CD	1:F:229:ARG:HH22	2.09	0.60
1:F:113:GLU:O	1:F:114:GLU:HG2	2.01	0.60
1:F:91:MET:HG2	1:F:107:TYR:CD1	2.36	0.60
1:C:106:ILE:CD1	1:C:399:THR:HG23	2.31	0.60
1:C:198:THR:CG2	1:C:389:GLY:H	2.15	0.60
1:G:193:LEU:C	1:G:193:LEU:HD23	2.26	0.60
1:G:251:GLU:CD	1:H:229:ARG:HH22	2.10	0.60
1:A:120:TYR:CE1	1:A:399:THR:HG22	2.37	0.60
1:D:58:ARG:HG2	1:D:66:PHE:CD1	2.36	0.60
1:G:112:HIS:HE1	1:G:115:GLY:HA2	1.66	0.60
1:D:1:MET:SD	1:D:2:ALA:HA	2.42	0.59
1:C:37:ARG:NH1	5:C:606:HOH:O	2.34	0.59
1:C:100:ALA:C	1:C:102:ALA:H	2.11	0.59
1:G:14:LEU:HD23	1:G:138:ALA:HB2	1.84	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:1:MET:HE3	1:D:422:ASN:HB3	1.85	0.59
1:B:332:LEU:HG	1:B:333:PHE:N	2.16	0.59
1:H:12:LYS:HZ1	1:H:15:ASP:CB	2.15	0.59
1:H:12:LYS:HZ2	1:H:15:ASP:HB3	1.68	0.59
1:B:6:ASP:HB3	1:B:418:MET:HE1	1.83	0.59
1:G:395:GLY:N	1:G:396:GLY:HA3	2.06	0.58
1:D:396:GLY:N	1:D:397:GLY:HA2	2.17	0.58
1:F:93:ARG:HG2	5:F:618:HOH:O	2.03	0.58
1:C:248:GLU:OE2	5:C:601:HOH:O	2.17	0.58
1:F:332:LEU:HG	1:F:333:PHE:N	2.18	0.58
1:G:18:ARG:O	1:G:22:ILE:HG13	2.04	0.58
1:E:332:LEU:HG	1:E:333:PHE:N	2.18	0.58
1:E:286:LYS:NZ	5:E:604:HOH:O	2.35	0.57
1:D:32:GLU:CD	1:D:37:ARG:HH22	2.12	0.57
1:D:91:MET:HE3	1:D:95:ASP:HB2	1.85	0.57
1:A:222:ARG:NH1	1:B:395:GLY:O	2.38	0.57
1:F:38:GLU:CG	1:F:88:ASP:HB3	2.35	0.57
1:G:116:ARG:HD3	1:G:400:TYR:CB	2.35	0.57
1:G:11:MET:HE2	1:G:11:MET:CA	2.32	0.57
1:A:402:LEU:N	1:A:402:LEU:HD12	2.20	0.56
1:A:423:ARG:HH21	1:A:423:ARG:HG3	1.70	0.56
1:F:89:THR:HG21	1:F:121:SER:HB2	1.88	0.56
1:A:124:ASN:OD1	3:A:502:6R8:O11	2.24	0.56
1:D:2:ALA:HB2	1:D:419:ASP:CB	2.31	0.56
1:F:114:GLU:CG	1:F:115:GLY:H	2.18	0.56
1:B:92:ALA:C	1:B:94:GLU:H	2.14	0.56
1:D:395:GLY:O	1:E:222:ARG:NH2	2.39	0.56
1:C:38:GLU:CG	1:C:88:ASP:HB3	2.36	0.56
1:A:229:ARG:HH22	1:B:251:GLU:CD	2.14	0.55
1:C:373:ARG:NH1	3:C:502:6R8:O12	2.39	0.55
1:G:332:LEU:HG	1:G:333:PHE:N	2.21	0.55
1:E:243:MET:CE	1:E:296:ILE:HD13	2.36	0.55
1:H:123:VAL:HG12	1:H:394:ALA:HB2	1.88	0.55
1:A:222:ARG:NH1	1:B:396:GLY:O	2.40	0.55
1:F:6:ASP:HB3	1:F:418:MET:HE1	1.88	0.55
1:F:91:MET:CE	1:F:102:ALA:HA	2.37	0.55
1:D:38:GLU:HG2	1:D:88:ASP:HB3	1.88	0.55
1:E:394:ALA:O	1:E:397:GLY:HA3	2.07	0.55
1:F:91:MET:HE1	1:F:102:ALA:HA	1.89	0.55
1:D:376:ASN:HB2	1:D:377:PRO:HD3	1.89	0.55
1:E:243:MET:CE	1:E:247:VAL:HG23	2.37	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:376:ASN:HB2	1:E:377:PRO:HD3	1.89	0.55
1:A:204:TRP:CE2	1:A:267:GLY:HA2	2.42	0.55
1:B:293:LEU:C	1:B:293:LEU:HD12	2.32	0.54
1:D:293:LEU:C	1:D:293:LEU:HD12	2.33	0.54
1:G:114:GLU:OE1	1:G:116:ARG:HB2	2.06	0.54
1:F:91:MET:N	5:F:608:HOH:O	2.39	0.54
1:B:391:GLY:HA3	1:B:401:PHE:CE1	2.42	0.54
1:D:217:PHE:HB2	1:D:325:LYS:HE3	1.90	0.54
1:E:243:MET:HE2	1:E:296:ILE:HD13	1.89	0.54
1:F:398:ASN:ND2	1:F:400:TYR:O	2.41	0.54
1:G:386:LEU:HD12	1:G:386:LEU:C	2.33	0.54
1:B:32:GLU:OE2	1:B:93:ARG:NE	2.34	0.54
1:B:38:GLU:CG	1:B:88:ASP:HB3	2.37	0.54
1:H:11:MET:HA	1:H:11:MET:HE2	1.89	0.54
1:G:17:MET:HE1	1:G:137:LYS:HG3	1.90	0.54
1:F:22:ILE:O	1:F:26:VAL:HG23	2.08	0.53
1:A:124:ASN:CG	3:A:502:6R8:O11	2.52	0.53
1:B:376:ASN:HB2	1:B:377:PRO:HD3	1.91	0.53
1:D:386:LEU:HD12	1:D:386:LEU:C	2.33	0.53
1:F:93:ARG:HD3	1:F:108:HIS:CD2	2.44	0.53
1:H:12:LYS:HA	1:H:15:ASP:OD1	2.08	0.53
1:A:394:ALA:O	1:A:397:GLY:HA3	2.08	0.53
1:A:386:LEU:C	1:A:386:LEU:HD12	2.33	0.53
1:C:198:THR:HG22	1:C:389:GLY:O	2.09	0.53
1:D:90:ILE:HG22	1:D:91:MET:N	2.23	0.53
1:F:305:ASP:HA	4:F:502:GOL:H11	1.90	0.53
1:A:22:ILE:HG23	1:A:117:ILE:HD11	1.90	0.53
1:A:101:ASP:OD1	1:A:101:ASP:N	2.42	0.53
1:A:162:GLU:HG3	1:A:332:LEU:HD22	1.91	0.53
1:H:376:ASN:HB2	1:H:377:PRO:HD3	1.90	0.53
1:G:32:GLU:HG2	1:G:37:ARG:HH21	1.73	0.53
1:G:116:ARG:C	1:G:117:ILE:HG12	2.33	0.53
1:D:7:VAL:O	1:D:11:MET:HG2	2.08	0.52
1:G:14:LEU:CD2	1:G:138:ALA:HB2	2.39	0.52
1:A:14:LEU:CD2	1:A:138:ALA:HB2	2.39	0.52
1:A:18:ARG:O	1:A:22:ILE:HG13	2.08	0.52
1:D:204:TRP:HB3	1:D:386:LEU:HB3	1.91	0.52
1:G:293:LEU:N	1:G:293:LEU:HD12	2.24	0.52
1:A:76:GLY:O	1:A:147:LYS:HB3	2.08	0.52
