



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 19, 2016 – 08:48 PM GMT

PDB ID : 4Z1Y
Title : Thermostable enolase from *Chloroflexus aurantiacus* with substrate 2-phosphoglycerate
Authors : Zadvornyy, O.A.; Peters, J.W.
Deposited on : 2015-03-27
Resolution : 2.53 Å(reported)

This is a Full wwPDB X-ray Structure Validation Report for a publicly released PDB entry.
We welcome your comments at validation@mail.wwpdb.org
A user guide is available at
<http://wwpdb.org/validation/2016/XrayValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

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

MolProbity : 4.02b-467
Mogul : 1.7.1 (RC1), CSD as537be (2016)
Xtriage (Phenix) : 1.9-1692
EDS : rb-20026982
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)
Refmac : 5.8.0135
CCP4 : 6.5.0
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : rb-20026982

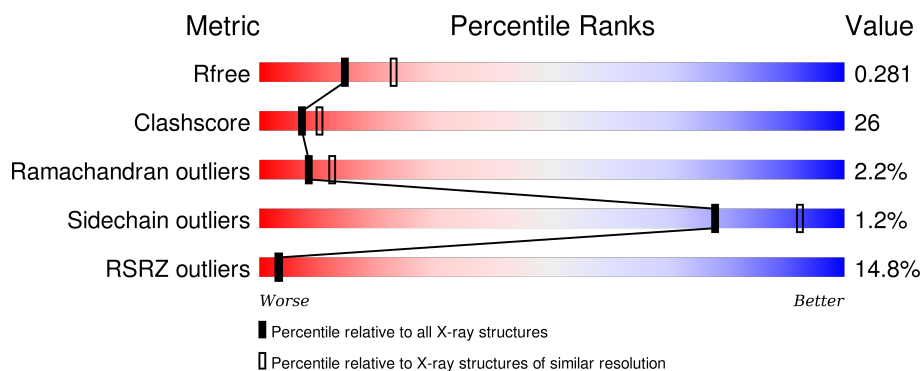
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.53 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	91344	4241 (2.54-2.50)
Clashscore	102246	4968 (2.54-2.50)
Ramachandran outliers	100387	4873 (2.54-2.50)
Sidechain outliers	100360	4875 (2.54-2.50)
RSRZ outliers	91569	4253 (2.54-2.50)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments on the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	426	<div> <div>10%</div> <div>80%</div> <div>16%</div> <div>.</div> </div>
1	B	426	<div> <div>20%</div> <div>75%</div> <div>20%</div> <div>...</div> </div>

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

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
2	MG	A	501	-	-	-	X
2	MG	B	501	-	-	-	X
3	2PG	A	502[B]	-	-	-	X
3	2PG	B	502[B]	-	-	X	X

2 Entry composition [i](#)

There are 4 unique types of molecules in this entry. The entry contains 6466 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.

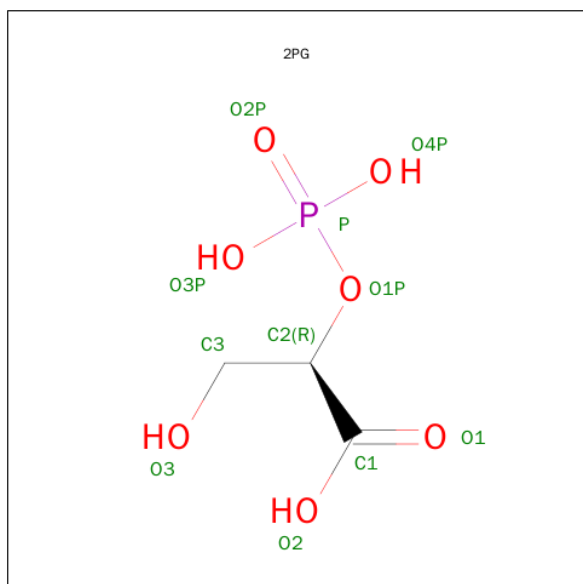
- Molecule 1 is a protein called Enolase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	424	Total	C	N	O	S	2	7	0
			3250	2037	572	633	8			
1	B	419	Total	C	N	O	S	0	0	0
			3169	1987	559	615	8			

- Molecule 2 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	B	1	Total	Mg	0	0
			1	1		
2	A	1	Total	Mg	0	0
			1	1		

- Molecule 3 is 2-PHOSPHOGLYCERIC ACID (three-letter code: 2PG) (formula: C₃H₇O₇P).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	A	1	Total	C	O	P	0	1
			11	3	7	1		
3	B	1	Total	C	O	P	0	1
			11	3	7	1		

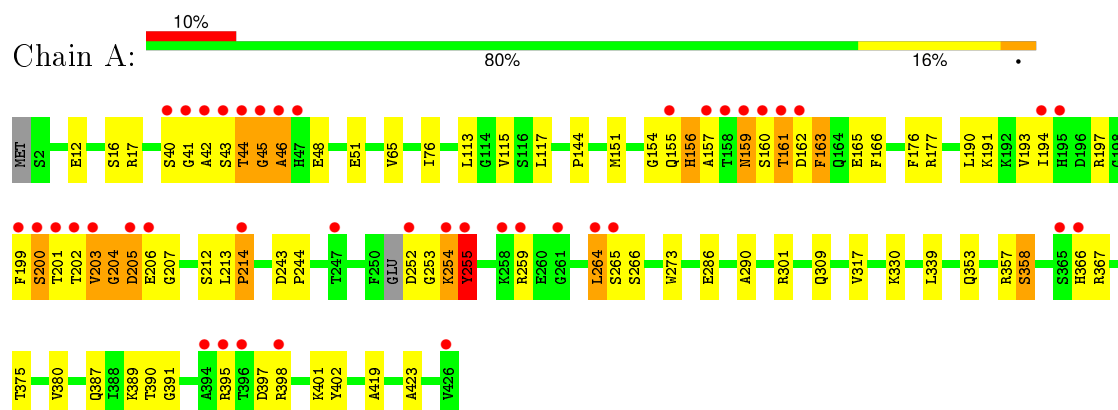
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	11	Total	O	0	0
			11	11		
4	B	12	Total	O	0	0
			12	12		

