



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 28, 2014 – 01:21 PM GMT

PDB ID : 2IOB
Title : E. coli Bifunctional glutathionylspermidinesynthetase/amidase Apo protein
Authors : Pai, C.H.; Chiang, B.Y.; Ko, T.P.; Chou, C.C.; Chong, C.M.; Yen, F.J.;
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Deposited on : 2006-10-10
Resolution : 2.20 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>

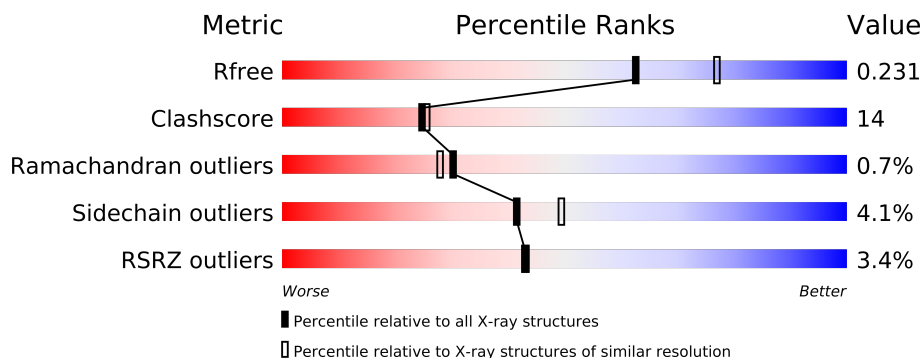
The following versions of software and data (see [references](#)) were used in the production of this report:

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 2.20 Å.

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



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	66092	2938 (2.20-2.20)
Clashscore	79885	3751 (2.20-2.20)
Ramachandran outliers	78287	3681 (2.20-2.20)
Sidechain outliers	78261	3682 (2.20-2.20)
RSRZ outliers	66119	2939 (2.20-2.20)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments 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	619	
1	B	619	

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 10550 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 Bifunctional glutathionylspermidinesynthetase/amidase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	571	Total	C	N	O	S	0	0	0
			4623	2964	787	854	18			
1	B	582	Total	C	N	O	S	0	0	0
			4703	3014	799	872	18			

- Molecule 2 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	596	Total	O	0	0
			596	596		
2	B	628	Total	O	0	0
			628	628		

4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	149.27Å 92.96Å 108.30Å 90.00° 109.37° 90.00°	Depositor
Resolution (Å)	50.00 – 2.20 46.77 – 2.20	Depositor EDS
% Data completeness (in resolution range)	(Not available) (50.00-2.20) 94.8 (46.77-2.20)	Depositor EDS
R_{merge}	0.08	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.32 (at 2.20Å)	Xtriage
Refinement program	XTALVIEW	Depositor
R, R_{free}	0.175 , 0.236 0.172 , 0.231	Depositor DCC
R_{free} test set	3431 reflections (5.36%)	DCC
Wilson B-factor (Å ²)	29.8	Xtriage
Anisotropy	0.472	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 47.8	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Outliers	0 of 67392 reflections	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	10550	wwPDB-VP
Average B, all atoms (Å ²)	38.0	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.

5 Model quality

5.1 Standard geometry

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	0.89	3/4744 (0.1%)	0.94	11/6445 (0.2%)
1	B	0.89	3/4823 (0.1%)	0.92	9/6553 (0.1%)
All	All	0.89	6/9567 (0.1%)	0.93	20/12998 (0.2%)

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	B	0	1

All (6) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	189	MET	SD-CE	-6.37	1.42	1.77
1	A	320	CYS	CB-SG	6.06	1.92	1.82
1	A	306	GLN	CB-CG	-6.03	1.36	1.52
1	B	328	VAL	CB-CG2	-5.63	1.41	1.52
1	B	601	GLU	CD-OE2	5.25	1.31	1.25
1	A	471	ASN	CB-CG	5.23	1.63	1.51