1:D:114:GLU:OE1	1:D:116:ARG:HD2	2.10	0.52
1:F:107:TYR:CD1	1:F:107:TYR:C	2.88	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:216:VAL:HG23	1:F:243:MET:CE	2.39	0.52
1:H:116:ARG:HD3	1:H:400:TYR:CD2	2.44	0.52
1:C:90:ILE:HD11	1:C:124:ASN:HD22	1.75	0.52
1:C:307:ASN:HA	4:C:503:GOL:H11	1.90	0.51
1:D:251:GLU:CD	1:E:229:ARG:HH22	2.17	0.51
1:A:89:THR:HG21	1:A:121:SER:HB2	1.92	0.51
1:D:1:MET:HB3	1:D:419:ASP:OD1	2.11	0.51
1:H:6:ASP:HB3	1:H:418:MET:CE	2.40	0.51
1:C:91:MET:CE	1:C:95:ASP:HB2	2.33	0.51
1:H:332:LEU:HG	1:H:333:PHE:N	2.25	0.51
1:A:14:LEU:HD23	1:A:138:ALA:HB2	1.93	0.51
1:D:229:ARG:HH22	1:E:251:GLU:CD	2.19	0.51
1:G:114:GLU:O	1:G:114:GLU:HG2	2.09	0.51
1:A:116:ARG:HD2	1:A:400:TYR:CE2	2.45	0.51
1:D:300:ILE:HG21	1:D:311:VAL:HG11	1.91	0.51
1:F:354:ARG:NH2	5:F:612:HOH:O	2.43	0.51
1:B:93:ARG:NH2	1:B:108:HIS:HB3	2.25	0.51
1:G:293:LEU:HD12	1:G:293:LEU:H	1.75	0.51
1:A:123:VAL:HG12	1:A:394:ALA:HB2	1.93	0.51
1:C:216:VAL:HG23	1:C:243:MET:CE	2.41	0.51
1:D:71:ARG:HD2	5:D:601:HOH:O	2.11	0.51
1:H:373:ARG:HG2	1:H:373:ARG:HH11	1.76	0.51
1:G:11:MET:HA	1:G:11:MET:CE	2.33	0.50
1:H:386:LEU:C	1:H:386:LEU:HD12	2.37	0.50
1:D:124:ASN:HB2	1:D:394:ALA:HB2	1.92	0.50
1:A:90:ILE:HD11	1:A:124:ASN:HD22	1.75	0.50
1:D:18:ARG:O	1:D:22:ILE:HG13	2.12	0.50
1:G:79:ALA:O	1:G:148:GLY:HA3	2.10	0.50
1:C:229:ARG:NH2	1:F:251:GLU:OE1	2.44	0.50
1:C:376:ASN:HB2	1:C:377:PRO:HD3	1.93	0.50
1:C:396:GLY:N	1:C:397:GLY:HA2	2.26	0.50
1:G:28:LEU:HG	1:G:44:TYR:CE1	2.45	0.50
1:G:105:ARG:HG3	1:G:109:GLU:CD	2.37	0.50
1:A:144:ALA:CB	1:A:418:MET:HE3	2.41	0.50
1:A:221:SER:C	1:A:222:ARG:HG2	2.36	0.50
1:B:89:THR:HG21	1:B:121:SER:HB2	1.94	0.50
1:B:93:ARG:HG2	1:B:108:HIS:CE1	2.46	0.50
1:C:222:ARG:NH1	1:F:395:GLY:O	2.41	0.50
1:G:358:GLY:C	1:G:359:ARG:HG2	2.37	0.50
1:E:373:ARG:NH1	5:E:603:HOH:O	2.45	0.49
1:D:7:VAL:HG23	5:D:615:HOH:O	2.12	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:396:GLY:N	1:F:397:GLY:HA2	2.26	0.49
1:C:137:LYS:O	1:C:141:GLU:HG3	2.12	0.49
1:C:274:VAL:O	1:F:229:ARG:NH1	2.44	0.49
1:H:12:LYS:HD2	1:H:15:ASP:CG	2.38	0.49
1:B:103:ASN:HA	1:B:108:HIS:CD2	2.47	0.49
1:D:332:LEU:HG	1:D:333:PHE:N	2.27	0.49
1:G:114:GLU:OE1	1:G:116:ARG:NE	2.46	0.49
1:B:91:MET:HG3	1:B:108:HIS:CE1	2.48	0.49
1:C:363:ARG:HG3	1:C:363:ARG:NH2	2.18	0.49
1:D:38:GLU:CG	1:D:88:ASP:HB3	2.42	0.49
1:D:58:ARG:HG2	1:D:66:PHE:CE1	2.48	0.49
1:F:6:ASP:HB3	1:F:418:MET:CE	2.42	0.49
1:A:22:ILE:HD11	1:A:403:VAL:HG11	1.95	0.49
1:D:92:ALA:HB3	1:D:95:ASP:OD1	2.12	0.49
1:F:300:ILE:HG21	1:F:311:VAL:HG11	1.95	0.49
1:H:191:TYR:OH	1:H:344:PRO:HG2	2.13	0.49
1:H:313:ARG:NH2	5:H:608:HOH:O	2.46	0.49
1:C:93:ARG:C	1:C:94:GLU:HG2	2.36	0.48
1:G:395:GLY:HA3	1:H:226:TYR:CE1	2.47	0.48
1:B:396:GLY:N	1:B:397:GLY:HA2	2.27	0.48
1:G:245:LYS:HE2	1:G:245:LYS:HA	1.94	0.48
1:G:116:ARG:CD	1:G:400:TYR:HB2	2.42	0.48
1:C:268:GLY:HA2	1:C:363:ARG:HH11	1.78	0.48
1:A:123:VAL:CG1	1:A:394:ALA:HB2	2.43	0.48
1:E:243:MET:HE2	1:E:247:VAL:HG23	1.96	0.48
1:A:92:ALA:HB1	1:A:94:GLU:OE2	2.13	0.48
1:F:114:GLU:HG2	1:F:115:GLY:N	2.28	0.48
1:H:79:ALA:O	1:H:148:GLY:HA3	2.14	0.48
1:B:366:SER:HB2	1:B:367:PRO:HD3	1.95	0.48
1:H:258:GLU:OE2	1:H:273:LYS:HG2	2.14	0.48
1:C:11:MET:HA	1:C:11:MET:HE2	1.94	0.48
1:D:4:SER:N	5:D:615:HOH:O	2.46	0.48
1:B:90:ILE:HD11	1:B:124:ASN:HD22	1.79	0.48
1:F:94:GLU:O	1:F:94:GLU:HG3	2.13	0.48
1:H:359:ARG:CD	1:H:360:PRO:HD2	2.44	0.48
1:A:13:THR:HG22	1:A:17:MET:HE3	1.96	0.47
1:B:106:ILE:HG23	1:B:120:TYR:CD1	2.49	0.47
1:D:123:VAL:HG12	1:D:394:ALA:HB2	1.95	0.47
1:G:92:ALA:O	1:G:95:ASP:HB2	2.14	0.47
1:G:153:THR:HG22	1:G:155:VAL:HG13	1.96	0.47
1:G:109:GLU:HB3	5:G:652:HOH:O	2.13	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:396:GLY:N	1:A:397:GLY:HA2	2.29	0.47
1:D:116:ARG:HG2	1:D:402:LEU:HD23	1.95	0.47
1:B:390:CYS:HB2	1:B:405:ASP:HB3	1.97	0.47
1:C:58:ARG:HG2	1:C:66:PHE:CD1	2.49	0.47
1:H:91:MET:HE2	1:H:107:TYR:CE1	2.50	0.47
1:E:317:ALA:O	1:E:321:LYS:HG2	2.15	0.47
1:C:366:SER:HB2	1:C:367:PRO:HD3	1.97	0.47
1:D:343:GLU:HB2	1:D:344:PRO:HD3	1.97	0.47
