



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 08:29 PM UTC

PDB ID : 6HPT / pdb_00006hpt
Title : Crystal structure of human Pif1 helicase, apoform.
Authors : Levnikov, V.M.; Dehghani-Tafti, S.; Bax, B.D.; Sanders, C.M.; Antson, A.A.
Deposited on : 2018-09-21
Resolution : 1.44 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

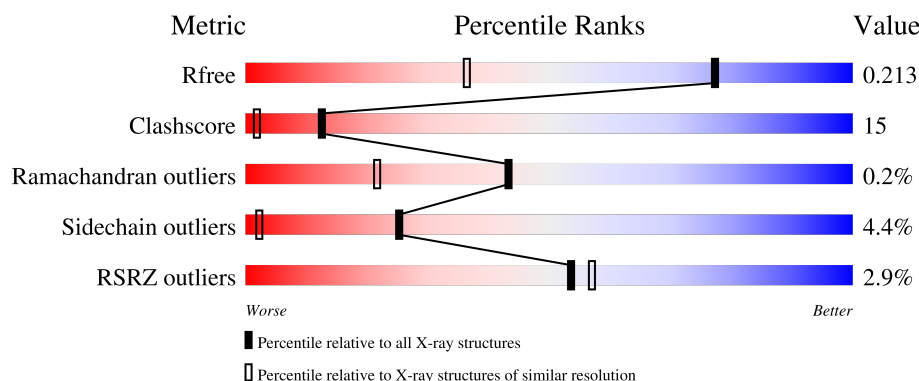
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.44 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	3234 (1.46-1.42)
Clashscore	190562	3289 (1.46-1.42)
Ramachandran outliers	187476	3248 (1.46-1.42)
Sidechain outliers	187428	3248 (1.46-1.42)
RSRZ outliers	180081	3234 (1.46-1.42)

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	439	

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	SO4	A	703	-	X	-	-

2 Entry composition [i](#)

There are 3 unique types of molecules in this entry. The entry contains 4195 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 ATP-dependent DNA helicase PIF1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	416	3204	2012	594	575	23	0	8	0

There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	203	SER	-	expression tag	UNP Q9H611
A	204	ARG	-	expression tag	UNP Q9H611
A	205	MET	-	expression tag	UNP Q9H611

- Molecule 2 is SULFATE ION (CCD ID: SO4) (formula: O₄S).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	A	1	Total	O	S	0	0
			5	4	1		
2	A	1	Total	O	S	0	0
			5	4	1		

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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	A	1	Total	O	S	0	0
			5	4	1		

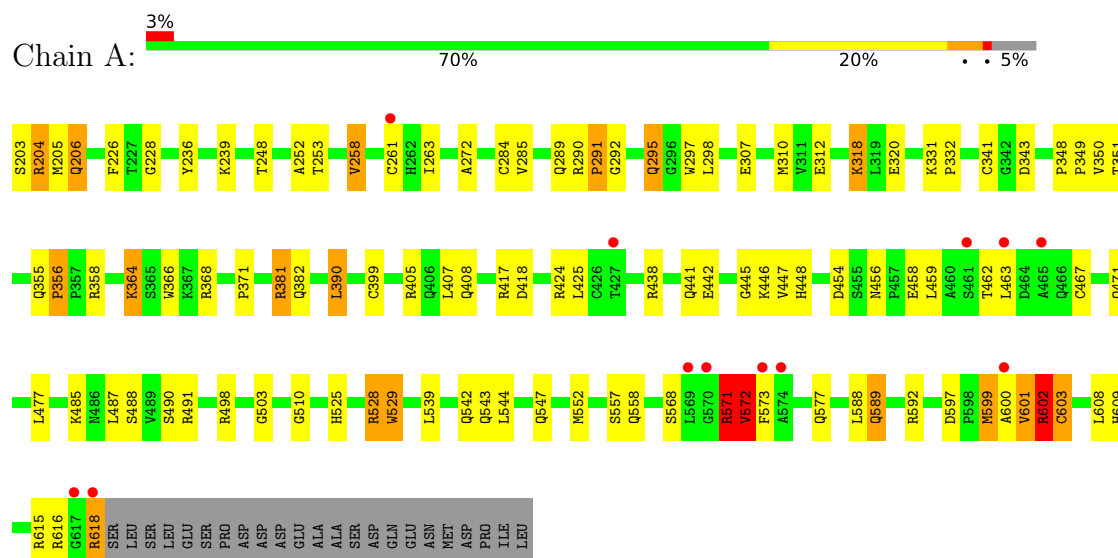
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	976	Total	O	0	0
			976	976		