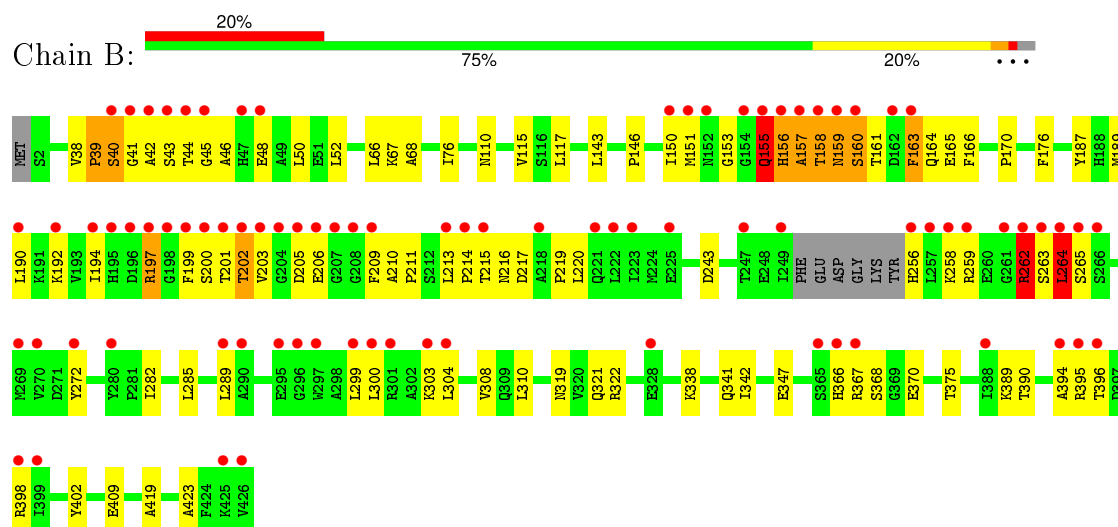
3 Residue-property plots

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red dot above a residue indicates a poor fit to the electron density ($RSRZ > 2$). 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: Enolase



• Molecule 1: Enolase



4 Data and refinement statistics

Property	Value	Source
Space group	I 4	Depositor
Cell constants a, b, c, α , β , γ	146.32Å 146.32Å 101.88Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	37.70 – 2.53 37.70 – 2.53	Depositor EDS
% Data completeness (in resolution range)	99.9 (37.70-2.53) 99.8 (37.70-2.53)	Depositor EDS
R_{merge}	0.05	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.08 (at 2.54Å)	Xtriage
Refinement program	BUSTER 2.10.1	Depositor
R, R_{free}	0.214 , 0.252 0.247 , 0.281	Depositor DCC
R_{free} test set	1794 reflections (5.26%)	DCC
Wilson B-factor (Å ²)	48.6	Xtriage
Anisotropy	0.273	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 44.6	EDS
Estimated twinning fraction	0.024 for -k,-h,-l	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.33$	Xtriage
Outliers	0 of 35899 reflections	Xtriage
F_o, F_c correlation	0.92	EDS
Total number of atoms	6466	wwPDB-VP
Average B, all atoms (Å ²)	61.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.76% 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, 0.375 respectively for untwinned datasets, and 0.333, 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: MG, 2PG

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	0.48	0/3300	0.74	4/4471 (0.1%)
1	B	0.60	4/3217 (0.1%)	1.02	20/4360 (0.5%)
All	All	0.55	4/6517 (0.1%)	0.89	24/8831 (0.3%)

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	A	0	1
1	B	0	4
All	All	0	5

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	158	THR	C-N	-12.79	1.04	1.34
1	B	155	GLN	C-N	-10.25	1.10	1.34
1	B	264	LEU	C-N	9.82	1.56	1.34
1	B	262	ARG	C-N	-9.19	1.12	1.34

All (24) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	265	SER	N-CA-CB	20.31	140.97	110.50
1	B	158	THR	O-C-N	-17.01	95.48	122.70
1	B	159	ASN	N-CA-CB	-14.99	83.61	110.60
1	B	262	ARG	O-C-N	-13.45	101.17	122.70
1	B	155	GLN	O-C-N	-13.12	101.70	122.70

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	156	HIS	N-CA-CB	-12.48	88.14	110.60
1	B	155	GLN	CB-CA-C	-11.33	87.74	110.40
1	B	262	ARG	CB-CA-C	-11.13	88.14	110.40
1	B	264	LEU	CB-CA-C	10.87	130.85	110.20
1	B	158	THR	CA-C-N	10.81	140.98	117.20
1	B	263	SER	N-CA-CB	-10.07	95.39	110.50
1	B	262	ARG	CA-C-N	9.95	139.09	117.20
1	A	264	LEU	CB-CA-C	9.61	128.45	110.20
1	B	155	GLN	N-CA-C	9.32	136.17	111.00
1	B	155	GLN	CA-C-N	7.78	134.32	117.20
1	B	159	ASN	N-CA-C	6.72	129.15	111.00
1	B	264	LEU	N-CA-C	-6.65	93.03	111.00
1	B	265	SER	N-CA-C	-6.62	93.12	111.00
1	A	205	ASP	N-CA-C	6.38	128.23	111.00
1	A	204	GLY	O-C-N	-6.03	113.05	122.70
1	A	255	TYR	CB-CA-C	5.95	122.30	110.40
1	B	158	THR	CB-CA-C	-5.76	96.04	111.60
1	B	262	ARG	C-N-CA	5.74	136.04	121.70
1	B	158	THR	N-CA-C	-5.67	95.69	111.00

There are no chirality outliers.

All (5) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	204	GLY	Mainchain
1	B	155	GLN	Mainchain
1	B	158	THR	Mainchain
1	B	262	ARG	Mainchain
1	B	264	LEU	Mainchain

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	3250	0	3244	130	0
1	B	3169	0	3171	229	0
2	A	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	B	1	0	0	0	0
3	A	11	0	4	0	0
3	B	11	0	4	4	0
4	A	11	0	0	0	0
4	B	12	0	0	0	0
All	All	6466	0	6423	334	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 26.