1:E:317:ALA:HB1	1:E:321:LYS:HE2	1.96	0.46
1:G:137:LYS:HE2	1:G:141:GLU:OE2	2.15	0.46
1:C:374:ASP:C	1:C:377:PRO:HD2	2.41	0.46
1:D:109:GLU:HB3	5:D:650:HOH:O	2.15	0.46
1:A:23:GLN:O	1:A:27:GLU:HG3	2.15	0.46
1:A:116:ARG:HD2	1:A:400:TYR:HD2	1.75	0.46
1:A:293:LEU:HD12	5:B:603:HOH:O	2.16	0.46
1:A:376:ASN:HB2	1:A:377:PRO:HD3	1.98	0.46
1:G:134:ILE:O	1:G:137:LYS:HB3	2.15	0.46
1:A:319:VAL:HG11	1:A:326:ALA:HB3	1.97	0.46
1:E:193:LEU:HD23	1:E:193:LEU:C	2.40	0.46
1:G:116:ARG:HD3	1:G:400:TYR:CG	2.51	0.46
1:G:343:GLU:HB2	1:G:344:PRO:HD3	1.96	0.46
1:F:103:ASN:N	1:F:107:TYR:CE2	2.82	0.46
1:G:204:TRP:CE2	1:G:267:GLY:HA2	2.51	0.46
1:H:91:MET:HE2	1:H:107:TYR:CD1	2.51	0.46
1:C:100:ALA:O	1:C:102:ALA:N	2.49	0.46
1:C:198:THR:HG23	1:C:201:LYS:N	2.25	0.46
1:G:248:GLU:HG3	5:G:638:HOH:O	2.14	0.46
1:C:162:GLU:CD	1:C:332:LEU:HD13	2.41	0.46
1:D:21:LEU:HD13	1:D:134:ILE:HG13	1.96	0.46
1:E:38:GLU:HG2	1:E:88:ASP:CB	2.32	0.46
1:F:73:ARG:HG2	5:F:739:HOH:O	2.14	0.46
1:A:115:GLY:O	1:A:403:VAL:HG23	2.16	0.46
1:C:6:ASP:C	1:C:418:MET:HE1	2.41	0.46
1:D:251:GLU:OE1	1:E:229:ARG:NH2	2.49	0.46
1:E:18:ARG:HD3	5:E:601:HOH:O	2.14	0.46
1:F:204:TRP:CE2	1:F:267:GLY:HA2	2.50	0.46
1:G:116:ARG:HG2	1:G:117:ILE:N	2.31	0.46
1:C:251:GLU:OE1	1:F:229:ARG:NH2	2.49	0.45
1:D:95:ASP:OD2	1:D:98:ARG:NH2	2.44	0.45
1:F:113:GLU:HB3	1:F:118:TYR:HE1	1.81	0.45
1:F:263:ARG:NH2	5:F:602:HOH:O	2.22	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:390:CYS:HB2	1:F:405:ASP:HB3	1.98	0.45
1:H:223:TYR:CG	1:H:225:PRO:HD2	2.50	0.45
1:E:20:GLY:N	5:E:606:HOH:O	2.38	0.45
1:C:100:ALA:C	1:C:102:ALA:N	2.74	0.45
1:C:374:ASP:O	1:C:377:PRO:HD2	2.17	0.45
1:F:224:THR:HB	1:F:225:PRO:HD3	1.98	0.45
1:A:193:LEU:C	1:A:193:LEU:HD23	2.41	0.45
1:C:300:ILE:HG21	1:C:311:VAL:HG11	1.99	0.45
1:D:91:MET:HE1	1:D:102:ALA:CA	2.45	0.45
1:D:106:ILE:HG13	1:D:120:TYR:HD1	1.82	0.45
1:D:307:ASN:HA	4:D:502:GOL:H11	1.97	0.45
1:H:393:GLY:O	1:H:397:GLY:HA2	2.15	0.45
1:A:114:GLU:OE2	1:A:116:ARG:HB3	2.16	0.45
1:H:204:TRP:CE2	1:H:267:GLY:HA2	2.52	0.45
1:H:12:LYS:HA	1:H:12:LYS:HD2	1.45	0.45
1:D:71:ARG:HD2	5:D:791:HOH:O	2.17	0.45
1:E:91:MET:HB2	1:E:91:MET:HE3	1.83	0.45
1:G:233:ALA:HB3	1:G:245:LYS:HD2	1.99	0.45
1:A:114:GLU:H	1:A:114:GLU:HG3	1.56	0.45
1:D:321:LYS:HB2	1:D:321:LYS:HE3	1.65	0.45
1:H:12:LYS:NZ	1:H:15:ASP:CB	2.72	0.45
1:B:124:ASN:HB2	1:B:394:ALA:HB2	1.97	0.45
1:F:386:LEU:C	1:F:386:LEU:HD12	2.42	0.45
1:A:229:ARG:NH2	1:B:251:GLU:OE1	2.50	0.45
1:C:386:LEU:C	1:C:386:LEU:HD12	2.42	0.45
1:D:204:TRP:CE2	1:D:267:GLY:HA2	2.52	0.45
1:B:363:ARG:CD	1:B:364:PRO:HD2	2.45	0.44
1:H:260:ARG:HH22	1:H:314:GLU:CD	2.26	0.44
1:B:73:ARG:NE	5:B:612:HOH:O	2.51	0.44
1:C:5:ASN:OD1	1:C:5:ASN:N	2.51	0.44
1:D:374:ASP:C	1:D:377:PRO:HD2	2.42	0.44
1:E:293:LEU:HD12	1:E:293:LEU:O	2.18	0.44
1:E:360:PRO:O	5:E:602:HOH:O	2.21	0.44
1:E:386:LEU:C	1:E:386:LEU:HD12	2.42	0.44
1:H:193:LEU:HD23	1:H:193:LEU:C	2.41	0.44
1:D:91:MET:HE2	1:D:91:MET:HB3	1.84	0.44
1:D:259:LYS:HA	1:D:259:LYS:HD3	1.68	0.44
1:G:91:MET:HE3	1:G:91:MET:HB2	1.60	0.44
1:E:118:TYR:CD1	1:E:400:TYR:HB3	2.52	0.44
1:B:374:ASP:C	1:B:377:PRO:HD2	2.43	0.44
1:G:49:MET:HE3	1:G:49:MET:HB3	1.86	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:193:LEU:C	1:B:193:LEU:HD23	2.43	0.44
1:D:58:ARG:HD3	1:D:66:PHE:CZ	2.53	0.44
1:G:283:VAL:HA	1:G:284:PRO:HD3	1.82	0.44
1:G:146:LEU:CD2	1:G:418:MET:HA	2.48	0.44
1:C:337:TYR:CE2	1:C:380:GLU:HB2	2.53	0.43
1:D:106:ILE:HG13	1:D:120:TYR:CD1	2.53	0.43
1:G:85:SER:OG	1:G:195:ALA:HB3	2.18	0.43
1:A:227:VAL:HG23	1:A:228:PRO:HD2	2.01	0.43
1:D:166:GLU:OE1	5:D:602:HOH:O	2.21	0.43
1:G:144:ALA:HB1	1:G:418:MET:HE3	1.99	0.43
1:G:395:GLY:N	1:G:396:GLY:CA	2.79	0.43
1:F:44:TYR:CD1	1:F:44:TYR:C	2.95	0.43
1:A:190:ASP:O	1:A:384:PRO:HD2	2.19	0.43
1:C:343:GLU:HB2	1:C:344:PRO:HD3	1.99	0.43
1:D:274:VAL:O	1:E:229:ARG:NH1	2.52	0.43
1:D:415:MET:HE2	1:D:415:MET:HB3	1.67	0.43
1:G:130:ALA:O	1:G:134:ILE:HG12	2.18	0.43
1:A:361:THR:HA	5:A:603:HOH:O	2.19	0.43
1:E:243:MET:HE3	1:E:247:VAL:HG23	2.01	0.43