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: ATP-dependent DNA helicase PIF1



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	63.54Å 81.40Å 91.48Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	60.89 – 1.44 60.81 – 1.44	Depositor EDS
% Data completeness (in resolution range)	99.8 (60.89-1.44) 99.8 (60.81-1.44)	Depositor EDS
R_{merge}	0.04	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.52 (at 1.44Å)	Xtriage
Refinement program	REFMAC 5.8.0151	Depositor
R, R_{free}	0.134 , 0.195 (Not available) , 0.213	Depositor DCC
R_{free} test set	4365 reflections (5.06%)	wwPDB-VP
Wilson B-factor (Å ²)	22.3	Xtriage
Anisotropy	0.190	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.27 , 46.7	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	0.98	EDS
Total number of atoms	4195	wwPDB-VP
Average B, all atoms (Å ²)	37.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.89% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: SO4

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	1.78	38/3280 (1.2%)	1.45	21/4436 (0.5%)

All (38) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	603[A]	CYS	CA-C	9.47	1.64	1.52
1	A	603[B]	CYS	CA-C	9.47	1.64	1.52
1	A	356	PRO	CA-C	9.12	1.56	1.51
1	A	568[A]	SER	C-O	-8.05	1.14	1.24
1	A	568[B]	SER	C-O	-8.05	1.14	1.24
1	A	253	THR	CA-C	7.20	1.61	1.52
1	A	568[A]	SER	CA-C	7.08	1.61	1.52
1	A	568[B]	SER	CA-C	7.08	1.61	1.52
1	A	349	PRO	CA-C	6.78	1.60	1.52
1	A	571	ARG	CA-C	6.67	1.62	1.53
1	A	343	ASP	CA-C	6.51	1.59	1.52
1	A	597	ASP	C-N	6.45	1.41	1.34
1	A	458	GLU	C-O	-6.41	1.14	1.24
1	A	228	GLY	CA-C	6.36	1.57	1.51
1	A	295	GLN	CA-C	6.24	1.61	1.52
1	A	390	LEU	C-O	6.21	1.31	1.24
1	A	539	LEU	N-CA	6.11	1.53	1.46
1	A	226	PHE	N-CA	6.08	1.53	1.46
1	A	503	GLY	N-CA	5.99	1.52	1.45
1	A	381	ARG	CD-NE	-5.89	1.38	1.46
1	A	510	GLY	C-O	5.84	1.30	1.24
1	A	542	GLN	CD-OE1	5.78	1.34	1.23
1	A	539	LEU	CA-C	5.78	1.59	1.52
1	A	252	ALA	N-CA	5.69	1.53	1.46
1	A	284	CYS	CA-CB	5.65	1.62	1.53
1	A	488	SER	C-O	5.63	1.30	1.23

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	341	CYS	N-CA	5.60	1.52	1.46
1	A	320	GLU	CA-C	5.57	1.60	1.52
1	A	263	ILE	CA-C	-5.48	1.45	1.52
1	A	445	GLY	N-CA	5.47	1.52	1.45
1	A	447	VAL	N-CA	5.32	1.52	1.46
1	A	454	ASP	CA-C	5.25	1.58	1.52
1	A	599	MET	CA-C	-5.25	1.45	1.52
1	A	441	GLN	C-O	5.15	1.30	1.24
1	A	408	GLN	CD-OE1	5.11	1.33	1.23
1	A	272	ALA	C-O	5.07	1.29	1.24
1	A	418	ASP	CG-OD2	-5.05	1.15	1.25
1	A	529	TRP	CA-C	5.01	1.58	1.52

