



Full wwPDB X-ray Structure Validation Report

Feb 27, 2014 – 11:28 PM GMT

PDB ID : 2FVC
Title : Crystal structure of NS5B BK strain (delta 24) in complex with a 3-(1,1-Dioxo-2H-(1,2,4)-benzothiadiazin-3-yl)-4-hydroxy-2(1H)-quinolinone
Authors : Concha, N.O.; Wonacott, A.; Singh, O.
Deposited on : 2006-01-30
Resolution : 2.00 Å(reported)

This is a full wwPDB 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/ValidationPDFNotes.html>

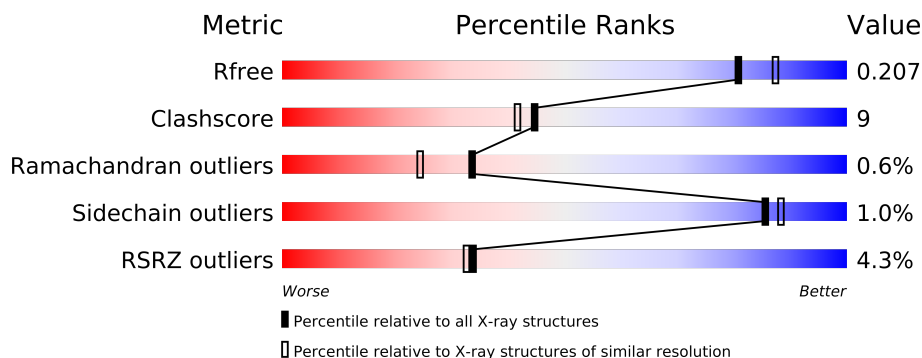
The following versions of software and data (see [references](#)) were used in the production of this report:

MolProbity : 4.02b-467
Mogul : 1.15 2013
Xtriage (Phenix) : dev-1323
EDS : stable22639
Percentile statistics : 21963
Refmac : 5.8.0049
CCP4 : 6.3.0 (Settle)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et. al. (1996)
Validation Pipeline (wwPDB-VP) : stable22683

1 Overall quality at a glance

The reported resolution of this entry is 2.00 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}	66092	4888 (2.00-2.00)
Clashscore	79885	6188 (2.00-2.00)
Ramachandran outliers	78287	6102 (2.00-2.00)
Sidechain outliers	78261	6100 (2.00-2.00)
RSRZ outliers	66119	4890 (2.00-2.00)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments on the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density.

Mol	Chain	Length	Quality of chain
1	A	563	
1	B	563	

The following table lists non-polymeric compounds that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Geometry	Electron density
2	888	A	901	-	X
2	888	B	902	-	X

2 Entry composition i

There are 3 unique types of molecules in this entry. The entry contains 9456 atoms, of which 0 are hydrogen and 0 are deuterium.

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.

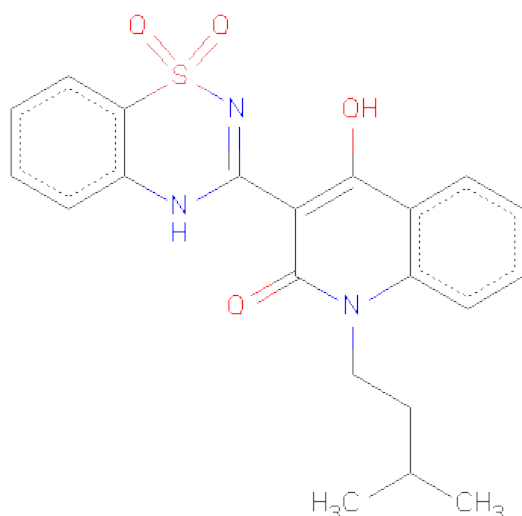
- Molecule 1 is a protein called polyprotein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	563	Total	C	N	O	S	14	2	0
			4376	2759	771	813	33			
1	B	563	Total	C	N	O	S	8	4	0
			4381	2764	771	813	33			

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	329	VAL	THR	SEE REMARK 999	GB 12831193
B	329	VAL	THR	SEE REMARK 999	GB 12831193

- Molecule 2 is 3-(1,1-DIOXIDO-4H-1,2,4-BENZOTHIADIAZIN-3-YL)-4-HYDROXY-1-(3-METHYLBUTYL)QUINOLIN-2(1H)-ONE (three-letter code: 888) (formula: C₂₁H₂₁N₃O₄S).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total	C	N	O	S	0	0
			29	21	3	4	1		

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	B	1	Total	C	N	O	S	0	0
			29	21	3	4	1		

- Molecule 3 is water.

