



Full wwPDB X-ray Structure Validation Report

Feb 28, 2014 – 02:44 PM GMT

PDB ID : 3DLK
Title : Crystal Structure of an engineered form of the HIV-1 Reverse Transcriptase, RT69A
Authors : Ho, W.C.; Bauman, J.D.; Himmel, D.M.; Das, K.; Arnold, E.
Deposited on : 2008-06-27
Resolution : 1.85 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>

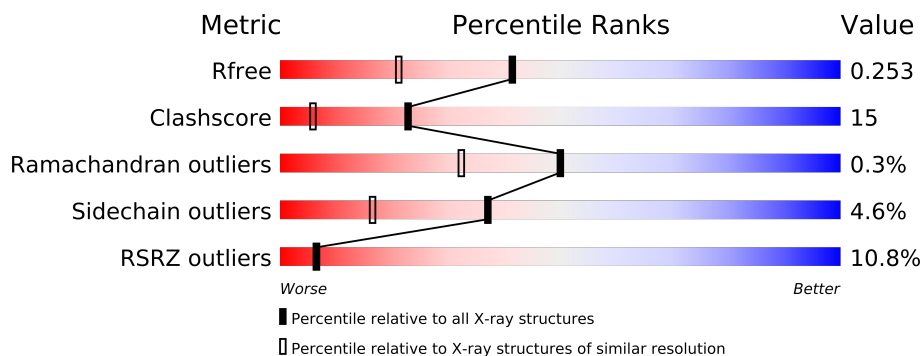
The following versions of software and data (see [references](#)) were used in the production of this report:

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 1.85 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	1269 (1.86-1.86)
Clashscore	79885	1470 (1.86-1.86)
Ramachandran outliers	78287	1451 (1.86-1.86)
Sidechain outliers	78261	1451 (1.86-1.86)
RSRZ outliers	66119	1269 (1.86-1.86)

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	556	
2	B	423	

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 8069 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 Reverse transcriptase/ribonucleaseH.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	552	Total	C	N	O	S	0	0	0
			4489	2902	748	832	7			

There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	0	MET	-	INITIATING METHIONINE	UNP P03366
A	160	SER	PHE	ENGINEERED	UNP P03366
A	280	SER	CYS	ENGINEERED	UNP P03366

- Molecule 2 is a protein called p51 RT.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	409	Total	C	N	O	S	0	0	0
			3388	2208	560	613	7			

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	280	SER	CYS	ENGINEERED	UNP P03366

- Molecule 3 is SULFATE ION (three-letter code: SO4) (formula: O₄S).



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

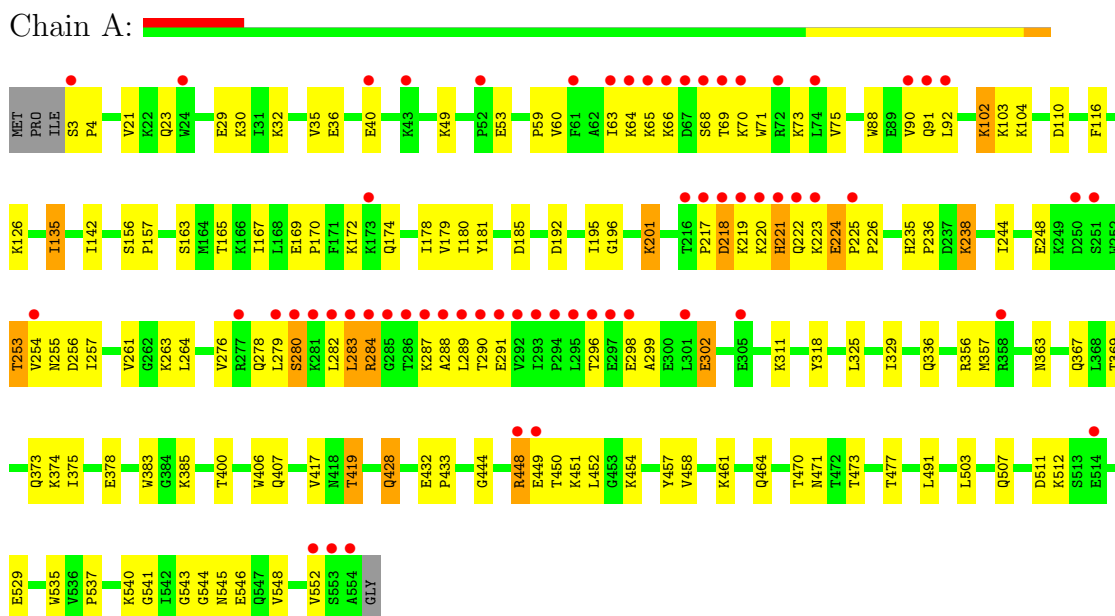
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	101	Total	O	0	0
			101	101		
4	B	86	Total	O	0	0
			86	86		