All (21) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	356	PRO	N-CA-C	7.83	117.99	110.47
1	A	310[A]	MET	CA-C-O	7.43	128.62	119.11
1	A	310[B]	MET	CA-C-O	7.43	128.62	119.11
1	A	602	ARG	NE-CZ-NH2	6.94	125.44	119.20
1	A	310[A]	MET	N-CA-C	6.81	121.42	113.18
1	A	310[B]	MET	N-CA-C	6.81	121.42	113.18
1	A	572	VAL	N-CA-CB	6.37	117.66	110.72
1	A	487	LEU	N-CA-C	6.03	117.94	111.36
1	A	599	MET	N-CA-C	5.91	119.59	112.38
1	A	318	LYS	CD-CE-NZ	5.84	130.57	111.90
1	A	571	ARG	O-C-N	-5.71	116.54	122.94
1	A	297	TRP	N-CA-C	5.57	117.03	111.07
1	A	601	VAL	CB-CA-C	5.41	118.88	111.31
1	A	407	LEU	N-CA-C	5.38	117.23	111.36
1	A	381	ARG	CG-CD-NE	-5.32	100.30	112.00
1	A	298	LEU	N-CA-C	5.29	117.05	111.28
1	A	366	TRP	N-CA-C	5.23	116.66	111.07
1	A	528	ARG	NE-CZ-NH1	-5.16	116.34	121.50
1	A	592	ARG	NE-CZ-NH2	5.12	123.81	119.20
1	A	602	ARG	NE-CZ-NH1	-5.07	116.43	121.50
1	A	263	ILE	N-CA-C	5.01	116.93	112.17

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	3204	0	3312	100	0
2	A	15	0	0	0	0
3	A	976	0	0	56	0
All	All	4195	0	3312	100	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 15.

All (100) 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:A:547:GLN:HG2	3:A:1341:HOH:O	1.30	1.23
1:A:205:MET:HB3	1:A:381:ARG:NH2	1.52	1.22
1:A:205:MET:CB	1:A:381:ARG:HH22	1.58	1.17
1:A:477:LEU:HD22	3:A:1323:HOH:O	1.47	1.12
1:A:599:MET:HE1	3:A:1675:HOH:O	1.48	1.09
1:A:205:MET:HB3	1:A:381:ARG:HH22	0.95	1.07
1:A:477:LEU:HD12	3:A:1599:HOH:O	1.55	1.06
1:A:600:ALA:HB1	3:A:881:HOH:O	1.61	1.00
1:A:618:ARG:NH2	3:A:801:HOH:O	1.96	0.97
1:A:348:PRO:HG3	3:A:1275:HOH:O	1.64	0.94
1:A:291:PRO:O	1:A:295:GLN:NE2	2.01	0.94
1:A:261:CYS:SG	3:A:1222:HOH:O	2.27	0.90
1:A:463:LEU:HD12	3:A:1093:HOH:O	1.74	0.86
1:A:602:ARG:HG2	1:A:602:ARG:HH21	1.39	0.85
1:A:558:GLN:HG2	3:A:1040:HOH:O	1.78	0.83
1:A:355:GLN:HB3	3:A:1469:HOH:O	1.78	0.82
1:A:399[B]:CYS:SG	1:A:601:VAL:HG11	2.20	0.82
1:A:206:GLN:O	1:A:381:ARG:NH1	2.13	0.82
1:A:205:MET:CB	1:A:381:ARG:NH2	2.30	0.78
1:A:543:GLN:HG3	1:A:544:LEU:N	1.99	0.77
1:A:477:LEU:HB3	3:A:1323:HOH:O	1.88	0.72
1:A:571:ARG:HD2	3:A:948:HOH:O	1.89	0.72
1:A:205:MET:HE3	1:A:236:TYR:CE1	2.24	0.71
1:A:205:MET:SD	1:A:381:ARG:NH2	2.63	0.71