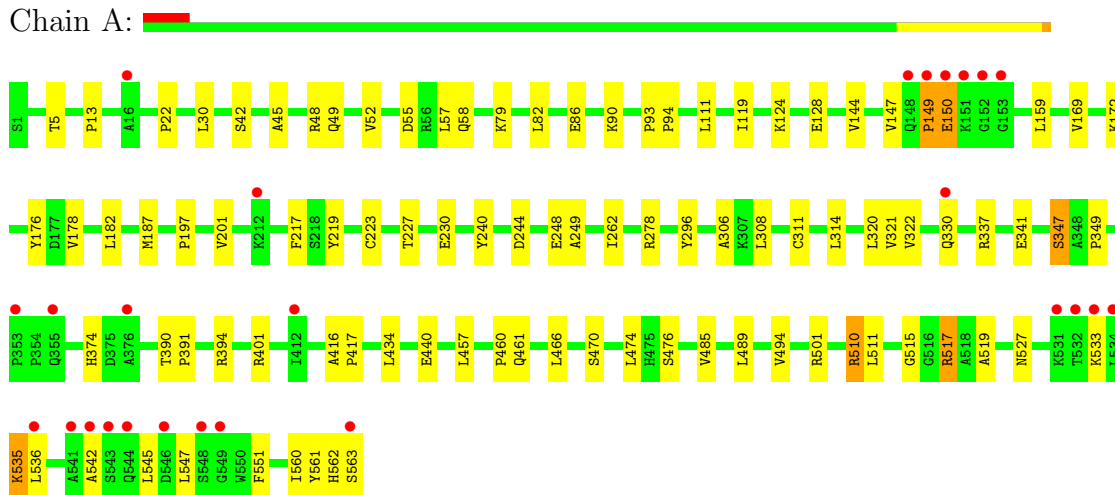
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	305	Total	O	0	0
			305	305		
3	B	336	Total	O	0	0
			336	336		

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 ($\text{RSRZ} > 2$). 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.

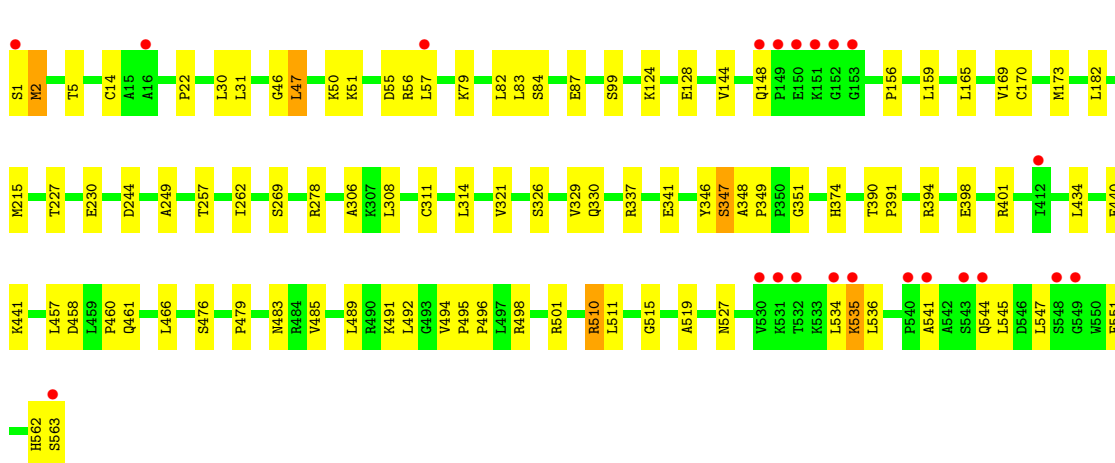
- Molecule 1: polypeptide

Chain A:



- Molecule 1: polypeptide

Chain B:



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	85.50Å 105.20Å 126.40Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	20.00 – 2.00 26.88 – 2.00	Depositor EDS
% Data completeness (in resolution range)	97.5 (20.00-2.00) 97.5 (26.88-2.00)	Depositor EDS
R_{merge}	0.08	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.41 (at 1.99Å)	Xtriage
Refinement program	CNS	Depositor
R, R_{free}	0.206 , 0.243 0.208 , 0.207	Depositor DCC
R_{free} test set	3743 reflections (4.95%)	DCC
Wilson B-factor (Å ²)	20.6	Xtriage
Anisotropy	0.437	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.42 , 40.8	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Outliers	2 of 75668 reflections (0.003%)	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	9456	wwPDB-VP
Average B, all atoms (Å ²)	22.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 45.88 % of the origin peak, indicating pseudo translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo translational symmetry is equal to 1.2407e-04. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

¹Intensities estimated from amplitudes.

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: 888

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	0.30	0/4482	0.57	0/6081
1	B	0.31	0/4497	0.59	2/6102 (0.0%)
All	All	0.30	0/8979	0.58	2/12183 (0.0%)

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	351	GLY	N-CA-C	-5.57	99.17	113.10
1	B	31	LEU	CA-CB-CG	5.02	126.85	115.30

There are no chirality outliers.

There are no planarity outliers.

5.2 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 hydrogens added by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, and the number in parentheses is this value normalized per 1000 atoms of the molecule in the chain. The Symm-Clashes column gives symmetry related clashes, in the same way as for the Clashes column.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	4376	0	4396	75	0
1	B	4381	0	4408	75	0
2	A	29	0	21	0	0
2	B	29	0	21	0	0
3	A	305	0	0	7	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	B	336	0	0	4	0
All	All	9456	0	8846	150	0

Clashscore is defined as the number of clashes calculated for the entry per 1000 atoms (including hydrogens) of the entry. The overall clashscore for this entry is 9.

All (150) close contacts within the same asymmetric unit are listed below.

Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:B:5:THR:HG23	1:B:278:ARG:HH12	1.17	1.07
1:A:5:THR:HG23	1:A:278:ARG:HH12	1.24	0.99
1:A:535:LYS:H	1:A:535:LYS:HD3	1.48	0.78
1:A:330:GLN:HB2	3:A:1201:HOH:O	1.88	0.72
1:B:308:LEU:HB3	1:B:311:CYS:SG	2.29	0.72
1:A:308:LEU:HB3	1:A:311:CYS:SG	2.30	0.71
1:A:5:THR:HG21	1:A:278:ARG:HH22	1.55	0.71
1:A:347:SER:O	1:A:349:PRO:HD3	1.91	0.70
1:B:510:ARG:HH11	1:B:510:ARG:HG2	1.58	0.68
1:B:5:THR:HG21	1:B:278:ARG:HH22	1.57	0.67
1:B:5:THR:HG23	1:B:278:ARG:NH1	2.00	0.67
1:A:149:PRO:HG2	1:A:150:GLU:H	1.58	0.67
1:B:337:ARG:O	1:B:341:GLU:HG3	1.95	0.66
1:A:517:ARG:HG2	1:A:517:ARG:HH11	1.60	0.66
1:B:527:ASN:HD21	1:B:534:LEU:H	1.45	0.65
1:B:535:LYS:HG3	1:B:536:LEU:H	1.61	0.65
1:B:1:SER:HB3	3:B:1214:HOH:O	1.96	0.65
1:A:178:VAL:HG23	3:A:1017:HOH:O	1.95	0.65
1:B:440:GLU:HG2	1:B:457:LEU:HD12	1.78	0.64
1:A:13:PRO:HG3	1:A:42:SER:OG	1.98	0.64
1:A:440:GLU:HG2	1:A:457:LEU:HD12	1.80	0.63
1:B:510:ARG:HG2	3:B:1205:HOH:O	1.99	0.63
1:B:182:LEU:HD23	1:B:182:LEU:C	2.19	0.63
1:A:466:LEU:HD22	1:A:551:PHE:HE2	1.62	0.62
1:A:176:TYR:OH	1:A:562:HIS:HE1	1.82	0.61
1:A:124:LYS:O	1:A:128:GLU:HG3	2.02	0.59
1:B:346:TYR:O	1:B:347:SER:HB3	2.01	0.59
1:A:22:PRO:HG2	1:A:401:ARG:HG3	1.85	0.59
1:A:52:VAL:HG12	1:A:223[B]:CYS:SG	2.43	0.58
1:B:170:CYS:HA	1:B:173:MET:HE3	1.85	0.58
1:A:337:ARG:O	1:A:341:GLU:HG3	2.03	0.57
1:A:182:LEU:HD23	1:A:182:LEU:C	2.24	0.57
1:A:510:ARG:HH11	1:A:510:ARG:HG2	1.70	0.56
1:B:169:VAL:HG12	1:B:173:MET:HE2	1.87	0.56