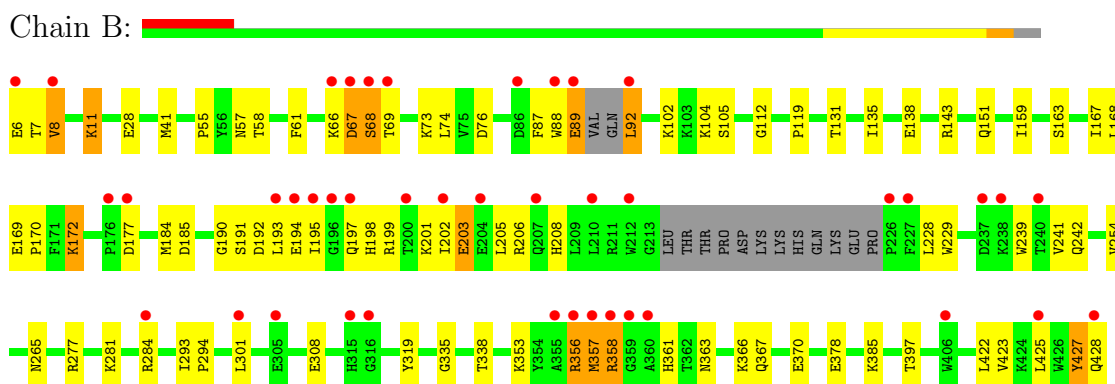
3 Residue-property plots

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: Reverse transcriptase/ribonucleaseH



• Molecule 2: p51 RT



4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	164.01Å 72.04Å 109.33Å 90.00° 104.38° 90.00°	Depositor
Resolution (Å)	40.66 – 1.85 40.66 – 1.85	Depositor EDS
% Data completeness (in resolution range)	94.3 (40.66-1.85) 94.3 (40.66-1.85)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.73 (at 1.86Å)	Xtriage
Refinement program	CNS	Depositor
R, R_{free}	0.237 , 0.250 0.237 , 0.253	Depositor DCC
R_{free} test set	2991 reflections (3.01%)	DCC
Wilson B-factor (Å ²)	32.1	Xtriage
Anisotropy	0.149	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.37 , 48.4	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	0 of 99442 reflections	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	8069	wwPDB-VP
Average B, all atoms (Å ²)	49.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.90% of the height of the origin peak. No significant pseudotranslation is detected.*

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: 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	0.33	0/4605	0.62	1/6256 (0.0%)
2	B	0.34	0/3486	0.61	0/4732
All	All	0.33	0/8091	0.61	1/10988 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	221	HIS	N-CA-C	-5.38	96.48	111.00

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	4489	0	4545	158	0
2	B	3388	0	3411	83	0
3	A	5	0	0	0	0
4	A	101	0	0	1	0
4	B	86	0	0	1	0
All	All	8069	0	7956	232	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 15.

All (232) close contacts within the same asymmetric unit are listed below.

Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:102:LYS:HE3	1:A:103:LYS:H	1.08	1.14
1:A:287:LYS:HB3	1:A:291:GLU:HG2	1.14	1.13
2:B:335:GLY:HA3	2:B:356:ARG:HG3	1.31	1.12
2:B:356:ARG:N	2:B:356:ARG:HD2	1.70	1.03
2:B:335:GLY:CA	2:B:356:ARG:HG3	1.91	1.00
1:A:102:LYS:HE3	1:A:103:LYS:N	1.81	0.96
2:B:131:THR:HG22	2:B:143:ARG:HE	1.34	0.92
1:A:287:LYS:HB3	1:A:291:GLU:CG	2.01	0.89
1:A:287:LYS:CB	1:A:291:GLU:HG2	2.02	0.88
2:B:356:ARG:HD2	2:B:356:ARG:H	1.35	0.87
2:B:6:GLU:O	2:B:119:PRO:HG2	1.75	0.86
1:A:503:LEU:HD23	2:B:422:LEU:HD21	1.58	0.85
1:A:254:VAL:HG12	1:A:291:GLU:HB2	1.58	0.85
2:B:11:LYS:HA	2:B:11:LYS:HE3	1.60	0.82
1:A:284:ARG:HB3	1:A:284:ARG:CZ	2.08	0.81
1:A:284:ARG:NH1	1:A:284:ARG:HB3	1.94	0.81
2:B:356:ARG:CD	2:B:356:ARG:N	2.43	0.81
2:B:57:ASN:OD1	2:B:131:THR:HG23	1.80	0.80
1:A:444:GLY:HA2	1:A:552:VAL:HG11	1.64	0.79
2:B:357:MET:SD	2:B:358:ARG:HD3	2.22	0.78
1:A:288:ALA:O	1:A:289:LEU:HB3	1.85	0.77
1:A:369:THR:O	1:A:373:GLN:HG2	1.86	0.76
1:A:279:LEU:HG	1:A:302:GLU:OE2	1.86	0.75
2:B:281:LYS:HE2	2:B:284:ARG:NH2	2.01	0.75
2:B:356:ARG:HG2	2:B:358:ARG:O	1.88	0.74
1:A:244:ILE:HD12	1:A:263:LYS:HZ1	1.52	0.74
1:A:223:LYS:HG2	1:A:224:GLU:H	1.53	0.74
1:A:278:GLN:HE21	1:A:298:GLU:CB	2.00	0.74
2:B:335:GLY:O	2:B:356:ARG:HG3	1.88	0.73
2:B:335:GLY:C	2:B:356:ARG:HG3	2.08	0.73
2:B:104:LYS:HG2	2:B:192:ASP:OD1	1.89	0.73
1:A:64:LYS:HA	1:A:70:LYS:O	1.88	0.72
1:A:503:LEU:CD2	2:B:422:LEU:HD21	2.19	0.71
1:A:278:GLN:HE21	1:A:298:GLU:HB3	1.53	0.71
2:B:172:LYS:HE2	2:B:172:LYS:HA	1.73	0.70
1:A:73:LYS:HZ3	1:A:75:VAL:HG23	1.57	0.70
2:B:335:GLY:HA3	2:B:356:ARG:CG	2.15	0.69
2:B:425:LEU:HD12	2:B:428:GLN:OE1	1.93	0.69
1:A:102:LYS:CE	1:A:102:LYS:HA	2.23	0.69