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:258:VAL:HG13	3:A:1343:HOH:O	1.90	0.70
1:A:204:ARG:HB2	1:A:204:ARG:CZ	2.20	0.69
1:A:285:VAL:O	1:A:289:GLN:HG2	1.93	0.69
1:A:572:VAL:HG12	3:A:920:HOH:O	1.91	0.68
1:A:424:ARG:HD2	3:A:971:HOH:O	1.92	0.68
1:A:485:LYS:HE2	1:A:529:TRP:CE2	2.28	0.68
1:A:348:PRO:CG	3:A:1275:HOH:O	2.29	0.67
1:A:491:ARG:NH1	3:A:808:HOH:O	2.27	0.67
1:A:485:LYS:HD2	3:A:839:HOH:O	1.97	0.65
1:A:292:GLY:HA2	3:A:821:HOH:O	1.96	0.65
1:A:438:ARG:HD3	3:A:1364:HOH:O	1.96	0.64
1:A:602:ARG:HH21	1:A:602:ARG:CG	2.12	0.62
1:A:600:ALA:C	3:A:805:HOH:O	2.43	0.60
1:A:348:PRO:HD3	3:A:1275:HOH:O	2.01	0.59
1:A:350:VAL:O	3:A:803:HOH:O	2.17	0.58
1:A:552[B]:MET:SD	1:A:557:SER:HB3	2.43	0.57
1:A:615:ARG:NH1	3:A:818:HOH:O	2.37	0.57
1:A:348:PRO:CD	3:A:1275:HOH:O	2.51	0.57
1:A:382:GLN:HG2	3:A:1421:HOH:O	2.05	0.56
1:A:601:VAL:O	3:A:802:HOH:O	2.17	0.56
1:A:205:MET:HE1	1:A:382:GLN:CD	2.30	0.56
1:A:528:ARG:HD2	3:A:1246:HOH:O	2.05	0.56
1:A:295:GLN:HG3	3:A:1316:HOH:O	2.05	0.56
1:A:399[B]:CYS:SG	1:A:601:VAL:CG1	2.94	0.56
1:A:446:LYS:HE2	3:A:1486:HOH:O	2.04	0.55
1:A:490:SER:HB3	3:A:1418:HOH:O	2.05	0.55
1:A:364:LYS:CE	3:A:1220:HOH:O	2.55	0.54
1:A:417:ARG:NE	3:A:807:HOH:O	2.26	0.54
1:A:248:THR:HG22	3:A:1431:HOH:O	2.06	0.54
1:A:368:ARG:HD3	3:A:1494:HOH:O	2.08	0.53
1:A:477:LEU:CD2	3:A:1323:HOH:O	2.25	0.53
1:A:448:HIS:HD2	3:A:978:HOH:O	1.90	0.53
1:A:205:MET:HB2	1:A:236:TYR:OH	2.09	0.53
1:A:602:ARG:CG	1:A:602:ARG:NH2	2.71	0.52
1:A:543:GLN:HE21	1:A:544:LEU:H	1.57	0.52
1:A:399[B]:CYS:SG	1:A:601:VAL:HG21	2.50	0.51
1:A:351:THR:HG21	3:A:1103:HOH:O	2.11	0.51
1:A:573:PHE:HB2	1:A:577:GLN:HB3	1.91	0.51
1:A:477:LEU:CB	3:A:1323:HOH:O	2.55	0.51
1:A:456:ASN:ND2	3:A:823:HOH:O	2.43	0.49
1:A:205:MET:HB3	1:A:381:ARG:CZ	2.35	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:543:GLN:HG3	1:A:544:LEU:H	1.77	0.48
1:A:600:ALA:CB	3:A:881:HOH:O	2.39	0.48
1:A:205:MET:HE1	1:A:382:GLN:NE2	2.29	0.47
1:A:307:GLU:HG2	3:A:1302:HOH:O	2.13	0.47
1:A:399[B]:CYS:SG	1:A:601:VAL:CB	3.03	0.47
1:A:390:LEU:C	1:A:390:LEU:HD23	2.40	0.47
1:A:203:SER:O	1:A:203:SER:OG	2.33	0.47
1:A:552[B]:MET:HE2	1:A:552[B]:MET:HB3	1.72	0.46
1:A:618:ARG:HA	1:A:618:ARG:HD3	1.47	0.46
1:A:258:VAL:HA	3:A:1281:HOH:O	2.16	0.46
1:A:603[A]:CYS:SG	1:A:608:LEU:HD11	2.56	0.46
1:A:442:GLU:HG3	3:A:1158:HOH:O	2.16	0.45
1:A:364:LYS:HB3	1:A:364:LYS:HE2	1.61	0.45
1:A:602:ARG:HG2	1:A:602:ARG:NH2	2.17	0.45
1:A:371:PRO:HG2	3:A:946:HOH:O	2.16	0.45
1:A:462:THR:HG21	3:A:804:HOH:O	2.16	0.44
1:A:355:GLN:HB2	1:A:356:PRO:HD2	2.01	0.43
1:A:205:MET:CG	1:A:381:ARG:NH2	2.81	0.43
1:A:498:ARG:CZ	1:A:498:ARG:HB3	2.49	0.42
1:A:295:GLN:HB2	3:A:821:HOH:O	2.18	0.42
1:A:307:GLU:OE2	1:A:558:GLN:NE2	2.52	0.42
1:A:599:MET:HA	3:A:816:HOH:O	2.19	0.42
1:A:205:MET:HB2	1:A:381:ARG:HH22	1.67	0.42
1:A:485:LYS:HE2	1:A:529:TRP:CZ2	2.54	0.42
1:A:609:HIS:HE1	3:A:1451:HOH:O	2.02	0.42
1:A:425:LEU:CD1	1:A:552[B]:MET:HE3	2.49	0.42
1:A:525:HIS:HE1	3:A:1429:HOH:O	2.02	0.42
1:A:589:GLN:NE2	3:A:835:HOH:O	2.53	0.41
1:A:588:LEU:HD12	3:A:1376:HOH:O	2.19	0.41
1:A:290:ARG:O	1:A:291:PRO:C	2.63	0.41
1:A:312:GLU:HG3	1:A:351:THR:HG23	2.02	0.40
1:A:599:MET:CE	3:A:1675:HOH:O	2.30	0.40
1:A:616:ARG:NH2	3:A:840:HOH:O	2.54	0.40
1:A:331:LYS:HB3	1:A:332:PRO:HD2	2.03	0.40
1:A:358:ARG:NH1	3:A:822:HOH:O	2.42	0.40