All (334) 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:209:PHE:CD2	1:B:211:PRO:HD3	1.46	1.46
1:B:156:HIS:N	1:B:157:ALA:CB	1.77	1.45
1:B:161:THR:CG2	1:B:216:ASN:OD1	1.73	1.36
1:B:156:HIS:N	1:B:157:ALA:HB2	1.01	1.31
1:A:42[A]:ALA:O	1:A:51:GLU:CG	1.78	1.29
1:B:156:HIS:CB	1:B:157:ALA:HB2	1.62	1.27
1:B:41:GLY:CA	1:B:367:ARG:HD3	1.64	1.26
1:A:395:ARG:NH1	1:B:395:ARG:CG	2.02	1.23
1:B:366:HIS:CD2	1:B:390:THR:HA	1.75	1.22
1:A:254:LYS:CB	1:A:264:LEU:O	1.88	1.20
1:A:254:LYS:HB3	1:A:264:LEU:O	1.06	1.18
1:A:160:SER:O	1:A:161:THR:CG2	1.92	1.17
1:A:160:SER:O	1:A:161:THR:HG22	1.02	1.17
1:B:262:ARG:NH1	1:B:272:TYR:CD2	2.12	1.17
1:B:156:HIS:CA	1:B:157:ALA:HB2	1.76	1.15
1:A:17:ARG:NH1	1:A:205:ASP:OD2	1.80	1.15
1:B:161:THR:HG23	1:B:216:ASN:OD1	1.32	1.14
1:B:156:HIS:HB3	1:B:157:ALA:HA	1.23	1.12
1:B:390:THR:O	1:B:398:ARG:HD2	1.49	1.13
1:B:41:GLY:HA3	1:B:367:ARG:HD3	1.16	1.12
1:A:395:ARG:NH1	1:B:395:ARG:HG2	1.60	1.12
1:B:44:THR:HB	1:B:45:GLY:CA	1.78	1.12
1:A:17:ARG:CZ	1:A:205:ASP:OD2	1.96	1.11
1:A:42[A]:ALA:O	1:A:51:GLU:HG2	0.93	1.11
1:B:209:PHE:CD2	1:B:211:PRO:CD	2.33	1.10
1:A:254:LYS:HG3	1:A:265:SER:HA	1.25	1.10
1:B:156:HIS:HB3	1:B:157:ALA:CA	1.79	1.10
1:B:209:PHE:HE2	1:B:211:PRO:CB	1.63	1.09

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:156:HIS:HB2	1:B:157:ALA:HB2	1.28	1.08
1:B:156:HIS:CB	1:B:157:ALA:CB	2.30	1.08
1:A:395:ARG:HH11	1:B:395:ARG:CG	1.63	1.06
1:A:395:ARG:HH22	1:B:203:VAL:HG21	1.18	1.06
1:A:395:ARG:NH2	1:B:203:VAL:HG21	1.71	1.04
1:B:304:LEU:HD13	1:B:308:VAL:CG2	1.86	1.04
1:B:366:HIS:HD2	1:B:390:THR:CA	1.70	1.04
1:B:213:LEU:HD13	1:B:219:PRO:HG3	1.38	1.03
1:A:395:ARG:HH11	1:B:395:ARG:HG2	0.90	1.03
1:B:262:ARG:NH1	1:B:272:TYR:HD2	1.48	1.03
1:A:395:ARG:NH2	1:B:203:VAL:CG2	2.22	1.03
1:B:370:GLU:CG	1:B:398:ARG:HH12	1.72	1.02
1:B:44:THR:HB	1:B:45:GLY:HA2	1.35	1.02
1:B:258:LYS:HA	1:B:259:ARG:HD2	1.40	1.01
1:B:366:HIS:HD2	1:B:390:THR:HA	0.90	1.01
1:B:41:GLY:N	1:B:367:ARG:HD3	1.76	1.00
1:B:41:GLY:HA3	1:B:367:ARG:CD	1.91	0.99
1:A:395:ARG:HH22	1:B:203:VAL:CG2	1.74	0.97
1:B:370:GLU:CB	1:B:398:ARG:HH12	1.77	0.96
1:B:209:PHE:CE2	1:B:211:PRO:CD	2.48	0.96
1:B:304:LEU:HD13	1:B:308:VAL:CB	1.93	0.96
1:B:304:LEU:CD1	1:B:308:VAL:HB	1.95	0.96
1:B:341:GLN:NE2	1:B:367:ARG:HH22	1.64	0.95
1:B:209:PHE:CE2	1:B:211:PRO:HB3	2.02	0.94
1:B:44:THR:HB	1:B:45:GLY:C	1.86	0.94
1:B:367:ARG:HG3	3:B:502[B]:2PG:O2P	1.67	0.94
1:A:252:ASP:HB2	1:A:253:GLY:HA2	1.48	0.94
1:A:395:ARG:NH1	1:B:395:ARG:HG3	1.80	0.93
1:B:213:LEU:CD1	1:B:219:PRO:HG3	1.98	0.93
1:B:209:PHE:HE2	1:B:211:PRO:HB3	1.32	0.92
1:B:209:PHE:CE2	1:B:211:PRO:CB	2.53	0.92
1:B:341:GLN:HE21	1:B:367:ARG:HH22	1.01	0.92
1:B:209:PHE:CE2	1:B:211:PRO:HD3	2.05	0.91
1:B:41:GLY:N	1:B:367:ARG:CD	2.32	0.91
1:B:338:LYS:HD3	1:B:341:GLN:NE2	1.85	0.90
1:B:304:LEU:HD13	1:B:308:VAL:HB	1.50	0.90
1:B:209:PHE:HD2	1:B:211:PRO:CD	1.75	0.90
1:B:161:THR:HG21	1:B:216:ASN:OD1	1.71	0.89
1:A:160:SER:HB2	1:A:212:SER:HA	1.54	0.89
1:B:156:HIS:CB	1:B:157:ALA:CA	2.46	0.89
1:B:44:THR:CG2	1:B:48:GLU:CG	2.51	0.89