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:163:SER:O	1:A:167:ILE:HG12	1.94	0.67
1:A:255:ASN:HD22	1:A:288:ALA:HB1	1.60	0.67
2:B:338:THR:HG21	2:B:427:TYR:O	1.95	0.67
2:B:366:LYS:O	2:B:370:GLU:HG3	1.95	0.66
2:B:335:GLY:O	2:B:356:ARG:CG	2.43	0.66
1:A:88:TRP:CD1	2:B:143:ARG:HD2	2.32	0.65
1:A:165:THR:O	1:A:169:GLU:HG3	1.97	0.64
1:A:325:LEU:HB2	1:A:385:LYS:HE3	1.78	0.64
1:A:223:LYS:HG2	1:A:224:GLU:N	2.13	0.63
1:A:102:LYS:HD3	1:A:236:PRO:O	1.98	0.63
1:A:329:ILE:HD11	1:A:375:ILE:HD12	1.80	0.63
1:A:244:ILE:HD12	1:A:263:LYS:NZ	2.14	0.63
1:A:276:VAL:O	1:A:276:VAL:HG22	1.99	0.63
2:B:361:HIS:HD2	2:B:363:ASN:H	1.47	0.62
1:A:178:ILE:CD1	1:A:201:LYS:HG2	2.29	0.62
1:A:356:ARG:HD2	1:A:357:MET:O	1.99	0.62
1:A:3:SER:N	1:A:4:PRO:HD2	2.14	0.62
2:B:361:HIS:CD2	2:B:363:ASN:H	2.17	0.62
2:B:28:GLU:HG3	2:B:135:ILE:HD11	1.82	0.61
1:A:219:LYS:HG3	1:A:219:LYS:O	2.01	0.61
2:B:358:ARG:NH1	2:B:361:HIS:ND1	2.49	0.61
2:B:11:LYS:HA	2:B:11:LYS:CE	2.30	0.61
2:B:41:MET:CE	2:B:73:LYS:HE2	2.31	0.61
1:A:444:GLY:CA	1:A:552:VAL:HG11	2.30	0.61
1:A:169:GLU:HB2	1:A:170:PRO:HD3	1.83	0.61
2:B:254:VAL:HG22	2:B:293:ILE:HD11	1.83	0.60
1:A:400:THR:HG21	1:A:428:GLN:HE22	1.65	0.60
2:B:143:ARG:HD3	4:B:455:HOH:O	2.00	0.59
1:A:261:VAL:HG13	1:A:276:VAL:HG21	1.83	0.59
1:A:543:GLY:C	1:A:545:ASN:H	2.06	0.59
1:A:279:LEU:HD23	1:A:299:ALA:HB1	1.83	0.59
1:A:261:VAL:HG13	1:A:276:VAL:CG2	2.33	0.58
1:A:541:GLY:HA2	1:A:546:GLU:HG3	1.86	0.58
1:A:284:ARG:NH1	1:A:284:ARG:CB	2.66	0.58
1:A:491:LEU:HB3	1:A:529:GLU:HG2	1.85	0.58
1:A:156:SER:HB2	1:A:157:PRO:HD3	1.85	0.57
1:A:253:THR:HA	1:A:291:GLU:O	2.03	0.57
1:A:511:ASP:O	1:A:512:LYS:HG3	2.05	0.57
2:B:169:GLU:N	2:B:170:PRO:HD2	2.18	0.57
2:B:281:LYS:HE2	2:B:284:ARG:CZ	2.35	0.57
2:B:356:ARG:HD3	2:B:356:ARG:O	2.05	0.57
1:A:64:LYS:HG3	1:A:71:TRP:CD2	2.40	0.56

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
2:B:168:LEU:HD22	2:B:205:LEU:HD11	1.86	0.56
2:B:67:ASP:OD1	2:B:68:SER:N	2.38	0.56
1:A:135:ILE:H	1:A:135:ILE:HD13	1.70	0.56
1:A:102:LYS:HD2	1:A:318:TYR:CD1	2.41	0.56
1:A:254:VAL:HG12	1:A:291:GLU:CB	2.34	0.55
1:A:64:LYS:HG2	1:A:70:LYS:C	2.26	0.55
1:A:282:LEU:O	1:A:283:LEU:HG	2.05	0.55
1:A:253:THR:HG22	1:A:256:ASP:OD2	2.07	0.55
1:A:135:ILE:N	1:A:135:ILE:HD13	2.22	0.55
1:A:64:LYS:HG2	1:A:70:LYS:O	2.07	0.55
1:A:102:LYS:HE3	1:A:102:LYS:HA	1.89	0.54
2:B:241:VAL:HG12	2:B:242:GLN:H	1.73	0.54
2:B:198:HIS:O	2:B:202:ILE:HG12	2.06	0.54
1:A:276:VAL:O	1:A:280:SER:HB2	2.07	0.54
1:A:543:GLY:H	1:A:546:GLU:HG2	1.71	0.54
1:A:226:PRO:HB3	1:A:235:HIS:CE1	2.43	0.54
1:A:223:LYS:HG2	1:A:224:GLU:HG3	1.88	0.54
1:A:167:ILE:O	1:A:170:PRO:HD2	2.07	0.54
1:A:279:LEU:N	1:A:302:GLU:OE2	2.40	0.54
1:A:23:GLN:OE1	1:A:60:VAL:HG12	2.08	0.54
1:A:287:LYS:CB	1:A:291:GLU:CG	2.76	0.53
1:A:461:LYS:NZ	1:A:461:LYS:HB3	2.24	0.53
1:A:552:VAL:O	1:A:552:VAL:HG12	2.08	0.53
1:A:255:ASN:HB2	1:A:288:ALA:HB1	1.89	0.53
1:A:543:GLY:C	1:A:545:ASN:N	2.61	0.53
2:B:335:GLY:O	2:B:356:ARG:HB3	2.10	0.52
1:A:540:LYS:HE3	2:B:265:ASN:OD1	2.09	0.52
1:A:21:VAL:HB	1:A:59:PRO:HD3	1.90	0.52
1:A:296:THR:HG22	1:A:299:ALA:HB2	1.91	0.52
1:A:135:ILE:H	1:A:135:ILE:CD1	2.23	0.52
1:A:90:VAL:O	1:A:91:GLN:HB3	2.09	0.52
2:B:87:PHE:O	2:B:88:TRP:CD1	2.62	0.52
1:A:400:THR:HG21	1:A:428:GLN:NE2	2.25	0.51
1:A:223:LYS:CG	1:A:224:GLU:H	2.22	0.51
1:A:110:ASP:OD1	1:A:217:PRO:HG2	2.10	0.51
1:A:543:GLY:O	1:A:545:ASN:N	2.36	0.51
1:A:104:LYS:HB3	1:A:192:ASP:HA	1.93	0.51
1:A:172:LYS:HE2	1:A:180:ILE:HB	1.93	0.50
1:A:373:GLN:HE22	2:B:397:THR:HG23	1.76	0.50
1:A:110:ASP:HA	1:A:185:ASP:O	2.11	0.50
2:B:112:GLY:HA3	2:B:151:GLN:HE21	1.77	0.50
2:B:241:VAL:HG12	2:B:242:GLN:N	2.26	0.50