All (20) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	65	ARG	NE-CZ-NH2	-12.79	113.91	120.30
1	B	414	ARG	NE-CZ-NH1	8.84	124.72	120.30
1	A	300	ARG	NE-CZ-NH1	-7.79	116.41	120.30
1	A	328	VAL	CB-CA-C	-7.09	97.94	111.40
1	B	65	ARG	NE-CZ-NH1	7.03	123.81	120.30
1	B	414	ARG	NE-CZ-NH2	-6.43	117.08	120.30
1	A	165	LEU	CA-CB-CG	6.18	129.51	115.30
1	B	322	ASP	CB-CG-OD2	5.78	123.50	118.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	132	VAL	CB-CA-C	-5.61	100.75	111.40
1	A	300	ARG	NE-CZ-NH2	5.53	123.06	120.30
1	A	416	LEU	CA-CB-CG	-5.52	102.61	115.30
1	B	328	VAL	CB-CA-C	-5.49	100.97	111.40
1	A	91	ARG	NE-CZ-NH1	5.44	123.02	120.30
1	A	130	GLY	N-CA-C	-5.42	99.55	113.10
1	A	284	ASP	CB-CG-OD1	5.26	123.03	118.30
1	B	189	MET	CG-SD-CE	-5.23	91.83	100.20
1	A	302	ARG	NE-CZ-NH1	5.19	122.89	120.30
1	A	387	ASP	CB-CG-OD1	5.09	122.88	118.30
1	B	65	ARG	CG-CD-NE	-5.08	101.13	111.80
1	A	598	ARG	NE-CZ-NH1	-5.00	117.80	120.30

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	B	567	TYR	Sidechain

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	4623	0	4486	136	0
1	B	4703	0	4576	123	0
2	A	596	0	0	13	0
2	B	628	0	0	25	0
All	All	10550	0	9062	256	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 14.

All (256) close contacts within the same asymmetric unit are listed below.

Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:B:24:ALA:O	1:B:65:ARG:NH2	2.00	0.94

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:28:SER:HG	1:A:30:TYR:HE1	1.11	0.92
1:A:269:GLU:HG2	1:A:273:MET:CE	1.99	0.92
1:A:269:GLU:HG2	1:A:273:MET:HE2	1.51	0.91
1:B:534:PRO:HA	1:B:565:ASN:ND2	1.86	0.89
1:A:516:ASP:H	1:A:569:GLN:HE21	0.90	0.88
1:B:316:ARG:HD3	1:B:584:CYS:HB3	1.58	0.83
1:B:533:LYS:HG2	1:B:543:ILE:HD12	1.63	0.80
1:A:33:LEU:HG	1:A:34:ASP:H	1.48	0.79
1:A:516:ASP:H	1:A:569:GLN:NE2	1.76	0.78
1:A:416:LEU:HD23	1:A:419:LEU:HD12	1.64	0.78
1:B:84:ILE:HG22	1:B:189:MET:CE	2.14	0.78
1:A:280:LYS:HE2	2:A:841:HOH:O	1.83	0.78
1:A:84:ILE:HG22	1:A:189:MET:CE	2.14	0.78
1:A:322:ASP:OD2	1:A:324:ARG:NH1	2.18	0.77
1:B:229:GLU:O	1:B:235:ASN:HB2	1.84	0.77
1:B:142:LYS:HE3	1:B:164:GLU:HG2	1.65	0.77
1:A:516:ASP:N	1:A:569:GLN:HE21	1.75	0.75
1:B:28:SER:H	1:B:152:HIS:HE1	1.33	0.74
1:B:40:ASP:O	1:B:43:VAL:HG22	1.90	0.71
1:B:303:LEU:HD13	1:B:307:ARG:NH1	2.05	0.71
1:A:139:HIS:ND1	1:A:144:ARG:NH2	2.38	0.71
1:A:84:ILE:HG22	1:A:189:MET:HE1	1.74	0.69
1:B:543:ILE:HG12	2:B:900:HOH:O	1.92	0.69
1:A:41:ASP:HB3	1:A:43:VAL:HG22	1.74	0.68
1:B:332:ASN:HD21	1:B:335:SER:H	1.41	0.68
1:B:141:ASN:HB3	2:B:662:HOH:O	1.94	0.68
1:B:144:ARG:HD3	1:B:161:TRP:CD1	2.29	0.67
1:B:13:GLY:N	2:B:940:HOH:O	2.26	0.67
1:A:311:HIS:HE2	1:A:377:ARG:NH2	1.91	0.67
1:A:170:GLU:HG2	1:A:171:ASN:ND2	2.10	0.66
1:B:84:ILE:HG22	1:B:189:MET:HE1	1.75	0.66
1:B:576:VAL:O	2:B:1069:HOH:O	2.13	0.65
1:A:606:LYS:CD	1:A:607:LYS:H	2.09	0.65
1:A:144:ARG:HD2	1:A:161:TRP:CD1	2.31	0.65
1:A:306:GLN:NE2	2:A:1036:HOH:O	2.29	0.65
1:B:84:ILE:HG22	1:B:189:MET:HE3	1.78	0.65
1:A:606:LYS:NZ	1:A:607:LYS:NZ	2.45	0.64
1:A:393:ASN:HD21	1:A:414:ARG:HE	1.45	0.64
1:A:171:ASN:HA	2:A:837:HOH:O	1.97	0.64
1:B:534:PRO:HA	1:B:565:ASN:HD22	1.62	0.64
1:B:534:PRO:HD2	1:B:543:ILE:HD13	1.79	0.64
1:A:28:SER:OG	1:A:30:TYR:HE1	1.80	0.64