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	422/439 (96%)	413 (98%)	8 (2%)	1 (0%)	43	22

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	291	PRO

5.3.2 Protein sidechains [i](#)

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	347/360 (96%)	332 (96%)	15 (4%)	26	2

All (15) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	204	ARG
1	A	206	GLN
1	A	239	LYS
1	A	258	VAL
1	A	318	LYS
1	A	364	LYS
1	A	405	ARG
1	A	459	LEU
1	A	467	CYS
1	A	471	GLN

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Mol	Chain	Res	Type
1	A	571	ARG
1	A	572	VAL
1	A	589	GLN
1	A	602	ARG
1	A	618	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	222	GLN
1	A	283	GLN
1	A	301	GLN
1	A	408	GLN
1	A	413	HIS
1	A	448	HIS
1	A	466	GLN
1	A	471	GLN
1	A	474	GLN
1	A	525	HIS
1	A	543	GLN
1	A	547	GLN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

3 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	$\# Z > 2$
2	SO4	A	703	-	4,4,4	1.42	1 (25%)	6,6,6	2.78	4 (66%)
2	SO4	A	702	-	4,4,4	0.86	0	6,6,6	0.92	0
2	SO4	A	701	-	4,4,4	0.22	0	6,6,6	1.25	0

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	703	SO4	O2-S	2.24	1.58	1.44

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	703	SO4	O3-S-O1	-3.62	90.61	109.56
2	A	703	SO4	O4-S-O1	3.59	128.32	109.56
2	A	703	SO4	O4-S-O2	-3.27	92.48	109.56
2	A	703	SO4	O4-S-O3	2.53	122.50	108.54

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Fit of model and data [i](#)

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

In the following table, the column labelled ‘#RSRZ > 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95th percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q < 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	A	416/439 (94%)	-0.04	12 (2%) 53 57	12, 29, 57, 109	9 (2%)

All (12) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	600	ALA	3.8
1	A	574	ALA	3.8
1	A	570	GLY	3.2
1	A	465	ALA	2.7
1	A	569	LEU	2.3
1	A	463	LEU	2.3
1	A	618	ARG	2.2
1	A	573	PHE	2.2
1	A	461	SER	2.1
1	A	617	GLY	2.1
1	A	427	THR	2.1
1	A	261	CYS	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(Å ²)	Q<0.9
2	SO4	A	703	5/5	0.90	0.19	36,42,46,50	5
2	SO4	A	702	5/5	0.99	0.03	22,24,30,31	0
2	SO4	A	701	5/5	0.99	0.03	21,25,25,29	0

6.5 Other polymers [i](#)

There are no such residues in this entry.