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:450:THR:O	1:A:451:LYS:HB2	2.11	0.50
1:A:451:LYS:HB3	1:A:471:ASN:HA	1.93	0.50
2:B:8:VAL:HG11	2:B:159:ILE:HG23	1.94	0.50
2:B:58:THR:HG23	2:B:76:ASP:O	2.12	0.49
1:A:544:GLY:O	1:A:548:VAL:HG12	2.12	0.49
1:A:181:TYR:CE2	2:B:138:GLU:HB3	2.48	0.49
2:B:88:TRP:O	2:B:89:GLU:HG3	2.12	0.49
1:A:278:GLN:HE21	1:A:298:GLU:HB2	1.75	0.49
1:A:296:THR:HG22	1:A:299:ALA:CB	2.43	0.48
1:A:458:VAL:HG12	1:A:464:GLN:HG2	1.95	0.48
1:A:503:LEU:O	1:A:507:GLN:HG3	2.13	0.48
2:B:191:SER:HG	2:B:198:HIS:HD1	1.61	0.48
1:A:218:ASP:C	1:A:220:LYS:N	2.67	0.48
1:A:102:LYS:CD	1:A:318:TYR:CD1	2.96	0.48
1:A:36:GLU:O	1:A:40:GLU:HG3	2.14	0.48
2:B:163:SER:O	2:B:167:ILE:HG13	2.13	0.48
2:B:6:GLU:HG2	2:B:7:THR:HG23	1.95	0.47
2:B:61:PHE:CZ	2:B:74:LEU:HD23	2.49	0.47
1:A:224:GLU:HB2	1:A:225:PRO:HD2	1.96	0.47
1:A:325:LEU:HD21	1:A:383:TRP:CE3	2.48	0.47
1:A:3:SER:N	1:A:4:PRO:CD	2.77	0.47
1:A:356:ARG:HG3	1:A:367:GLN:NE2	2.30	0.47
1:A:181:TYR:CD2	2:B:138:GLU:HB3	2.49	0.47
1:A:244:ILE:CD1	1:A:263:LYS:HZ1	2.24	0.47
2:B:41:MET:HE1	2:B:73:LYS:HE2	1.96	0.47
2:B:254:VAL:HG22	2:B:293:ILE:CD1	2.45	0.47
1:A:253:THR:CG2	1:A:256:ASP:OD2	2.62	0.47
2:B:105:SER:O	2:B:190:GLY:HA2	2.14	0.47
2:B:335:GLY:O	2:B:356:ARG:CB	2.62	0.47
2:B:11:LYS:CA	2:B:11:LYS:HE3	2.38	0.47
1:A:235:HIS:HB2	1:A:238:LYS:O	2.14	0.47
2:B:194:GLU:H	2:B:197:GLN:HE21	1.63	0.47
2:B:193:LEU:CD1	2:B:201:LYS:HG3	2.44	0.47
1:A:546:GLU:OE1	1:A:546:GLU:HA	2.14	0.46
1:A:253:THR:HG23	1:A:256:ASP:H	1.80	0.46
2:B:242:GLN:HE21	2:B:353:LYS:HB2	1.80	0.46
1:A:473:THR:O	1:A:477:THR:HG23	2.16	0.46
2:B:358:ARG:HB3	2:B:361:HIS:HB2	1.99	0.45
1:A:53:GLU:OE1	1:A:53:GLU:N	2.49	0.45
1:A:179:VAL:CG2	1:A:181:TYR:CZ	2.99	0.45
1:A:374:LYS:O	1:A:378:GLU:HG3	2.17	0.45
1:A:276:VAL:CG2	1:A:276:VAL:O	2.65	0.45