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:370:GLU:HG3	1:B:398:ARG:NH1	1.88	0.89
1:B:370:GLU:CG	1:B:398:ARG:NH1	2.37	0.88
1:B:41:GLY:CA	1:B:367:ARG:CD	2.50	0.88
1:B:197:ARG:CG	1:B:199:PHE:HE2	1.87	0.88
1:B:156:HIS:HB2	1:B:157:ALA:CB	1.98	0.88
1:B:209:PHE:HE2	1:B:211:PRO:CA	1.87	0.88
1:A:252:ASP:HB2	1:A:253:GLY:CA	2.05	0.87
1:A:395:ARG:HH12	1:B:395:ARG:HG3	1.35	0.86
1:B:44:THR:CB	1:B:45:GLY:C	2.43	0.86
1:B:342:ILE:HD11	1:B:347:GLU:HB3	1.57	0.86
1:B:197:ARG:CG	1:B:199:PHE:CE2	2.59	0.86
1:B:338:LYS:CD	1:B:341:GLN:NE2	2.39	0.86
1:A:254:LYS:CG	1:A:265:SER:HA	2.03	0.86
1:B:44:THR:HG22	1:B:45:GLY:O	1.75	0.85
1:B:156:HIS:N	1:B:157:ALA:HB3	1.90	0.85
1:A:390:THR:HG22	1:A:390:THR:O	1.77	0.85
1:B:262:ARG:HH12	1:B:272:TYR:HD2	1.06	0.85
1:B:304:LEU:HD13	1:B:308:VAL:HG21	1.57	0.85
1:B:42:ALA:HB1	1:B:43:SER:HA	1.57	0.84
1:B:44:THR:CG2	1:B:45:GLY:O	2.26	0.84
1:A:202:THR:O	1:A:203:VAL:HG13	1.77	0.84
1:B:205:ASP:O	1:B:395:ARG:NH1	2.10	0.84
1:B:197:ARG:HG3	1:B:199:PHE:CE2	2.12	0.83
1:B:44:THR:CB	1:B:45:GLY:O	2.26	0.83
1:A:309:GLN:HE22	1:A:387:GLN:HE22	1.26	0.83
1:A:366:HIS:ND1	1:A:390:THR:HA	1.95	0.82
1:B:370:GLU:HB2	1:B:398:ARG:HH12	1.41	0.82
1:A:206:GLU:HA	1:A:398:ARG:HE	1.43	0.82
1:B:44:THR:HG23	1:B:48:GLU:CD	2.00	0.82
1:B:44:THR:HB	1:B:45:GLY:O	1.79	0.82
1:B:209:PHE:CE2	1:B:211:PRO:N	2.48	0.81
1:B:390:THR:O	1:B:398:ARG:CD	2.28	0.81
1:B:44:THR:CA	1:B:45:GLY:C	2.48	0.81
1:A:12:GLU:HG3	1:A:65:VAL:HG12	1.62	0.81
1:A:366:HIS:ND1	1:A:389:LYS:O	2.12	0.81
1:B:342:ILE:CD1	1:B:347:GLU:HB3	2.10	0.81
1:B:48:GLU:O	1:B:50:LEU:HD22	1.82	0.79
1:B:197:ARG:HG3	1:B:199:PHE:CD2	2.18	0.79
1:A:206:GLU:HA	1:A:398:ARG:NE	1.95	0.79
1:A:202:THR:O	1:A:203:VAL:CG1	2.30	0.79
1:A:160:SER:HB2	1:A:212:SER:CA	2.13	0.79