1:G:141:GLU:C	1:G:143:GLY:H	2.27	0.43
1:A:402:LEU:N	1:A:402:LEU:CD1	2.82	0.43
1:G:118:TYR:N	5:G:601:HOH:O	2.17	0.43
1:D:5:ASN:C	1:D:7:VAL:N	2.75	0.43
1:G:116:ARG:HG2	1:G:117:ILE:H	1.84	0.43
1:B:92:ALA:C	1:B:94:GLU:N	2.77	0.43
1:B:300:ILE:HG21	1:B:311:VAL:HG11	2.00	0.43
1:C:204:TRP:CE2	1:C:267:GLY:HA2	2.53	0.43
1:E:204:TRP:CE2	1:E:267:GLY:HA2	2.53	0.43
1:F:216:VAL:HG23	1:F:243:MET:HE2	2.00	0.43
1:G:254:ALA:HB1	1:G:274:VAL:HB	2.01	0.43
1:B:58:ARG:HG2	1:B:66:PHE:CD2	2.54	0.42
1:B:96:THR:HG22	1:B:96:THR:O	2.19	0.42
1:C:116:ARG:HD3	1:C:400:TYR:CD2	2.54	0.42
1:C:193:LEU:HD23	1:C:193:LEU:C	2.43	0.42
1:G:117:ILE:O	1:G:400:TYR:HA	2.18	0.42
1:H:174:ALA:HB3	5:H:642:HOH:O	2.18	0.42
1:C:273:LYS:HD3	1:F:227:VAL:HG12	2.01	0.42
1:D:386:LEU:HD12	1:D:386:LEU:O	2.19	0.42
1:A:113:GLU:HG3	1:A:118:TYR:CD2	2.54	0.42
1:A:113:GLU:HB3	1:A:114:GLU:H	1.45	0.42
1:G:89:THR:HG21	1:G:121:SER:HB2	2.01	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:146:LEU:HD21	1:G:418:MET:HA	2.00	0.42
1:H:424:THR:HA	1:H:425:PRO:HD3	1.89	0.42
1:B:162:GLU:CD	1:B:332:LEU:HD13	2.44	0.42
1:C:224:THR:HB	1:C:225:PRO:HD3	2.00	0.42
1:D:117:ILE:HG22	1:D:122:VAL:HG21	2.02	0.42
1:F:415:MET:HE2	1:F:415:MET:HB3	1.83	0.42
1:D:58:ARG:HD3	1:D:66:PHE:CE1	2.54	0.42
1:G:116:ARG:HD3	1:G:400:TYR:HD2	1.82	0.42
1:A:353:HIS:CD2	1:A:361:THR:HG22	2.54	0.42
1:D:193:LEU:C	1:D:193:LEU:HD23	2.44	0.42
1:E:243:MET:HE2	1:E:247:VAL:CG2	2.49	0.42
1:G:37:ARG:NH1	1:G:37:ARG:HB3	2.35	0.42
1:H:300:ILE:HG21	1:H:311:VAL:HG11	2.02	0.42
1:A:224:THR:HB	1:A:225:PRO:HD3	2.01	0.42
1:C:216:VAL:HG23	1:C:243:MET:HE2	2.02	0.42
1:D:116:ARG:HG3	1:D:116:ARG:HH11	1.84	0.42
1:E:245:LYS:HA	1:E:245:LYS:HD2	1.89	0.42
1:F:190:ASP:O	1:F:384:PRO:HD2	2.18	0.42
1:H:123:VAL:CG1	1:H:394:ALA:HB2	2.50	0.42
1:A:343:GLU:HB2	1:A:344:PRO:HD3	2.02	0.42
1:G:49:MET:HE1	1:G:70:GLY:N	2.34	0.42
1:G:224:THR:HB	1:G:225:PRO:HD3	2.01	0.42
1:H:6:ASP:C	1:H:418:MET:HE1	2.45	0.42
1:B:109:GLU:HB3	5:B:614:HOH:O	2.18	0.42
1:C:93:ARG:HA	1:C:93:ARG:HD3	1.71	0.42
1:D:1:MET:SD	1:D:3:GLY:N	2.86	0.42
1:H:400:TYR:CD1	1:H:400:TYR:N	2.88	0.42
1:H:211:PHE:HB2	1:H:332:LEU:HB3	2.02	0.42
1:E:374:ASP:C	1:E:377:PRO:HD2	2.44	0.41
1:F:321:LYS:HB2	1:F:321:LYS:HE3	1.64	0.41
1:G:363:ARG:HA	5:G:710:HOH:O	2.19	0.41
1:H:6:ASP:HB3	1:H:418:MET:HE1	2.01	0.41
1:B:322:LEU:HD23	1:B:322:LEU:HA	1.85	0.41
1:E:396:GLY:N	1:E:397:GLY:HA2	2.35	0.41
1:F:245:LYS:HA	1:F:245:LYS:HD2	1.89	0.41
1:H:374:ASP:C	1:H:377:PRO:HD2	2.45	0.41
1:B:124:ASN:HB2	1:B:394:ALA:CB	2.50	0.41
1:B:392:GLY:H	1:B:398:ASN:HD22	1.68	0.41
1:C:322:LEU:HD23	1:C:322:LEU:HA	1.85	0.41
1:D:188:ILE:HG13	1:H:309:LEU:HD21	2.03	0.41
1:F:322:LEU:HD23	1:F:322:LEU:HA	1.87	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:265:TYR:OH	1:G:305:ASP:OD2	2.31	0.41
1:F:343:GLU:HB2	1:F:344:PRO:HD3	2.01	0.41
1:F:364:PRO:HG2	1:F:369:CYS:SG	2.60	0.41
1:G:162:GLU:CD	1:G:332:LEU:HD13	2.45	0.41
1:B:6:ASP:C	1:B:418:MET:HE1	2.45	0.41
1:C:251:GLU:CD	1:F:229:ARG:NH2	2.78	0.41
1:G:57:GLU:HG2	5:G:653:HOH:O	2.19	0.41
1:H:396:GLY:N	1:H:397:GLY:HA2	2.35	0.41
1:G:162:GLU:HG3	1:G:332:LEU:HD13	2.02	0.41
1:A:300:ILE:HG21	1:A:311:VAL:HG11	2.03	0.41
1:A:368:GLU:HA	1:A:371:MET:HE3	2.03	0.41
1:E:116:ARG:NH1	1:E:400:TYR:CE2	2.89	0.41
1:F:116:ARG:HD3	1:F:400:TYR:CE2	2.56	0.41
1:H:359:ARG:HG3	1:H:360:PRO:HD2	2.02	0.41
1:A:160:ASP:HB2	1:B:288:TYR:HB3	2.02	0.40
1:D:283:VAL:HA	1:D:284:PRO:HD3	1.89	0.40
1:E:134:ILE:HD13	1:E:134:ILE:HA	1.90	0.40
1:C:417:ALA:O	1:C:421:CYS:HB2	2.22	0.40
1:E:343:GLU:HB3	1:E:344:PRO:HD3	2.04	0.40
1:G:76:GLY:O	1:G:147:LYS:HB3	2.22	0.40
1:G:211:PHE:HB2	1:G:332:LEU:HB3	2.03	0.40
1:B:204:TRP:HB3	1:B:386:LEU:HB3	2.02	0.40
1:D:227:VAL:HG23	1:D:228:PRO:HD2	2.02	0.40
1:E:8:ALA:O	1:E:12:LYS:HG3	2.22	0.40
1:C:44:TYR:CD1	1:C:44:TYR:C	3.00	0.40
1:E:197:ALA:HA	1:E:390:CYS:O	2.22	0.40
1:E:210:VAL:HA	1:E:332:LEU:O	2.20	0.40
1:H:322:LEU:HD23	1:H:322:LEU:HA	1.84	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)
5:F:797:HOH:O	5:G:763:HOH:O[6_445]	2.15	0.05