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:373:GLN:NE2	2:B:397:THR:OG1	2.50	0.45
1:A:29:GLU:HG3	1:A:30:LYS:N	2.31	0.45
2:B:69:THR:O	2:B:69:THR:HG22	2.17	0.45
1:A:102:LYS:CD	1:A:236:PRO:O	2.65	0.45
2:B:335:GLY:HA2	2:B:367:GLN:OE1	2.18	0.44
1:A:218:ASP:C	1:A:220:LYS:H	2.20	0.44
1:A:63:ILE:O	1:A:63:ILE:HG13	2.17	0.44
1:A:419:THR:OG1	1:A:419:THR:O	2.34	0.44
2:B:92:LEU:HD23	2:B:92:LEU:N	2.32	0.44
1:A:49:LYS:HE3	1:A:142:ILE:HG23	1.98	0.44
1:A:373:GLN:NE2	2:B:397:THR:HA	2.33	0.44
1:A:244:ILE:CG2	1:A:263:LYS:HZ1	2.30	0.44
1:A:110:ASP:OD1	1:A:217:PRO:HD2	2.18	0.44
1:A:179:VAL:HG22	1:A:181:TYR:CE2	2.53	0.44
1:A:512:LYS:HD2	4:A:640:HOH:O	2.16	0.44
1:A:179:VAL:HG13	1:A:179:VAL:O	2.18	0.43
1:A:92:LEU:HA	1:A:92:LEU:HD23	1.76	0.43
1:A:432:GLU:HB3	1:A:433:PRO:HD2	2.00	0.43
1:A:253:THR:O	1:A:257:ILE:HG13	2.18	0.43
1:A:195:ILE:HG23	1:A:196:GLY:N	2.32	0.43
1:A:503:LEU:HD22	1:A:535:TRP:HB2	2.00	0.43
2:B:88:TRP:C	2:B:89:GLU:HG3	2.38	0.43
2:B:112:GLY:C	2:B:151:GLN:HE21	2.22	0.43
1:A:102:LYS:CA	1:A:102:LYS:HE3	2.48	0.43
1:A:66:LYS:C	1:A:68:SER:H	2.22	0.43
1:A:254:VAL:HG22	1:A:254:VAL:O	2.18	0.43
1:A:63:ILE:HA	1:A:71:TRP:HZ3	1.83	0.43
1:A:64:LYS:HG3	1:A:71:TRP:CE2	2.53	0.43
2:B:67:ASP:OD1	2:B:229:TRP:HH2	2.02	0.43
1:A:537:PRO:HB2	1:A:540:LYS:HG3	2.01	0.42
2:B:308:GLU:OE1	2:B:308:GLU:HA	2.19	0.42
1:A:457:TYR:C	1:A:457:TYR:CD1	2.92	0.42
2:B:228:LEU:HD23	2:B:228:LEU:O	2.18	0.42
1:A:102:LYS:CE	1:A:103:LYS:H	2.01	0.42
1:A:282:LEU:O	1:A:283:LEU:CG	2.67	0.42
1:A:283:LEU:O	1:A:283:LEU:CG	2.67	0.42
1:A:254:VAL:CG1	1:A:287:LYS:O	2.67	0.42
2:B:28:GLU:HG3	2:B:135:ILE:CD1	2.50	0.42
2:B:195:ILE:HG12	2:B:199:ARG:CD	2.49	0.42
2:B:319:TYR:OH	2:B:385:LYS:HE2	2.20	0.42
1:A:311:LYS:HD2	1:A:311:LYS:HA	1.82	0.42
2:B:151:GLN:HB3	2:B:185:ASP:OD2	2.20	0.42