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:262:ARG:NH1	1:B:272:TYR:CE2	2.50	0.79
1:A:202:THR:HB	1:B:202:THR:OG1	1.84	0.78
1:A:395:ARG:NH2	1:B:203:VAL:HG22	1.97	0.77
1:B:338:LYS:HB2	1:B:341:GLN:OE1	1.85	0.77
1:B:44:THR:HA	1:B:45:GLY:C	2.04	0.77
1:B:366:HIS:CD2	1:B:390:THR:CA	2.54	0.77
1:A:254:LYS:O	1:A:255:TYR:HB2	1.85	0.76
1:A:45[B]:GLY:O	1:A:46[B]:ALA:HB3	1.86	0.76
1:B:197:ARG:NH2	1:B:199:PHE:CZ	2.54	0.76
1:A:154:GLY:H	1:A:161:THR:HG23	1.51	0.75
1:A:160:SER:HB3	1:A:213:LEU:O	1.86	0.75
1:B:44:THR:CB	1:B:45:GLY:CA	2.56	0.74
1:A:202:THR:CB	1:B:202:THR:HG21	2.19	0.72
1:B:44:THR:HG22	1:B:48:GLU:HG2	1.71	0.72
1:B:338:LYS:HD3	1:B:367:ARG:NH2	2.03	0.72
1:B:42:ALA:H	1:B:367:ARG:NH1	1.88	0.72
1:B:209:PHE:CE2	1:B:211:PRO:CA	2.71	0.72
1:B:40:SER:C	1:B:367:ARG:HD2	2.09	0.72
1:A:203:VAL:HG23	1:A:203:VAL:O	1.90	0.72
1:A:390:THR:O	1:A:398:ARG:HD2	1.90	0.71
1:A:252:ASP:CB	1:A:253:GLY:CA	2.68	0.71
1:B:197:ARG:CD	1:B:199:PHE:HE2	2.02	0.71
1:B:197:ARG:NH2	1:B:199:PHE:CE2	2.58	0.71
1:B:341:GLN:NE2	1:B:367:ARG:NH2	2.37	0.71
1:B:258:LYS:HG2	1:B:259:ARG:CD	2.21	0.71
1:A:252:ASP:CB	1:A:253:GLY:HA2	2.18	0.71
1:B:42:ALA:CB	1:B:43:SER:HA	2.16	0.70
1:A:357:ARG:O	1:A:358:SER:OG	2.09	0.70
1:B:200:SER:O	1:B:209:PHE:CE1	2.44	0.70
1:B:42:ALA:H	1:B:367:ARG:HH11	1.36	0.70
1:A:202:THR:HB	1:B:202:THR:HG21	1.73	0.70
1:B:341:GLN:HE21	1:B:367:ARG:NH2	1.85	0.70
1:B:42:ALA:HB1	1:B:43:SER:CA	2.23	0.69
1:B:256:HIS:NE2	1:B:264:LEU:HD23	2.08	0.69
1:B:41:GLY:N	1:B:367:ARG:HD2	2.08	0.69
1:B:200:SER:O	1:B:209:PHE:HE1	1.77	0.68
1:A:390:THR:O	1:A:390:THR:CG2	2.41	0.68
1:A:45[B]:GLY:O	1:A:46[B]:ALA:CB	2.42	0.68
1:B:163:PHE:HD2	1:B:166:PHE:CZ	2.13	0.66
1:B:338:LYS:HB2	1:B:341:GLN:CD	2.16	0.66
1:A:43[B]:SER:C	1:A:44[B]:THR:HG1	1.99	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:44:THR:CB	1:B:45:GLY:HA2	2.20	0.66
1:A:254:LYS:HG3	1:A:265:SER:CA	2.14	0.66
1:A:12:GLU:HG3	1:A:65:VAL:CG1	2.25	0.65
1:B:338:LYS:HD2	1:B:341:GLN:NE2	2.12	0.65
1:A:395:ARG:HH12	1:B:395:ARG:CG	1.89	0.65
1:A:154:GLY:O	1:A:157:ALA:HB3	1.96	0.65
1:A:203:VAL:HG12	1:A:207:GLY:O	1.96	0.65
1:A:160:SER:HB3	1:A:213:LEU:N	2.12	0.64
1:B:41:GLY:HA3	1:B:367:ARG:CG	2.27	0.64
1:B:44:THR:CG2	1:B:48:GLU:HG2	2.24	0.64
1:B:143:LEU:HD13	1:B:409:GLU:HB2	1.79	0.64
1:B:209:PHE:CD2	1:B:210:ALA:N	2.66	0.64
1:B:48:GLU:O	1:B:50:LEU:CD2	2.46	0.64
1:B:338:LYS:CD	1:B:341:GLN:CD	2.66	0.64
1:A:202:THR:HB	1:B:202:THR:CG2	2.29	0.63
1:A:191:LYS:HE3	1:A:201:THR:HG21	1.80	0.63
1:A:202:THR:C	1:A:203:VAL:HG13	2.19	0.63
1:B:213:LEU:HD13	1:B:219:PRO:CG	2.25	0.62
1:B:258:LYS:HG2	1:B:259:ARG:HD3	1.81	0.62
1:B:370:GLU:CB	1:B:398:ARG:NH1	2.59	0.62
1:B:258:LYS:HG2	1:B:259:ARG:HD2	1.81	0.62
1:B:44:THR:CG2	1:B:48:GLU:HG3	2.30	0.62
1:B:153:GLY:HA2	1:B:160:SER:OG	2.00	0.62
1:B:197:ARG:HD2	1:B:199:PHE:CE2	2.35	0.61
1:A:202:THR:HB	1:B:202:THR:CB	2.31	0.61
1:B:367:ARG:NH1	3:B:502[B]:2PG:O4P	2.33	0.61
1:A:43[B]:SER:O	1:A:44[B]:THR:OG1	2.13	0.61
1:B:44:THR:CG2	1:B:48:GLU:CD	2.69	0.60
1:A:177:ARG:HH22	1:B:66:LEU:HD21	1.66	0.60
1:B:202:THR:CG2	1:B:203:VAL:N	2.64	0.60
1:B:76:ILE:HG21	1:B:115:VAL:HG21	1.83	0.60
1:A:202:THR:HA	1:B:202:THR:HG21	1.82	0.60
1:B:52:LEU:HD21	1:B:67:LYS:HB3	1.83	0.59
1:A:165:GLU:HG3	1:A:243:ASP:HB3	1.85	0.59
1:B:44:THR:HG21	1:B:48:GLU:HG3	1.85	0.59
1:B:209:PHE:CE2	1:B:211:PRO:CG	2.85	0.59
1:B:256:HIS:NE2	1:B:264:LEU:CD2	2.66	0.58
1:B:39:PRO:O	1:B:40:SER:HB3	2.02	0.58
1:B:304:LEU:CD1	1:B:308:VAL:CB	2.66	0.58
1:A:202:THR:CA	1:B:202:THR:HG21	2.34	0.58
1:B:197:ARG:HH21	1:B:199:PHE:HZ	1.48	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:151:MET:SD	1:B:219:PRO:HB3	2.44	0.58
1:A:44[B]:THR:O	1:A:45[B]:GLY:C	2.42	0.58
1:B:209:PHE:HE2	1:B:211:PRO:CG	2.16	0.57
1:B:44:THR:HA	1:B:46:ALA:CB	2.33	0.57
1:B:338:LYS:HD3	1:B:341:GLN:CD	2.24	0.57
1:A:395:ARG:CZ	1:B:203:VAL:HG21	2.33	0.57
1:B:202:THR:HG23	1:B:203:VAL:N	2.20	0.57
1:B:366:HIS:CD2	1:B:390:THR:C	2.78	0.57
1:B:209:PHE:HD2	1:B:211:PRO:HD3	0.78	0.57
1:A:254:LYS:O	1:A:255:TYR:CB	2.51	0.57
1:B:44:THR:HA	1:B:46:ALA:N	2.21	0.56
1:A:17:ARG:NH2	1:A:205:ASP:OD2	2.35	0.56
1:A:155:GLN:C	1:A:157:ALA:H	2.09	0.56
1:A:206:GLU:HA	1:A:398:ARG:CZ	2.35	0.56
1:B:40:SER:C	1:B:367:ARG:CD	2.73	0.56
1:A:254:LYS:HD2	1:A:266:SER:H	1.70	0.56
1:A:194:ILE:HG23	1:A:199:PHE:HB2	1.87	0.56
1:B:197:ARG:NH2	1:B:199:PHE:HZ	2.04	0.55
1:B:258:LYS:HA	1:B:259:ARG:CD	2.26	0.55
1:B:341:GLN:HG3	1:B:367:ARG:HH21	1.70	0.55
1:B:163:PHE:HD2	1:B:166:PHE:HZ	1.53	0.55
1:B:165:GLU:HB2	1:B:243:ASP:HB3	1.88	0.55
1:B:285:LEU:HD23	1:B:310:LEU:HD22	1.88	0.54
1:A:205:ASP:O	1:A:398:ARG:NH2	2.40	0.54
1:A:160:SER:O	1:A:161:THR:CB	2.55	0.54
1:B:190:LEU:HG	1:B:194:ILE:HD12	1.88	0.54
1:B:143:LEU:HD11	1:B:409:GLU:HA	1.90	0.54
1:A:214:PRO:HA	1:A:259:ARG:HH21	1.73	0.54
1:B:143:LEU:CD1	1:B:409:GLU:HB2	2.38	0.53
1:A:40[A]:SER:O	1:A:367:ARG:HB3	2.08	0.53