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:121:ASP:OD1	1:A:122:LYS:N	2.28	0.63
1:A:322:ASP:OD1	1:A:324:ARG:HG3	1.99	0.63
1:A:564:LYS:HE3	2:A:1137:HOH:O	1.98	0.63
1:A:329:TYR:HE1	1:A:573:LEU:HD21	1.63	0.63
1:A:181:ASP:HB2	2:A:939:HOH:O	1.98	0.63
1:A:269:GLU:HG2	1:A:273:MET:HE1	1.79	0.62
1:B:28:SER:H	1:B:152:HIS:CE1	2.15	0.62
1:B:95:ASN:ND2	2:B:864:HOH:O	2.32	0.61
1:A:606:LYS:HD2	1:A:607:LYS:H	1.65	0.61
1:A:84:ILE:HG22	1:A:189:MET:HE3	1.81	0.61
1:B:300:ARG:NH1	2:B:1181:HOH:O	2.34	0.61
1:B:498:LYS:HE3	1:B:534:PRO:O	2.00	0.60
1:B:494:ILE:HB	1:B:495:PRO:HD3	1.84	0.60
1:A:303:LEU:HD21	1:B:72:GLY:HA3	1.83	0.60
1:A:12:PHE:CG	1:A:13:GLY:N	2.62	0.60
1:B:119:ILE:CD1	1:B:132:VAL:HG13	2.32	0.59
1:B:366:ILE:HG12	2:B:1143:HOH:O	2.03	0.59
1:A:240:ALA:HB2	1:A:390:ILE:HG22	1.84	0.58
1:B:122:LYS:HB2	1:B:127:LYS:O	2.02	0.58
1:A:431:GLU:HG2	2:A:1103:HOH:O	2.03	0.58
1:B:21:GLY:HA3	1:B:70:ASN:HD21	1.68	0.58
1:A:416:LEU:HD23	1:A:419:LEU:CD1	2.33	0.58
1:B:465:ARG:HD3	2:B:1016:HOH:O	2.03	0.58
1:B:605:ILE:HG23	1:B:609:SER:OG	2.03	0.58
1:B:34:ASP:OD2	1:B:36:GLN:HB3	2.03	0.57
1:B:246:ASN:H	1:B:246:ASN:HD22	1.52	0.57
1:A:31:SER:O	1:A:33:LEU:N	2.38	0.57
1:B:206:GLY:O	1:B:323:GLU:HA	2.05	0.56
1:A:416:LEU:HD13	2:A:976:HOH:O	2.05	0.56
1:A:121:ASP:HB2	1:A:186:LEU:HG	1.88	0.56
1:B:81:ALA:HB1	1:B:132:VAL:HG22	1.87	0.55
1:B:436:ASN:HD22	1:B:436:ASN:C	2.10	0.55
1:A:469:PRO:CB	1:A:470:GLN:HE22	2.19	0.55
1:B:572:CYS:HB3	1:B:603:LEU:HD21	1.88	0.55
1:B:603:LEU:HD22	2:B:790:HOH:O	2.07	0.55
1:A:38:TYR:HA	1:A:44:PHE:CD1	2.42	0.55
1:A:207:GLU:OE2	1:A:210:LYS:HE2	2.06	0.54
1:B:173:CYS:HB2	2:B:742:HOH:O	2.07	0.54
1:A:38:TYR:HA	1:A:44:PHE:CE1	2.43	0.54
1:A:474:ARG:HB2	1:A:477:ASP:OD2	2.07	0.54
1:B:251:HIS:HE1	1:B:577:ASP:OD2	1.90	0.54
1:B:498:LYS:HG2	2:B:764:HOH:O	2.06	0.54