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	419/425 (99%)	403 (96%)	13 (3%)	3 (1%)	18	19
1	B	419/425 (99%)	406 (97%)	11 (3%)	2 (0%)	24	27
1	C	420/425 (99%)	405 (96%)	13 (3%)	2 (0%)	24	27
1	D	423/425 (100%)	403 (95%)	19 (4%)	1 (0%)	43	51
1	E	421/425 (99%)	408 (97%)	11 (3%)	2 (0%)	24	27
1	F	423/425 (100%)	409 (97%)	12 (3%)	2 (0%)	24	27
1	G	419/425 (99%)	399 (95%)	19 (4%)	1 (0%)	43	51
1	H	420/425 (99%)	407 (97%)	11 (3%)	2 (0%)	24	27
All	All	3364/3400 (99%)	3240 (96%)	109 (3%)	15 (0%)	30	34

All (15) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	113	GLU
1	C	101	ASP
1	F	114	GLU
1	F	160	ASP
1	A	160	ASP
1	C	160	ASP
1	E	160	ASP
1	G	160	ASP
1	H	160	ASP
1	B	160	ASP
1	A	218	ALA
1	B	218	ALA
1	D	160	ASP
1	E	218	ALA
1	H	218	ALA

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	328/330 (99%)	321 (98%)	7 (2%)	47	63
1	B	328/330 (99%)	322 (98%)	6 (2%)	51	68
1	C	329/330 (100%)	321 (98%)	8 (2%)	43	58
1	D	330/330 (100%)	329 (100%)	1 (0%)	86	93
1	E	329/330 (100%)	327 (99%)	2 (1%)	78	89
1	F	330/330 (100%)	324 (98%)	6 (2%)	51	68
1	G	328/330 (99%)	323 (98%)	5 (2%)	57	73
1	H	329/330 (100%)	323 (98%)	6 (2%)	51	68
All	All	2631/2640 (100%)	2590 (98%)	41 (2%)	55	71