1:B:159:ASN:O	1:B:159:ASN:CG	2.46	0.53
1:A:160:SER:CB	1:A:213:LEU:N	2.72	0.53
1:B:43:SER:O	1:B:44:THR:OG1	2.25	0.53
1:B:341:GLN:CG	1:B:367:ARG:NH2	2.72	0.53
1:A:76:ILE:HG21	1:A:115:VAL:HG21	1.91	0.53
1:B:215:THR:HG22	1:B:217:ASP:H	1.73	0.53
1:A:160:SER:C	1:A:161:THR:HG22	2.09	0.52
1:A:390:THR:HG21	1:A:401:LYS:HB2	1.91	0.52
1:B:143:LEU:CD1	1:B:409:GLU:HG3	2.40	0.52
1:B:304:LEU:HD12	1:B:308:VAL:HB	1.84	0.51
1:B:197:ARG:HH21	1:B:199:PHE:HE2	1.46	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:143:LEU:CD1	1:B:409:GLU:CB	2.88	0.51
1:B:143:LEU:CD1	1:B:409:GLU:CG	2.89	0.51
1:B:209:PHE:HE2	1:B:211:PRO:N	1.94	0.51
1:B:42:ALA:O	1:B:367:ARG:NH1	2.43	0.51
1:B:155:GLN:C	1:B:157:ALA:CB	2.61	0.51
1:A:254:LYS:CG	1:A:264:LEU:O	2.58	0.50
1:A:395:ARG:NH1	1:B:395:ARG:CD	2.73	0.50
1:B:197:ARG:O	1:B:197:ARG:HD3	2.11	0.50
1:B:44:THR:HA	1:B:46:ALA:HB3	1.93	0.50
1:B:338:LYS:HD2	1:B:341:GLN:CD	2.31	0.50
1:A:162:ASP:O	1:A:163:PHE:O	2.30	0.50
1:B:161:THR:HG23	1:B:216:ASN:CG	2.23	0.50
1:B:38:VAL:HG11	1:B:110:ASN:HA	1.94	0.49
1:B:370:GLU:HB2	1:B:398:ARG:NH1	2.19	0.49
1:B:44:THR:HG23	1:B:48:GLU:OE1	2.12	0.49
1:A:254:LYS:HD2	1:A:266:SER:N	2.27	0.49
1:B:197:ARG:CD	1:B:197:ARG:O	2.60	0.49
1:A:395:ARG:HG2	1:B:395:ARG:HE	1.76	0.49
1:A:151:MET:HB3	1:A:166:PHE:HB2	1.94	0.49
1:A:206:GLU:HA	1:A:398:ARG:NH2	2.28	0.49
1:B:159:ASN:O	1:B:159:ASN:OD1	2.30	0.49
1:B:209:PHE:HE2	1:B:211:PRO:CD	2.07	0.49
1:A:254:LYS:CD	1:A:265:SER:HA	2.43	0.49
1:A:16:SER:O	1:B:394:ALA:O	2.30	0.48
1:A:200:SER:OG	1:A:201:THR:N	2.46	0.48
1:B:197:ARG:CD	1:B:199:PHE:CE2	2.85	0.48
1:B:319:ASN:HD22	1:B:322:ARG:HG2	1.78	0.48
1:A:206:GLU:O	1:A:398:ARG:HG3	2.14	0.48
1:B:366:HIS:CD2	1:B:389:LYS:O	2.67	0.47
1:A:144:PRO:HG3	1:A:380:VAL:HG11	1.96	0.47
1:A:203:VAL:HB	1:A:207:GLY:HA2	1.96	0.47
1:A:203:VAL:CG2	1:A:203:VAL:O	2.61	0.47
1:B:258:LYS:CA	1:B:259:ARG:HD2	2.29	0.47
1:B:419:ALA:HB1	1:B:423:ALA:HB2	1.95	0.47
1:A:390:THR:O	1:A:398:ARG:CD	2.60	0.47
1:A:255:TYR:OH	1:A:290:ALA:N	2.39	0.47
1:A:46[B]:ALA:O	1:A:317:VAL:HG11	2.15	0.47
1:A:253:GLY:O	1:A:254:LYS:HE2	2.14	0.46
1:B:52:LEU:HD23	1:B:68:ALA:N	2.30	0.46
1:B:338:LYS:CD	1:B:341:GLN:HE22	2.25	0.46
1:B:338:LYS:HD2	1:B:341:GLN:HE22	1.78	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:367:ARG:CG	3:B:502[B]:2PG:O2P	2.51	0.46
1:B:289:LEU:HD12	1:B:300:LEU:HD22	1.97	0.46
1:A:44[B]:THR:O	1:A:45[B]:GLY:O	2.34	0.45
1:A:397:ASP:HB3	1:B:396:THR:OG1	2.16	0.45
1:A:46[B]:ALA:N	1:A:48:GLU:OE1	2.37	0.45
1:B:164:GLN:HB3	1:B:243:ASP:O	2.17	0.45
1:B:319:ASN:HB3	1:B:322:ARG:HG2	1.97	0.45
1:A:113:LEU:HD11	1:A:339:LEU:HG	1.99	0.45
1:B:215:THR:HG22	1:B:216:ASN:N	2.32	0.45
1:A:391:GLY:HA3	1:A:398:ARG:HD2	1.98	0.44
1:A:42[A]:ALA:O	1:A:51:GLU:CD	2.49	0.44
1:B:341:GLN:CG	1:B:367:ARG:HH21	2.30	0.44
1:B:189:MET:HA	1:B:192:LYS:HD2	1.99	0.44
1:B:367:ARG:HG2	1:B:368:SER:H	1.83	0.44
1:A:252:ASP:HB2	1:A:253:GLY:HA3	1.93	0.44
1:A:154:GLY:N	1:A:163:PHE:O	2.51	0.44
1:B:367:ARG:O	1:B:398:ARG:NH2	2.49	0.44
1:B:206:GLU:OE2	3:B:502[B]:2PG:C3	2.65	0.44
1:B:367:ARG:HG2	1:B:368:SER:N	2.32	0.44
1:A:397:ASP:OD1	1:A:398:ARG:HG2	2.18	0.44
1:A:254:LYS:HD2	1:A:265:SER:HA	2.00	0.44
1:B:256:HIS:CD2	1:B:264:LEU:HD23	2.51	0.44
1:B:48:GLU:H	1:B:48:GLU:HG2	1.63	0.43
1:B:209:PHE:CG	1:B:210:ALA:N	2.85	0.43
1:B:143:LEU:HD12	1:B:409:GLU:HG3	2.01	0.43
1:B:163:PHE:CD2	1:B:166:PHE:HZ	2.34	0.43
1:A:117:LEU:HD22	1:A:375:THR:HG21	2.01	0.43
1:A:419:ALA:HB1	1:A:423:ALA:HB2	2.00	0.43
1:B:220:LEU:HD21	1:B:282:ILE:HD11	2.00	0.43
1:A:176:PHE:HZ	1:A:402:TYR:HD1	1.67	0.43
1:A:160:SER:CB	1:A:212:SER:C	2.87	0.43
1:B:319:ASN:HD21	1:B:321:GLN:HB3	1.84	0.42
1:B:176:PHE:HZ	1:B:402:TYR:HD1	1.67	0.42
1:A:160:SER:OG	1:A:212:SER:HB3	2.18	0.42
1:A:202:THR:O	1:A:203:VAL:HG12	2.14	0.42
1:A:44[A]:THR:CG2	1:A:45[A]:GLY:N	2.83	0.42
1:B:163:PHE:CD2	1:B:166:PHE:CZ	3.00	0.42
1:B:299:LEU:HD11	1:B:303:LYS:HE2	2.01	0.42
1:A:40[A]:SER:HA	1:A:41[A]:GLY:HA3	1.64	0.42
1:A:395:ARG:HB2	1:A:397:ASP:OD1	2.19	0.42
1:A:157:ALA:HB1	1:A:160:SER:O	2.18	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:44[A]:THR:HG22	1:A:45[A]:GLY:N	2.34	0.42
1:B:190:LEU:HG	1:B:194:ILE:CD1	2.49	0.42
1:B:150:ILE:HG22	1:B:187:TYR:HD1	1.84	0.42
1:A:206:GLU:CA	1:A:398:ARG:HE	2.22	0.42
1:B:52:LEU:HD23	1:B:68:ALA:HA	2.00	0.42
1:A:353:GLN:O	1:A:357:ARG:HG2	2.20	0.42
1:A:254:LYS:HD3	1:A:254:LYS:HA	1.36	0.41
1:A:357:ARG:O	1:A:358:SER:CB	2.68	0.41
1:B:52:LEU:HD23	1:B:68:ALA:CA	2.49	0.41
1:B:117:LEU:HD22	1:B:375:THR:HG21	2.03	0.41
1:A:190:LEU:HG	1:A:194:ILE:HD12	2.02	0.41
1:B:146:PRO:HD2	1:B:170:PRO:HD2	2.02	0.41
1:B:338:LYS:HD2	1:B:341:GLN:OE1	2.20	0.41
1:A:301:ARG:HD3	1:A:330:LYS:O	2.20	0.41
1:A:40[B]:SER:O	1:A:367:ARG:HB3	2.21	0.40
1:A:193:VAL:O	1:A:197:ARG:HG2	2.22	0.40
1:A:163:PHE:CE1	1:A:273:TRP:HH2	2.39	0.40
1:A:244:PRO:HD2	1:A:286:GLU:O	2.20	0.40
1:A:155:GLN:C	1:A:157:ALA:N	2.75	0.40