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:284:ARG:CB	1:A:284:ARG:HH11	2.30	0.42
1:A:417:VAL:O	1:A:417:VAL:HG13	2.19	0.41
1:A:65:LYS:HB2	1:A:68:SER:O	2.20	0.41
1:A:218:ASP:O	1:A:220:LYS:N	2.53	0.41
1:A:174:GLN:HB2	1:A:174:GLN:HE21	1.65	0.41
1:A:102:LYS:HD3	1:A:318:TYR:CE1	2.56	0.41
1:A:449:GLU:N	1:A:449:GLU:OE1	2.53	0.41
2:B:239:TRP:CH2	2:B:378:GLU:HA	2.55	0.41
2:B:112:GLY:CA	2:B:151:GLN:HE21	2.33	0.41
1:A:452:LEU:CD2	1:A:470:THR:HG22	2.51	0.41
1:A:356:ARG:HG3	1:A:367:GLN:CD	2.41	0.41
2:B:293:ILE:HA	2:B:294:PRO:HD3	1.95	0.41
1:A:406:TRP:CE2	1:A:407:GLN:HG3	2.56	0.41
1:A:135:ILE:N	1:A:135:ILE:CD1	2.83	0.41
1:A:417:VAL:HG22	1:A:419:THR:HG22	2.03	0.41
1:A:69:THR:O	1:A:70:LYS:CG	2.70	0.40
1:A:73:LYS:HZ3	1:A:75:VAL:CG2	2.28	0.40
2:B:203:GLU:HA	2:B:206:ARG:HB2	2.03	0.40
1:A:454:LYS:HB2	1:A:552:VAL:HG13	2.03	0.40
1:A:363:ASN:OD1	1:A:363:ASN:C	2.59	0.40
1:A:178:ILE:HD11	1:A:201:LYS:HG2	2.01	0.40
1:A:448:ARG:HG2	1:A:449:GLU:OE1	2.21	0.40
1:A:32:LYS:O	1:A:35:VAL:HG12	2.21	0.40
2:B:67:ASP:OD1	2:B:229:TRP:CH2	2.74	0.40
2:B:242:GLN:NE2	2:B:353:LYS:HB2	2.36	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	550/556 (99%)	517 (94%)	32 (6%)	1 (0%)	56	38
2	B	403/423 (95%)	385 (96%)	16 (4%)	2 (0%)	38	19
All	All	953/979 (97%)	902 (95%)	48 (5%)	3 (0%)	50	32

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	222	GLN
2	B	66	LYS
2	B	423	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	493/496 (99%)	472 (96%)	21 (4%)	40	19
2	B	371/385 (96%)	352 (95%)	19 (5%)	33	13
All	All	864/881 (98%)	824 (95%)	40 (5%)	37	16

All (40) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	102	LYS
1	A	116	PHE
1	A	126	LYS
1	A	135	ILE
1	A	201	LYS
1	A	218	ASP
1	A	221	HIS
1	A	224	GLU
1	A	238	LYS
1	A	248	GLU
1	A	253	THR
1	A	264	LEU
1	A	280	SER
1	A	283	LEU
1	A	284	ARG
1	A	290	THR
1	A	302	GLU
1	A	336	GLN
1	A	419	THR
1	A	428	GLN
1	A	448	ARG

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Mol	Chain	Res	Type
2	B	8	VAL
2	B	11	LYS
2	B	55	PRO
2	B	67	ASP
2	B	68	SER
2	B	89	GLU
2	B	92	LEU
2	B	102	LYS
2	B	172	LYS
2	B	177	ASP
2	B	184	MET
2	B	203	GLU
2	B	208	HIS
2	B	277	ARG
2	B	301	LEU
2	B	356	ARG
2	B	357	MET
2	B	358	ARG
2	B	427	TYR

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (20) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	151	GLN
1	A	161	GLN
1	A	174	GLN
1	A	182	GLN
1	A	235	HIS
1	A	258	GLN
1	A	278	GLN
1	A	373	GLN
1	A	394	GLN
1	A	428	GLN
1	A	475	GLN
1	A	509	GLN
1	A	524	GLN
2	B	151	GLN
2	B	182	GLN
2	B	197	GLN
2	B	242	GLN
2	B	278	GLN
2	B	330	GLN

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Mol	Chain	Res	Type
2	B	340	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 ⓘ

1 ligand is modelled in this entry.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
3	SO4	A	556	-	4,4,4	0.32	0	6,6,6	0.06	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	SO4	A	556	-	-	0/0/0/0	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.