All (41) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	12	LYS
1	A	91	MET
1	A	94	GLU
1	A	114	GLU
1	A	313	ARG
1	A	366	SER
1	A	402	LEU
1	B	6	ASP
1	B	103	ASN
1	B	248	GLU
1	B	355	GLU
1	B	363	ARG
1	B	368	GLU
1	C	5	ASN
1	C	19	GLU
1	C	96	THR
1	C	104	ASP
1	C	198	THR
1	C	222	ARG

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Mol	Chain	Res	Type
1	C	355	GLU
1	C	363	ARG
1	D	90	ILE
1	E	91	MET
1	E	424	THR
1	F	95	ASP
1	F	107	TYR
1	F	108	HIS
1	F	114	GLU
1	F	293	LEU
1	F	321	LYS
1	G	91	MET
1	G	114	GLU
1	G	117	ILE
1	G	293	LEU
1	G	359	ARG
1	H	12	LYS
1	H	47	GLU
1	H	94	GLU
1	H	248	GLU
1	H	355	GLU
1	H	399	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (7) such sidechains are listed below:

Mol	Chain	Res	Type
1	B	347	ASN
1	C	103	ASN
1	C	340	GLN
1	D	108	HIS
1	F	108	HIS
1	G	5	ASN
1	G	112	HIS

5.3.3 RNA ⓘ

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 22 ligands modelled in this entry, 8 are monoatomic - leaving 14 for Mogul analysis.

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
4	GOL	B	503	-	5,5,5	0.38	0	5,5,5	0.58	0
3	6R8	E	502	2	10,14,14	4.41	4 (40%)	9,21,21	2.33	4 (44%)
4	GOL	F	502	-	5,5,5	0.44	0	5,5,5	0.55	0
4	GOL	C	503	-	5,5,5	0.49	0	5,5,5	0.29	0
4	GOL	G	503	-	5,5,5	0.45	0	5,5,5	0.25	0
4	GOL	H	503	-	5,5,5	0.45	0	5,5,5	0.38	0
3	6R8	A	502	2	10,14,14	4.29	4 (40%)	9,21,21	2.06	2 (22%)
4	GOL	D	502	-	5,5,5	0.46	0	5,5,5	0.27	0
4	GOL	E	503	-	5,5,5	0.48	0	5,5,5	0.56	0
3	6R8	B	502	2	10,14,14	4.45	5 (50%)	9,21,21	1.87	1 (11%)
4	GOL	A	503	-	5,5,5	0.38	0	5,5,5	0.49	0
3	6R8	G	502	2	10,14,14	4.26	4 (40%)	9,21,21	1.85	1 (11%)
3	6R8	C	502	2	10,14,14	4.38	5 (50%)	9,21,21	1.98	2 (22%)
3	6R8	H	502	2	10,14,14	4.27	5 (50%)	9,21,21	2.09	3 (33%)

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
4	GOL	B	503	-	-	3/4/4/4	-
3	6R8	E	502	2	-	6/6/24/24	0/1/1/1
4	GOL	F	502	-	-	1/4/4/4	-
4	GOL	C	503	-	-	4/4/4/4	-
4	GOL	G	503	-	-	1/4/4/4	-
4	GOL	H	503	-	-	2/4/4/4	-
3	6R8	A	502	2	-	6/6/24/24	0/1/1/1
4	GOL	D	502	-	-	2/4/4/4	-
4	GOL	E	503	-	-	3/4/4/4	-
3	6R8	B	502	2	-	6/6/24/24	0/1/1/1
4	GOL	A	503	-	-	2/4/4/4	-
3	6R8	G	502	2	-	6/6/24/24	0/1/1/1
3	6R8	C	502	2	-	6/6/24/24	0/1/1/1
3	6R8	H	502	2	-	4/6/24/24	0/1/1/1

All (27) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	B	502	6R8	O08-N07	9.71	1.39	1.22
3	C	502	6R8	O08-N07	9.63	1.39	1.22
3	E	502	6R8	O08-N07	9.49	1.39	1.22
3	G	502	6R8	O08-N07	9.45	1.39	1.22
3	A	502	6R8	O08-N07	9.36	1.39	1.22
3	H	502	6R8	O08-N07	9.13	1.38	1.22
3	H	502	6R8	C02-C03	-7.53	1.35	1.50
3	E	502	6R8	C02-C03	-7.49	1.35	1.50
3	C	502	6R8	C02-C03	-7.18	1.36	1.50
3	G	502	6R8	C02-C03	-7.10	1.36	1.50
3	B	502	6R8	C02-C03	-7.09	1.36	1.50
3	A	502	6R8	C02-C03	-7.08	1.36	1.50
3	B	502	6R8	O14-C01	5.96	1.49	1.40
3	E	502	6R8	O14-C01	5.73	1.48	1.40
3	A	502	6R8	O14-C01	5.60	1.48	1.40
3	C	502	6R8	O14-C01	5.55	1.48	1.40
3	H	502	6R8	O14-C01	5.18	1.47	1.40
3	G	502	6R8	O14-C01	5.09	1.47	1.40
3	B	502	6R8	C03-C04	2.74	1.42	1.34
3	C	502	6R8	C03-C04	2.54	1.41	1.34
3	A	502	6R8	C03-C04	2.50	1.41	1.34
3	G	502	6R8	C03-C04	2.42	1.41	1.34
3	E	502	6R8	C03-C04	2.38	1.41	1.34

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	B	502	6R8	O12-C10	2.20	1.28	1.22
3	H	502	6R8	O12-C10	2.16	1.27	1.22
3	H	502	6R8	C03-C04	2.08	1.40	1.34
3	C	502	6R8	O12-C10	2.03	1.27	1.22

All (13) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	C	502	6R8	C01-C02-C03	4.94	122.05	113.06
3	G	502	6R8	C01-C02-C03	4.92	122.02	113.06
3	E	502	6R8	C01-C02-C03	4.91	122.00	113.06
3	A	502	6R8	C01-C02-C03	4.85	121.90	113.06
3	H	502	6R8	C01-C02-C03	4.80	121.81	113.06
3	B	502	6R8	C01-C02-C03	4.71	121.63	113.06
3	E	502	6R8	O11-C10-C06	2.93	120.87	114.84
3	E	502	6R8	C05-C06-C10	-2.68	115.16	120.67
3	H	502	6R8	O11-C10-C06	2.42	119.82	114.84
3	C	502	6R8	O11-C10-C06	2.20	119.36	114.84
3	A	502	6R8	O11-C10-C06	2.18	119.32	114.84
3	E	502	6R8	O12-C10-C06	-2.09	118.56	122.53
3	H	502	6R8	O12-C10-C06	-2.09	118.56	122.53

There are no chirality outliers.