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:B:600:ASP:OD1	1:B:602:SER:HB3	2.08	0.54
1:A:606:LYS:HZ1	1:A:607:LYS:NZ	2.06	0.53
1:B:92:GLU:HG2	2:B:864:HOH:O	2.07	0.53
1:B:27:SER:HB2	1:B:152:HIS:ND1	2.23	0.53
1:B:66:PHE:CE2	1:B:134:ILE:HG21	2.43	0.53
1:A:606:LYS:NZ	1:A:607:LYS:HZ1	2.05	0.53
1:A:606:LYS:HZ1	1:A:607:LYS:HZ1	1.55	0.53
1:B:316:ARG:HD2	1:B:318:ASP:OD1	2.07	0.53
1:A:517:THR:HG23	1:A:568:GLN:HB2	1.90	0.53
1:B:131:HIS:HE1	1:B:147:GLU:OE1	1.92	0.53
1:B:143:VAL:HG21	1:B:176:LEU:HD21	1.91	0.53
1:A:320:CYS:HB2	1:A:329:TYR:CZ	2.44	0.52
1:B:131:HIS:HD2	2:B:879:HOH:O	1.92	0.52
1:B:568:GLN:HG2	2:B:1117:HOH:O	2.10	0.52
1:B:228:ASP:OD1	1:B:230:LYS:N	2.35	0.52
1:B:337:SER:O	1:B:338:CYS:HB2	2.08	0.52
1:B:522:ASN:O	1:B:526:VAL:HG23	2.09	0.52
1:A:606:LYS:NZ	1:A:607:LYS:HZ2	2.08	0.52
1:B:280:LYS:HD3	1:B:503:ILE:HG23	1.90	0.52
1:B:60:VAL:HG12	2:B:685:HOH:O	2.09	0.52
1:B:30:TYR:O	1:B:33:LEU:HB2	2.09	0.52
1:B:389:ASP:C	1:B:389:ASP:OD2	2.46	0.52
1:A:469:PRO:CB	1:A:470:GLN:NE2	2.73	0.51
1:A:139:HIS:CG	1:A:144:ARG:HH21	2.27	0.51
1:A:245:ILE:HG23	1:A:246:ASN:N	2.25	0.51
1:A:606:LYS:O	1:A:609:SER:HB2	2.10	0.51
1:B:352:GLN:NE2	1:B:352:GLN:HA	2.26	0.51
1:A:96:ASP:O	1:A:276:HIS:CE1	2.63	0.51
1:B:31:SER:C	1:B:33:LEU:H	2.14	0.51
1:A:56:LYS:HD3	1:A:57:TRP:CZ2	2.45	0.51
1:B:56:LYS:NZ	2:B:682:HOH:O	2.44	0.51
1:B:300:ARG:NH2	1:B:482:PRO:HG3	2.27	0.50
1:B:171:ASN:ND2	1:B:171:ASN:O	2.44	0.50
1:B:119:ILE:HD13	1:B:132:VAL:HG13	1.93	0.50
1:B:122:LYS:NZ	2:B:886:HOH:O	2.43	0.50
1:B:393:ASN:OD1	1:B:414:ARG:NH1	2.45	0.50
1:A:324:ARG:HH11	1:A:324:ARG:CG	2.25	0.50
1:A:498:LYS:HD3	1:A:533:LYS:HD3	1.94	0.50
1:A:96:ASP:O	1:A:276:HIS:HE1	1.94	0.49
1:B:245:ILE:HG23	1:B:246:ASN:N	2.27	0.49
1:A:361:PRO:HD3	1:A:616:VAL:HG23	1.94	0.49
1:B:171:ASN:C	1:B:171:ASN:HD22	2.15	0.49