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:347:SER:C	1:A:349:PRO:HD3	2.25	0.56
1:A:306:ALA:HB3	1:A:308:LEU:HD13	1.88	0.56
1:B:50:LYS:HD2	1:B:50:LYS:N	2.19	0.56
1:B:47:LEU:HD22	1:B:51:LYS:NZ	2.20	0.56
1:B:314:LEU:HB3	1:B:321:VAL:HG12	1.89	0.55
1:A:308:LEU:CB	1:A:311:CYS:SG	2.94	0.55
1:B:124:LYS:O	1:B:128:GLU:HG3	2.06	0.55
1:B:515:GLY:HA2	1:B:519:ALA:HB2	1.89	0.55
1:B:510:ARG:NH1	1:B:510:ARG:HG2	2.21	0.55
1:A:314:LEU:HB3	1:A:321:VAL:CG1	2.36	0.55
1:A:314:LEU:HB3	1:A:321:VAL:HG12	1.89	0.54
1:A:501:ARG:NH1	1:A:501:ARG:HB2	2.22	0.54
1:B:227:THR:HB	1:B:347:SER:O	2.07	0.54
1:A:517:ARG:HG2	1:A:517:ARG:NH1	2.23	0.54
1:A:230:GLU:HG3	1:A:262:ILE:HG23	1.90	0.54
1:B:348:ALA:N	1:B:349:PRO:HD3	2.23	0.54
1:A:501:ARG:HB2	1:A:501:ARG:HH11	1.73	0.53
1:A:5:THR:HG23	1:A:278:ARG:NH1	2.08	0.53
1:A:460:PRO:HB2	1:A:461:GLN:HE21	1.74	0.53
1:A:535:LYS:HE3	3:A:1204:HOH:O	2.09	0.53
1:A:390:THR:HB	1:A:391:PRO:HD3	1.91	0.53
1:B:374:HIS:HD2	1:B:476:SER:HB2	1.74	0.53
1:A:434:LEU:HD21	1:A:511:LEU:HD23	1.90	0.53
1:A:240:TYR:OH	3:A:1193:HOH:O	2.14	0.53
1:B:82:LEU:HD13	1:B:249:ALA:HB2	1.89	0.52
1:B:390:THR:HB	1:B:391:PRO:HD3	1.91	0.52
1:B:541:ALA:O	1:B:544:GLN:HG2	2.10	0.52
1:A:230:GLU:HG3	1:A:262:ILE:CG2	2.40	0.52
1:B:215:MET:HB2	1:B:326:SER:HB2	1.91	0.52
1:B:230:GLU:HG3	1:B:262[A]:ILE:CG2	2.39	0.52
1:A:248:GLU:HB3	3:A:1075:HOH:O	2.09	0.52
1:A:535:LYS:HG2	3:A:1204:HOH:O	2.09	0.51
1:B:308:LEU:CB	1:B:311:CYS:SG	2.97	0.51
1:B:47:LEU:HD13	1:B:156:PRO:HG3	1.92	0.51
1:B:394:ARG:O	1:B:398:GLU:HG3	2.10	0.51
1:A:5:THR:CG2	1:A:278:ARG:HH12	2.11	0.51
1:A:144:VAL:HB	1:A:394:ARG:HG2	1.92	0.51
1:B:314:LEU:HB3	1:B:321:VAL:CG1	2.42	0.50
1:B:22:PRO:HG2	1:B:401:ARG:HG3	1.92	0.50
1:B:535:LYS:O	1:B:536:LEU:HB2	2.12	0.50
1:B:466:LEU:HD22	1:B:551:PHE:HE2	1.75	0.50
1:A:545:LEU:HB3	1:A:547:LEU:CD1	2.42	0.50