All (52) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	502	6R8	C01-C06-C10-O11
3	A	502	6R8	C05-C06-C10-O11
3	A	502	6R8	C01-C06-C10-O12
3	A	502	6R8	C05-C06-C10-O12
3	A	502	6R8	C03-C04-N07-O08
3	A	502	6R8	C05-C04-N07-O08
3	B	502	6R8	C05-C06-C10-O11
3	B	502	6R8	C01-C06-C10-O12
3	B	502	6R8	C05-C06-C10-O12
3	B	502	6R8	C03-C04-N07-O08
3	B	502	6R8	C05-C04-N07-O08
3	C	502	6R8	C01-C06-C10-O11
3	C	502	6R8	C05-C06-C10-O11
3	C	502	6R8	C05-C06-C10-O12
3	C	502	6R8	C05-C04-N07-O08
3	E	502	6R8	C01-C06-C10-O11

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Mol	Chain	Res	Type	Atoms
3	E	502	6R8	C05-C06-C10-O11
3	E	502	6R8	C01-C06-C10-O12
3	E	502	6R8	C05-C06-C10-O12
3	E	502	6R8	C05-C04-N07-O08
3	G	502	6R8	C01-C06-C10-O11
3	G	502	6R8	C05-C06-C10-O11
3	G	502	6R8	C01-C06-C10-O12
3	G	502	6R8	C05-C06-C10-O12
3	G	502	6R8	C03-C04-N07-O08
3	G	502	6R8	C05-C04-N07-O08
3	H	502	6R8	C01-C06-C10-O12
4	A	503	GOL	C1-C2-C3-O3
4	B	503	GOL	O1-C1-C2-C3
4	C	503	GOL	C1-C2-C3-O3
4	E	503	GOL	O1-C1-C2-C3
3	H	502	6R8	C05-C04-N07-O08
4	C	503	GOL	O1-C1-C2-C3
4	D	502	GOL	C1-C2-C3-O3
4	H	503	GOL	O1-C1-C2-C3
4	A	503	GOL	O2-C2-C3-O3
4	C	503	GOL	O1-C1-C2-O2
3	C	502	6R8	C03-C04-N07-O08
3	E	502	6R8	C03-C04-N07-O08
4	B	503	GOL	O1-C1-C2-O2
4	C	503	GOL	O2-C2-C3-O3
4	E	503	GOL	O1-C1-C2-O2
4	D	502	GOL	O2-C2-C3-O3
4	F	502	GOL	O2-C2-C3-O3
3	C	502	6R8	C01-C06-C10-O12
3	B	502	6R8	C01-C06-C10-O11
3	H	502	6R8	C01-C06-C10-O11
4	B	503	GOL	O2-C2-C3-O3
4	E	503	GOL	O2-C2-C3-O3
4	H	503	GOL	O1-C1-C2-O2
4	G	503	GOL	O1-C1-C2-C3
3	H	502	6R8	C05-C06-C10-O12

There are no ring outliers.

6 monomers are involved in 7 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	F	502	GOL	1	0

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Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	C	503	GOL	1	0
3	A	502	6R8	2	0
4	D	502	GOL	1	0
3	C	502	6R8	1	0
3	H	502	6R8	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	421/425 (99%)	0.14	36 (8%)	16	14	19, 30, 63, 95	0
1	B	421/425 (99%)	-0.28	25 (5%)	28	25	17, 26, 58, 106	0
1	C	422/425 (99%)	-0.33	25 (5%)	28	25	17, 25, 55, 105	0
1	D	425/425 (100%)	-0.09	35 (8%)	17	15	17, 26, 71, 123	0
1	E	423/425 (99%)	-0.30	15 (3%)	47	44	18, 26, 52, 80	0
1	F	425/425 (100%)	-0.12	31 (7%)	21	18	17, 26, 70, 128	0
1	G	421/425 (99%)	0.21	38 (9%)	15	12	18, 31, 67, 102	0
1	H	422/425 (99%)	-0.19	19 (4%)	38	35	18, 28, 55, 87	0
All	All	3380/3400 (99%)	-0.12	224 (6%)	24	21	17, 27, 63, 128	0

All (224) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	F	107	TYR	8.6
1	D	3	GLY	8.4
1	D	102	ALA	7.4
1	B	102	ALA	7.2
1	A	115	GLY	7.2
1	F	102	ALA	7.1
1	C	4	SER	6.8
1	D	397	GLY	6.6
1	D	396	GLY	6.4
1	F	396	GLY	6.3
1	G	397	GLY	6.2
1	D	92	ALA	6.2
1	G	115	GLY	6.0
1	D	4	SER	5.9
1	C	102	ALA	5.9
1	F	120	TYR	5.3

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Mol	Chain	Res	Type	RSRZ
1	B	101	ASP	5.2
1	D	393	GLY	5.1
1	G	102	ALA	5.1
1	F	395	GLY	5.1
1	D	114	GLU	5.0
1	B	394	ALA	4.9
1	F	108	HIS	4.9
1	D	2	ALA	4.8
1	G	395	GLY	4.7
1	F	101	ASP	4.7
1	F	103	ASN	4.6
1	F	92	ALA	4.5
1	D	101	ASP	4.5
1	C	101	ASP	4.4
1	D	99	PHE	4.4
1	H	395	GLY	4.4
1	H	15	ASP	4.4
1	C	396	GLY	4.3
1	G	114	GLU	4.3
1	F	397	GLY	4.2
1	D	120	TYR	4.2
1	C	397	GLY	4.2
1	F	100	ALA	4.2
1	D	5	ASN	4.1
1	D	93	ARG	4.1
1	A	120	TYR	4.1
1	H	4	SER	4.1
1	E	395	GLY	4.0
1	E	102	ALA	4.0
1	G	100	ALA	4.0
1	B	5	ASN	4.0
1	C	96	THR	4.0
1	F	392	GLY	4.0
1	B	96	THR	3.9
1	F	96	THR	3.9
1	F	99	PHE	3.9
1	F	394	ALA	3.9
1	D	103	ASN	3.9
1	F	94	GLU	3.9
1	A	102	ALA	3.9
1	A	5	ASN	3.9
1	E	115	GLY	3.8

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Mol	Chain	Res	Type	RSRZ
1	G	5	ASN	3.8
1	A	94	GLU	3.8
1	D	96	THR	3.8
1	D	394	ALA	3.8
1	G	101	ASP	3.7
1	B	395	GLY	3.7
1	G	103	ASN	3.7
1	G	394	ALA	3.7
1	C	99	PHE	3.7
1	D	395	GLY	3.7
1	H	5	ASN	3.7
1	B	91	MET	3.6
1	B	103	ASN	3.6
1	A	396	GLY	3.6
1	E	4	SER	3.6
1	C	103	ASN	3.6
1	F	393	GLY	3.5
1	G	396	GLY	3.5
1	C	92	ALA	3.5
1	D	392	GLY	3.5
1	H	396	GLY	3.5
1	A	199	ASN	3.5
1	D	100	ALA	3.5
1	H	12	LYS	3.4
1	A	398	ASN	3.4
1	G	112	HIS	3.4
1	B	396	GLY	3.4
1	A	101	ASP	3.4
1	D	91	MET	3.4
1	F	5	ASN	3.4
1	G	118	TYR	3.3
1	A	400	TYR	3.3
1	G	111	TRP	3.3
1	G	400	TYR	3.3
1	A	397	GLY	3.3
1	B	397	GLY	3.3
1	G	392	GLY	3.3
1	D	106	ILE	3.3
1	F	93	ARG	3.3
1	A	392	GLY	3.2
1	A	395	GLY	3.2
1	B	393	GLY	3.2