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:91:ARG:HD3	1:A:272:LEU:HD21	1.94	0.49
1:A:305:TRP:CH2	1:A:309:ARG:HD3	2.47	0.49
1:A:56:LYS:HB3	1:A:57:TRP:CE2	2.46	0.49
1:A:51:GLU:OE1	1:A:91:ARG:NH2	2.46	0.49
1:A:476:ILE:O	1:A:476:ILE:HG13	2.12	0.49
1:B:228:ASP:OD1	1:B:228:ASP:C	2.50	0.49
1:B:352:GLN:HE21	1:B:352:GLN:CA	2.25	0.49
1:A:142:LYS:HB3	1:A:164:GLU:HG2	1.95	0.49
1:A:254:THR:HA	1:A:615:ILE:O	2.13	0.48
1:A:30:TYR:O	1:A:32:SER:N	2.46	0.48
1:B:314:THR:OG1	1:B:339:HIS:HE1	1.95	0.48
1:A:532:VAL:HG22	1:A:567:TYR:CD2	2.48	0.48
1:A:30:TYR:N	1:A:30:TYR:CD1	2.79	0.48
1:B:246:ASN:N	1:B:246:ASN:HD22	2.09	0.48
1:A:324:ARG:HG3	1:A:324:ARG:HH11	1.78	0.48
1:B:303:LEU:HD13	1:B:307:ARG:HH11	1.76	0.48
1:A:16:LEU:HD21	1:A:27:SER:HB3	1.96	0.48
1:A:469:PRO:HB3	1:A:470:GLN:HE22	1.78	0.48
1:B:215:ARG:NH1	2:B:632:HOH:O	2.34	0.48
1:A:337:SER:O	1:A:338:CYS:HB2	2.14	0.48
1:A:117:LEU:HD23	1:A:134:ILE:CD1	2.44	0.48
1:A:240:ALA:CB	1:A:390:ILE:HG22	2.44	0.47
1:B:597:LEU:HG	1:B:614:LEU:HD22	1.95	0.47
1:A:56:LYS:HB3	1:A:57:TRP:CD2	2.49	0.47
1:B:332:ASN:HD22	1:B:332:ASN:C	2.18	0.47
1:A:137:GLN:NE2	1:B:458:GLU:OE2	2.46	0.47
1:B:56:LYS:HB3	1:B:57:TRP:CD2	2.49	0.47
1:A:319:PHE:CE2	1:A:328:VAL:HG13	2.49	0.47
1:B:94:VAL:HG23	2:B:923:HOH:O	2.14	0.47
1:B:319:PHE:CD2	1:B:326:LEU:HD22	2.49	0.47
1:A:30:TYR:O	1:A:31:SER:C	2.53	0.47
1:B:505:TRP:CH2	1:B:510:HIS:HA	2.50	0.47
1:A:33:LEU:HD12	2:A:1148:HOH:O	2.15	0.47
1:B:543:ILE:CG1	2:B:900:HOH:O	2.58	0.47
1:B:303:LEU:HD23	1:B:303:LEU:HA	1.73	0.46
1:A:458:GLU:O	1:B:137:GLN:HA	2.16	0.46
1:A:324:ARG:NH1	1:A:324:ARG:HG3	2.30	0.46
1:B:323:GLU:HG2	2:B:668:HOH:O	2.15	0.46
1:A:530:TYR:O	1:A:530:TYR:CG	2.67	0.46
1:A:597:LEU:HG	1:A:614:LEU:HD22	1.98	0.46
1:A:606:LYS:CG	1:A:607:LYS:N	2.78	0.46
1:A:56:LYS:HA	1:A:57:TRP:HA	1.74	0.46