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	552/556 (99%)	0.72	62 (11%) 6 6	22, 47, 98, 146	0
2	B	409/423 (96%)	0.58	42 (10%) 7 7	23, 43, 83, 99	0
All	All	961/979 (98%)	0.66	104 (10%) 6 6	22, 45, 90, 146	0

All (104) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	289	LEU	21.5
1	A	220	LYS	9.9
1	A	221	HIS	9.7
1	A	67	ASP	9.6
1	A	290	THR	8.9
1	A	222	GLN	8.8
1	A	288	ALA	8.4
1	A	283	LEU	8.3
1	A	554	ALA	8.1
2	B	92	LEU	7.7
2	B	360	ALA	7.4
1	A	218	ASP	7.1
2	B	357	MET	6.9
1	A	68	SER	6.5
1	A	284	ARG	6.4
1	A	281	LYS	6.4
1	A	70	LYS	6.3
1	A	66	LYS	6.2
1	A	91	GLN	6.1
1	A	69	THR	6.0
1	A	223	LYS	6.0
1	A	286	THR	5.9
2	B	212	TRP	5.8
1	A	65	LYS	5.8

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Mol	Chain	Res	Type	RSRZ
1	A	301	LEU	5.4
1	A	282	LEU	5.4
1	A	219	LYS	5.3
2	B	358	ARG	5.3
1	A	297	GLU	5.2
2	B	359	GLY	5.1
1	A	293	ILE	5.0
2	B	88	TRP	4.9
1	A	291	GLU	4.9
2	B	89	GLU	4.9
2	B	6	GLU	4.8
2	B	69	THR	4.7
1	A	24	TRP	4.7
1	A	92	LEU	4.5
1	A	277	ARG	4.4
1	A	298	GLU	4.1
2	B	237	ASP	4.0
2	B	66	LYS	3.9
1	A	279	LEU	3.8
2	B	226	PRO	3.8
1	A	254	VAL	3.7
1	A	295	LEU	3.7
1	A	296	THR	3.7
1	A	64	LYS	3.7
2	B	284	ARG	3.6
1	A	292	VAL	3.4
1	A	90	VAL	3.4
1	A	251	SER	3.4
1	A	553	SER	3.4
2	B	67	ASP	3.3
1	A	3	SER	3.3
2	B	240	THR	3.2
2	B	356	ARG	3.2
1	A	250	ASP	3.2
1	A	225	PRO	3.2
1	A	287	LYS	3.2
2	B	315	HIS	3.1
2	B	195	ILE	3.0
1	A	285	GLY	3.0
1	A	63	ILE	3.0
2	B	355	ALA	2.8
2	B	177	ASP	2.8

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Mol	Chain	Res	Type	RSRZ
2	B	301	LEU	2.8
2	B	425	LEU	2.7
1	A	280	SER	2.7
1	A	216	THR	2.7
1	A	217	PRO	2.6
1	A	294	PRO	2.6
1	A	72	ARG	2.6
1	A	358	ARG	2.6
2	B	210	LEU	2.6
2	B	197	GLN	2.5
1	A	449	GLU	2.4
1	A	52	PRO	2.4
2	B	238	LYS	2.4
1	A	61	PHE	2.4
2	B	194	GLU	2.4
2	B	176	PRO	2.4
2	B	428	GLN	2.3
1	A	552	VAL	2.3
2	B	207	GLN	2.3
1	A	40	GLU	2.3
1	A	305	GLU	2.3
2	B	305	GLU	2.3
2	B	316	GLY	2.3
2	B	202	ILE	2.2
2	B	200	THR	2.2
2	B	193	LEU	2.1
1	A	74	LEU	2.1
2	B	196	GLY	2.1
2	B	227	PHE	2.1
1	A	514	GLU	2.1
2	B	8	VAL	2.0
1	A	448	ARG	2.0
2	B	68	SER	2.0
2	B	204	GLU	2.0
2	B	406	TRP	2.0
1	A	43	LYS	2.0
1	A	173	LYS	2.0
2	B	86	ASP	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(Å ²)	Q<0.9
3	SO4	A	556	5/5	0.25	1.83	65,65,66,70	0

6.5 Other polymers

There are no such residues in this entry.