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:B:306:ALA:HB3	1:B:308:LEU:HD13	1.94	0.49
1:A:461:GLN:HB2	1:A:545:LEU:HD11	1.92	0.49
1:B:230:GLU:HG3	1:B:262[A]:ILE:HG23	1.94	0.49
1:B:47:LEU:HD22	1:B:51:LYS:HZ3	1.78	0.49
1:B:5:THR:CG2	1:B:278:ARG:HH22	2.26	0.49
1:A:545:LEU:HB3	1:A:547:LEU:HD13	1.94	0.49
1:B:329:VAL:HG23	1:B:330:GLN:N	2.28	0.49
1:B:545:LEU:HB3	1:B:547:LEU:CD1	2.43	0.49
1:B:144:VAL:HB	1:B:394:ARG:HG2	1.94	0.49
1:A:57:LEU:HD12	1:A:57:LEU:N	2.28	0.48
1:B:170:CYS:HA	1:B:173:MET:CE	2.44	0.48
1:B:2:MET:H	1:B:55:ASP:HA	1.77	0.48
1:B:169:VAL:HG12	1:B:173:MET:CE	2.43	0.48
1:A:510:ARG:NH1	1:A:510:ARG:HG2	2.28	0.48
1:A:86:GLU:HG3	1:A:111:LEU:HD11	1.94	0.48
1:A:48:ARG:HG2	1:A:159:LEU:HD13	1.96	0.48
1:A:440:GLU:HG2	1:A:457:LEU:CD1	2.43	0.48
1:B:440:GLU:HG2	1:B:457:LEU:CD1	2.44	0.47
1:B:182:LEU:HD23	1:B:182:LEU:O	2.14	0.47
1:A:172:LYS:HE3	1:A:560:ILE:HD13	1.97	0.47
1:B:491:LYS:HE3	1:B:492:LEU:CD1	2.45	0.47
1:A:119:ILE:HD13	1:A:169:VAL:HG11	1.95	0.47
1:A:374:HIS:HD2	1:A:476:SER:HB2	1.79	0.47
1:A:176:TYR:OH	1:A:562:HIS:CE1	2.64	0.46
1:B:434:LEU:HD21	1:B:511:LEU:HD23	1.96	0.46
1:B:55:ASP:OD2	1:B:57:LEU:HD11	2.16	0.46
1:A:86:GLU:O	1:A:90:LYS:HG2	2.16	0.46
1:B:56:ARG:C	1:B:57:LEU:HD12	2.36	0.46
1:A:561:TYR:CE2	1:A:563:SER:HB2	2.51	0.46
1:A:535:LYS:CD	1:A:535:LYS:H	2.24	0.46
1:A:485:VAL:O	1:A:489:LEU:HG	2.16	0.45
1:B:491:LYS:HE3	1:B:492:LEU:HD11	1.98	0.45
1:B:461:GLN:HB2	1:B:545:LEU:HD11	1.98	0.45
1:A:82:LEU:HD13	1:A:249:ALA:HB2	1.99	0.45
1:A:45:ALA:O	1:A:49:GLN:HG3	2.17	0.45
1:B:14[A]:CYS:SG	1:B:269:SER:HB2	2.57	0.44
1:A:501:ARG:NH1	3:A:1195:HOH:O	2.50	0.44
1:A:227:THR:HB	1:A:347:SER:O	2.16	0.44
1:B:84:SER:OG	1:B:87:GLU:HG3	2.17	0.44
1:B:1:SER:N	3:B:1226:HOH:O	2.35	0.44
1:A:219:TYR:HB3	1:A:320:LEU:HD23	1.98	0.44
1:A:515:GLY:HA2	1:A:519:ALA:HB2	2.00	0.43