There are no symmetry-related clashes.

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
1	A	427/426 (100%)	383 (90%)	30 (7%)	14 (3%)	5 6
1	B	415/426 (97%)	379 (91%)	29 (7%)	7 (2%)	11 19
All	All	842/852 (99%)	762 (90%)	59 (7%)	21 (2%)	8 10

All (21) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	159	ASN
1	A	163	PHE
1	B	264	LEU
1	A	45[A]	GLY
1	A	45[B]	GLY
1	A	46[A]	ALA
1	A	46[B]	ALA
1	A	203	VAL
1	A	255	TYR
1	B	40	SER
1	A	44[A]	THR
1	A	44[B]	THR
1	A	156	HIS
1	A	358	SER
1	B	157	ALA
1	B	155	GLN
1	B	163	PHE
1	A	161	THR
1	B	39	PRO
1	A	214	PRO
1	B	214	PRO

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	333/332 (100%)	329 (99%)	4 (1%)	78	92
1	B	326/332 (98%)	322 (99%)	4 (1%)	78	92
All	All	659/664 (99%)	651 (99%)	8 (1%)	78	92

All (8) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	156	HIS
1	A	159	ASN
1	A	200	SER

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Mol	Chain	Res	Type
1	A	254	LYS
1	B	160	SER
1	B	197	ARG
1	B	201	THR
1	B	202	THR

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

Mol	Chain	Res	Type
1	A	93	GLN
1	A	256	HIS
1	A	309	GLN
1	B	88	GLN
1	B	319	ASN
1	B	341	GLN
1	B	366	HIS

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no carbohydrates in this entry.