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Mol	Chain	Res	Type	RSRZ
1	D	108	HIS	3.2
1	B	90	ILE	3.2
1	B	100	ALA	3.2
1	B	392	GLY	3.2
1	F	91	MET	3.2
1	D	107	TYR	3.2
1	E	3	GLY	3.2
1	H	102	ALA	3.2
1	H	425	PRO	3.1
1	A	93	ARG	3.1
1	A	114	GLU	3.1
1	D	398	ASN	3.1
1	E	5	ASN	3.1
1	G	199	ASN	3.1
1	B	120	TYR	3.1
1	C	93	ARG	3.1
1	G	91	MET	3.1
1	D	105	ARG	3.1
1	B	92	ALA	3.0
1	G	7	VAL	3.0
1	A	118	TYR	3.0
1	E	396	GLY	3.0
1	C	90	ILE	3.0
1	B	363	ARG	3.0
1	D	104	ASP	3.0
1	F	95	ASP	3.0
1	G	6	ASP	3.0
1	A	106	ILE	2.9
1	C	5	ASN	2.9
1	H	115	GLY	2.9
1	E	91	MET	2.9
1	D	94	GLU	2.9
1	B	398	ASN	2.9
1	D	6	ASP	2.9
1	H	101	ASP	2.9
1	B	93	ARG	2.8
1	C	100	ALA	2.8
1	F	106	ILE	2.8
1	C	104	ASP	2.8
1	G	107	TYR	2.8
1	G	358	GLY	2.7
1	A	91	MET	2.7

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Mol	Chain	Res	Type	RSRZ
1	G	398	ASN	2.7
1	C	94	GLU	2.7
1	A	116	ARG	2.7
1	C	394	ALA	2.7
1	G	92	ALA	2.6
1	B	99	PHE	2.6
1	D	95	ASP	2.6
1	D	98	ARG	2.6
1	G	90	ILE	2.6
1	G	116	ARG	2.6
1	A	6	ASP	2.6
1	C	107	TYR	2.6
1	G	106	ILE	2.6
1	A	359	ARG	2.6
1	G	359	ARG	2.6
1	E	101	ASP	2.6
1	F	398	ASN	2.6
1	D	1	MET	2.6
1	A	12	LYS	2.6
1	A	112	HIS	2.5
1	F	90	ILE	2.5
1	B	94	GLU	2.5
1	G	113	GLU	2.5
1	H	359	ARG	2.5
1	A	402	LEU	2.5
1	E	392	GLY	2.5
1	A	104	ASP	2.5
1	A	111	TRP	2.5
1	G	94	GLU	2.5
1	B	107	TYR	2.5
1	A	197	ALA	2.5
1	G	22	ILE	2.4
1	A	8	ALA	2.4
1	F	3	GLY	2.4
1	C	108	HIS	2.4
1	G	399	THR	2.4
1	A	16	GLY	2.4
1	C	120	TYR	2.3
1	H	103	ASN	2.3
1	H	120	TYR	2.3
1	H	398	ASN	2.3
1	A	391	GLY	2.3

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Mol	Chain	Res	Type	RSRZ
1	A	399	THR	2.3
1	G	99	PHE	2.3
1	H	94	GLU	2.3
1	G	120	TYR	2.3
1	C	359	ARG	2.3
1	F	105	ARG	2.3
1	E	103	ASN	2.3
1	B	108	HIS	2.3
1	F	115	GLY	2.3
1	E	394	ALA	2.3
1	F	114	GLU	2.3
1	B	95	ASP	2.2
1	E	400	TYR	2.2
1	G	16	GLY	2.2
1	A	394	ALA	2.2
1	A	107	TYR	2.2
1	F	4	SER	2.2
1	C	98	ARG	2.2
1	A	113	GLU	2.2
1	E	359	ARG	2.1
1	G	402	LEU	2.1
1	E	95	ASP	2.1
1	G	403	VAL	2.1
1	G	401	PHE	2.1
1	F	1	MET	2.1
1	F	104	ASP	2.1
1	D	116	ARG	2.1
1	H	91	MET	2.1
1	D	113	GLU	2.1
1	C	398	ASN	2.1
1	A	363	ARG	2.1
1	H	400	TYR	2.1
1	B	359	ARG	2.1
1	H	399	THR	2.0
1	H	100	ALA	2.0
1	C	95	ASP	2.0
1	C	392	GLY	2.0
1	C	91	MET	2.0
1	A	423	ARG	2.0
1	D	90	ILE	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
3	6R8	C	502	14/14	0.69	0.19	34,47,56,56	0
3	6R8	B	502	14/14	0.72	0.18	40,46,56,61	0
3	6R8	E	502	14/14	0.78	0.18	36,42,57,59	0
3	6R8	G	502	14/14	0.82	0.16	42,52,62,63	0
3	6R8	A	502	14/14	0.84	0.14	41,46,55,62	0
3	6R8	H	502	14/14	0.86	0.14	33,40,49,54	0
4	GOL	E	503	6/6	0.88	0.13	25,31,38,38	0
4	GOL	B	503	6/6	0.89	0.11	22,31,35,35	0
4	GOL	A	503	6/6	0.89	0.12	25,33,34,41	0
4	GOL	F	502	6/6	0.91	0.12	27,30,36,40	0
2	ZN	F	501	1/1	0.92	0.14	39,39,39,39	1
2	ZN	D	501	1/1	0.93	0.11	38,38,38,38	1
4	GOL	D	502	6/6	0.94	0.09	29,31,33,37	0
4	GOL	C	503	6/6	0.95	0.07	28,29,31,33	0
4	GOL	G	503	6/6	0.95	0.09	27,33,37,38	0
4	GOL	H	503	6/6	0.95	0.09	23,29,32,37	0
2	ZN	A	501	1/1	0.96	0.13	38,38,38,38	1
2	ZN	G	501	1/1	0.97	0.10	67,67,67,67	0
2	ZN	H	501	1/1	0.97	0.10	34,34,34,34	1
2	ZN	E	501	1/1	0.98	0.12	33,33,33,33	1
2	ZN	C	501	1/1	0.98	0.12	30,30,30,30	1
2	ZN	B	501	1/1	0.98	0.11	33,33,33,33	1

6.5 Other polymers [i](#)

There are no such residues in this entry.