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:B:99:SER:HB2	1:B:165:LEU:HB3	2.00	0.43
1:A:79:LYS:HA	1:A:244:ASP:HB3	1.99	0.43
1:B:479:PRO:O	1:B:483:ASN:ND2	2.52	0.43
1:B:441:LYS:HD3	3:B:1148:HOH:O	2.17	0.43
1:B:46:GLY:O	1:B:50:LYS:HD3	2.19	0.43
1:A:5:THR:CG2	1:A:278:ARG:HH22	2.29	0.42
1:A:416:ALA:N	1:A:417:PRO:CD	2.82	0.42
1:B:257:THR:O	1:B:262[B]:ILE:HG23	2.19	0.42
1:B:562:HIS:O	1:B:563:SER:C	2.57	0.42
1:B:498:ARG:HA	1:B:501:ARG:NH1	2.34	0.42
1:A:561:TYR:CZ	1:A:563:SER:HB2	2.54	0.42
1:A:93:PRO:HA	1:A:94:PRO:HD3	1.98	0.42
1:A:470:SER:O	1:A:474:LEU:HG	2.19	0.42
1:A:58:GLN:HG2	1:A:347:SER:HB3	2.01	0.42
1:B:458:ASP:HA	1:B:461:GLN:NE2	2.35	0.42
1:A:197:PRO:O	1:A:201:VAL:HG23	2.20	0.42
1:A:461:GLN:HB3	1:A:542:ALA:HA	2.01	0.42
1:B:461:GLN:N	1:B:461:GLN:OE1	2.48	0.41
1:A:187:MET:HE3	1:A:296:TYR:HB2	2.01	0.41
1:A:217:PHE:CE1	1:A:322:VAL:HB	2.55	0.41
1:B:79:LYS:HA	1:B:244:ASP:HB3	2.02	0.41
1:A:30:LEU:O	1:A:494:VAL:HG22	2.21	0.41
1:B:485:VAL:O	1:B:489:LEU:HG	2.20	0.41
1:B:83:LEU:HB2	1:B:173:MET:HA	2.01	0.41
1:B:169:VAL:O	1:B:173:MET:HE3	2.20	0.41
1:A:55:ASP:OD2	1:A:57:LEU:HD11	2.21	0.41
1:B:515:GLY:CA	1:B:519:ALA:HB2	2.51	0.41
1:B:460:PRO:HB2	1:B:461:GLN:OE1	2.21	0.41
1:B:30:LEU:O	1:B:494:VAL:HG22	2.21	0.41
1:A:149:PRO:HG2	1:A:150:GLU:N	2.32	0.40
1:B:374:HIS:CD2	1:B:476:SER:HB2	2.56	0.40
1:B:495:PRO:HA	1:B:496:PRO:HD3	1.94	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	563/563 (100%)	542 (96%)	17 (3%)	4 (1%)	30	20
1	B	565/563 (100%)	546 (97%)	16 (3%)	3 (0%)	38	29
All	All	1128/1126 (100%)	1088 (96%)	33 (3%)	7 (1%)	33	24

All (7) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	149	PRO
1	B	347	SER
1	B	535	LYS
1	A	533	LYS
1	A	536	LEU
1	B	2	MET
1	A	147	VAL

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	481/479 (100%)	475 (99%)	6 (1%)	82	84
1	B	483/479 (101%)	479 (99%)	4 (1%)	89	92
All	All	964/958 (101%)	954 (99%)	10 (1%)	85	88

All (10) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	150	GLU
1	A	347	SER
1	A	510	ARG
1	A	517	ARG
1	A	527	ASN
1	A	535	LYS
1	B	47	LEU
1	B	148	GLN

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Mol	Chain	Res	Type
1	B	159	LEU
1	B	510	ARG

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (15) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	35	ASN
1	A	49	GLN
1	A	273	ASN
1	A	309	GLN
1	A	374	HIS
1	A	461	GLN
1	A	544	GLN
1	A	562	HIS
1	B	49	GLN
1	B	120	HIS
1	B	273	ASN
1	B	374	HIS
1	B	483	ASN
1	B	527	ASN
1	B	544	GLN

5.3.3 RNA ⓘ

There are no RNA chains in this entry.

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

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

5.5 Carbohydrates ⓘ

There are no carbohydrates in this entry.

5.6 Ligand geometry ⓘ

2 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	888	A	901	-	32,32,32	1.64	7 (21%)	45,48,48	2.08	9 (20%)
2	888	B	902	-	32,32,32	1.68	6 (18%)	45,48,48	1.97	10 (22%)

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
2	888	A	901	-	-	0/8/24/24	0/0/4/4
2	888	B	902	-	-	0/8/24/24	0/0/4/4