5.6 Ligand geometry [i](#)

Of 4 ligands modelled in this entry, 2 are monoatomic - leaving 2 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
3	2PG	A	502[B]	-	5,10,10	0.67	0	6,14,14	1.17	0
3	2PG	B	502[B]	2	5,10,10	0.62	0	6,14,14	1.02	0

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	2PG	A	502[B]	-	-	0/7/11/11	0/0/0/0
3	2PG	B	502[B]	2	-	0/7/11/11	0/0/0/0

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

1 monomer is involved in 4 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	B	502[B]	2PG	4	0

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
1	B	3

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	B	262:ARG	C	263:SER	N	1.12
1	B	155:GLN	C	156:HIS	N	1.10
1	B	158:THR	C	159:ASN	N	1.04

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	424/426 (99%)	0.65	41 (9%) 10 11	30, 49, 97, 120	0
1	B	419/426 (98%)	1.18	84 (20%) 1 1	27, 58, 128, 144	0
All	All	843/852 (98%)	0.91	125 (14%) 3 3	27, 53, 111, 144	0

All (125) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	44	THR	11.4
1	A	44[A]	THR	11.2
1	B	426	VAL	9.8
1	B	42	ALA	8.6
1	B	157	ALA	8.6
1	B	196	ASP	8.2
1	A	202	THR	8.1
1	B	155	GLN	8.0
1	A	264	LEU	7.9
1	B	261	GLY	7.3
1	A	43[A]	SER	7.1
1	A	42[A]	ALA	7.1
1	A	46[A]	ALA	7.0
1	B	218	ALA	7.0
1	B	43	SER	6.7
1	A	159	ASN	6.6
1	B	262	ARG	6.5
1	A	252	ASP	6.5
1	A	158	THR	6.5
1	A	45[A]	GLY	6.5
1	B	207	GLY	6.5
1	B	201	THR	6.2
1	B	209	PHE	6.1
1	B	203	VAL	6.1

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Mol	Chain	Res	Type	RSRZ
1	A	261	GLY	6.1
1	B	156	HIS	5.9
1	B	213	LEU	5.9
1	B	159	ASN	5.9
1	B	256	HIS	5.7
1	B	160	SER	5.7
1	A	203	VAL	5.7
1	A	41[A]	GLY	5.7
1	B	264	LEU	5.7
1	B	47	HIS	5.5
1	B	206	GLU	5.4
1	B	195	HIS	5.3
1	B	198	GLY	5.3
1	B	199	PHE	5.3
1	B	200	SER	5.2
1	B	214	PRO	5.1
1	B	204	GLY	5.0
1	B	158	THR	5.0
1	A	200	SER	4.8
1	A	47	HIS	4.8
1	B	259	ARG	4.8
1	A	201	THR	4.6
1	B	194	ILE	4.5
1	B	151	MET	4.4
1	B	154	GLY	4.4
1	B	208	GLY	4.4
1	B	45	GLY	4.4
1	B	202	THR	4.4
1	B	263	SER	4.2
1	A	258	LYS	4.2
1	B	258	LYS	4.1
1	A	205	ASP	4.1
1	B	249	ILE	4.1
1	B	197	ARG	4.1
1	A	199	PHE	3.8
1	A	162	ASP	3.8
1	A	254	LYS	3.7
1	B	290	ALA	3.7
1	B	163	PHE	3.7
1	A	395	ARG	3.7
1	A	426	VAL	3.7
1	A	160	SER	3.7

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Mol	Chain	Res	Type	RSRZ
1	A	161	THR	3.6
1	B	152	ASN	3.6
1	B	304	LEU	3.6
1	B	215	THR	3.6
1	B	205	ASP	3.6
1	B	225	GLU	3.5
1	B	222	LEU	3.5
1	B	192	LYS	3.4
1	B	41	GLY	3.4
1	A	157	ALA	3.3
1	B	150	ILE	3.3
1	A	194	ILE	3.2
1	A	195	HIS	3.2
1	A	396	THR	3.1
1	B	247	THR	3.1
1	B	396	THR	3.1
1	B	328	GLU	3.1
1	B	266	SER	3.1
1	B	398	ARG	2.9
1	A	255	TYR	2.9
1	B	300	LEU	2.8
1	B	295	GLU	2.8
1	B	221	GLN	2.7
1	A	398	ARG	2.7
1	B	162	ASP	2.7
1	B	280	TYR	2.7
1	A	394	ALA	2.7
1	B	367	ARG	2.7
1	B	365	SER	2.6
1	B	48	GLU	2.6
1	A	247	THR	2.6
1	A	40[A]	SER	2.6
1	B	269	MET	2.5
1	B	297	TRP	2.5
1	B	190	LEU	2.5
1	B	303	LYS	2.5
1	B	265	SER	2.4
1	B	270	VAL	2.4
1	B	289	LEU	2.4
1	A	214	PRO	2.4
1	B	40	SER	2.4
1	A	206	GLU	2.4

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Mol	Chain	Res	Type	RSRZ
1	B	296	GLY	2.4
1	B	399	ILE	2.4
1	B	301	ARG	2.4
1	B	394	ALA	2.3
1	B	299	LEU	2.3
1	A	366	HIS	2.3
1	B	388	ILE	2.2
1	B	366	HIS	2.2
1	B	272	TYR	2.2
1	B	395	ARG	2.2
1	A	265	SER	2.2
1	A	259	ARG	2.1
1	B	425	LYS	2.1
1	A	365	SER	2.1
1	B	257	LEU	2.1
1	A	155	GLN	2.1
1	B	223	ILE	2.0

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

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

6.3 Carbohydrates ⓘ

There are no carbohydrates in this entry.

6.4 Ligands ⓘ

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(Å ²)	Q<0.9
2	MG	A	501	1/1	0.92	0.38	4.78	41,41,41,41	0
2	MG	B	501	1/1	0.88	0.36	4.34	56,56,56,56	0
3	2PG	A	502[B]	11/11	0.64	0.72	3.67	93,95,100,100	11
3	2PG	B	502[B]	11/11	0.68	0.59	1.86	97,99,104,104	11

6.5 Other polymers

There are no such residues in this entry.