All (13) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	902	888	C20-C15	3.75	1.53	1.43
2	A	901	888	C20-C15	3.71	1.53	1.43
2	B	902	888	C6-S11	3.33	1.78	1.74
2	B	902	888	C18-N19	3.31	1.43	1.38
2	A	901	888	C6-S11	3.24	1.78	1.74
2	A	901	888	C18-N19	3.13	1.43	1.38
2	B	902	888	C1-N14	-2.94	1.34	1.39
2	A	901	888	C1-N14	-2.56	1.35	1.39
2	A	901	888	C23-C24	2.33	1.42	1.36
2	B	902	888	C23-C24	2.25	1.41	1.36
2	A	901	888	C16-C17	2.13	1.48	1.43
2	B	902	888	C16-C17	2.13	1.48	1.43
2	A	901	888	C5-C6	2.03	1.41	1.39

All (19) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	901	888	C32-C31-N19	10.25	120.65	112.31
2	B	902	888	C32-C31-N19	8.95	119.59	112.31

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	902	888	C15-C13-N12	3.42	123.39	118.86
2	B	902	888	C15-C16-C17	-3.36	118.88	122.29
2	A	901	888	C15-C16-C17	-3.31	118.93	122.29
2	A	901	888	C15-C13-N12	2.97	122.79	118.86
2	B	902	888	O46-S11-N12	-2.70	105.86	109.15
2	A	901	888	O46-S11-N12	-2.67	105.88	109.15
2	B	902	888	C1-N14-C13	2.42	129.90	123.71
2	B	902	888	O47-S11-O46	2.39	118.60	115.73
2	A	901	888	C17-C18-N19	2.36	120.81	118.50
2	A	901	888	C31-N19-C18	2.36	121.01	118.92
2	A	901	888	C1-N14-C13	2.27	129.51	123.71
2	B	902	888	C17-C18-N19	2.26	120.70	118.50
2	B	902	888	C31-N19-C18	2.20	120.86	118.92
2	A	901	888	C21-C17-C18	2.11	120.47	118.11
2	A	901	888	O47-S11-O46	2.10	118.26	115.73
2	B	902	888	C21-C17-C18	2.10	120.46	118.11
2	B	902	888	C20-C15-C16	2.07	120.22	117.56

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

5.7 Other polymers ⓘ

There are no such residues in this entry.

5.8 Polymer linkage issues

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	563/563 (100%)	0.07	26 (4%) 31 30	10, 21, 42, 61	3 (0%)
1	B	563/563 (100%)	-0.03	22 (3%) 37 37	10, 19, 37, 60	2 (0%)
All	All	1126/1126 (100%)	0.02	48 (4%) 34 32	10, 20, 40, 61	5 (0%)

All (48) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	150	GLU	6.5
1	A	149	PRO	5.5
1	B	532	THR	5.4
1	A	152	GLY	5.4
1	B	152	GLY	5.2
1	B	149	PRO	5.0
1	B	151	LYS	4.9
1	B	150	GLU	4.6
1	B	563	SER	4.3
1	A	534	LEU	4.3
1	A	151	LYS	4.3
1	A	531	LYS	4.2
1	B	535	LYS	3.9
1	B	531	LYS	3.8
1	A	549	GLY	3.6
1	A	532	THR	3.6
1	B	549	GLY	3.5
1	B	534	LEU	3.5
1	B	544	GLN	3.3
1	B	153	GLY	3.3
1	B	148	GLN	3.2
1	B	1	SER	3.0
1	A	412	ILE	2.9
1	A	542	ALA	2.9

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Mol	Chain	Res	Type	RSRZ
1	A	544	GLN	2.9
1	A	548	SER	2.8
1	A	546	ASP	2.7
1	A	543	SER	2.6
1	A	212	LYS	2.6
1	A	16	ALA	2.6
1	A	536	LEU	2.6
1	A	563	SER	2.5
1	A	541	ALA	2.5
1	A	148	GLN	2.5
1	A	353	PRO	2.4
1	A	533	LYS	2.3
1	B	541	ALA	2.3
1	B	548	SER	2.3
1	A	355	GLN	2.3
1	B	543	SER	2.3
1	B	530	VAL	2.2
1	B	57	LEU	2.1
1	A	330	GLN	2.1
1	A	376	ALA	2.1
1	B	16	ALA	2.1
1	B	412	ILE	2.1
1	B	540	PRO	2.0
1	A	153	GLY	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	RSR	LLDF	B-factors(\AA^2)	Q<0.9
2	888	B	902	29/29	0.15	2.75	17,20,22,27	0
2	888	A	901	29/29	0.16	2.41	20,23,26,33	0

6.5 Other polymers ⓘ

There are no such residues in this entry.