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:102:GLN:O	1:A:189:MET:HA	2.15	0.46
1:A:393:ASN:ND2	1:A:414:ARG:HE	2.09	0.46
1:A:469:PRO:HD3	2:B:931:HOH:O	2.14	0.46
1:A:144:ARG:HD3	1:A:161:TRP:CE2	2.51	0.46
1:B:95:ASN:ND2	1:B:97:ASN:OD1	2.48	0.46
1:A:395:HIS:HE1	2:A:894:HOH:O	1.98	0.45
1:A:94:VAL:HG23	2:A:1006:HOH:O	2.16	0.45
1:B:352:GLN:NE2	1:B:352:GLN:CA	2.79	0.45
1:B:196:GLU:HG2	1:B:197:TYR:CD1	2.51	0.45
1:A:12:PHE:O	1:A:14:THR:N	2.50	0.45
1:A:360:ASN:ND2	1:A:362:ALA:H	2.14	0.45
1:B:530:TYR:HA	1:B:570:LEU:HG	1.99	0.45
1:A:322:ASP:CG	1:A:324:ARG:NH1	2.70	0.45
1:B:170:GLU:O	1:B:171:ASN:HB3	2.16	0.45
1:B:38:TYR:CD2	1:B:44:PHE:CE2	3.05	0.45
1:B:584:CYS:SG	1:B:598:ARG:HD3	2.56	0.45
1:A:532:VAL:HG22	1:A:567:TYR:HD2	1.82	0.45
1:B:270:LEU:HD13	1:B:328:VAL:CG2	2.47	0.45
1:B:603:LEU:CD2	2:B:790:HOH:O	2.65	0.45
1:A:111:ALA:HB2	1:A:174:TYR:CE1	2.52	0.45
1:B:518:ASP:OD1	1:B:519:PHE:N	2.50	0.45
1:B:92:GLU:CG	2:B:864:HOH:O	2.64	0.44
1:A:605:ILE:HG23	1:A:609:SER:CB	2.47	0.44
1:B:533:LYS:HG2	1:B:543:ILE:CD1	2.40	0.44
1:B:16:LEU:HD21	1:B:27:SER:HB3	1.99	0.44
1:B:416:LEU:HD21	1:B:475:LEU:HA	1.99	0.44
1:B:67:LEU:HD11	1:B:117:LEU:HD21	1.99	0.44
1:B:468:HIS:CG	1:B:469:PRO:HD2	2.53	0.44
1:A:165:LEU:CD2	1:A:179:THR:HG23	2.48	0.44
1:B:252:TYR:HB2	1:B:613:PRO:HB2	2.00	0.44
1:A:28:SER:HB2	1:A:57:TRP:O	2.18	0.44
1:A:91:ARG:CD	1:A:272:LEU:HD21	2.48	0.44
1:A:348:ARG:NE	1:A:348:ARG:HA	2.33	0.44
1:A:421:TRP:HE3	1:A:471:ASN:ND2	2.16	0.44
1:A:142:LYS:HB3	1:A:164:GLU:CG	2.48	0.44
1:A:120:TRP:HB2	1:A:131:HIS:HB3	2.00	0.44
1:A:33:LEU:HG	1:A:34:ASP:N	2.26	0.43
1:A:452:ARG:NH1	2:A:858:HOH:O	2.50	0.43
1:B:226:TRP:HB2	1:B:352:GLN:HG2	1.98	0.43
1:B:199:LEU:HA	1:B:200:PRO:HD3	1.87	0.43
1:A:136:THR:HG21	1:A:146:ALA:HB2	2.01	0.43
1:B:301:LEU:CD1	1:B:491:TRP:HA	2.49	0.43

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:324:ARG:NH2	1:A:572:CYS:O	2.49	0.43
1:A:417:ASP:HB2	2:A:1183:HOH:O	2.18	0.43
1:A:600:ASP:HB2	1:A:605:ILE:HD13	2.01	0.43
1:B:37:GLU:C	1:B:39:GLU:H	2.21	0.43
1:B:254:THR:HA	1:B:615:ILE:O	2.19	0.43
1:B:564:LYS:HA	1:B:564:LYS:HD2	1.81	0.43
1:B:31:SER:O	1:B:33:LEU:N	2.52	0.43
1:A:117:LEU:HD23	1:A:134:ILE:HD13	2.00	0.43
1:A:95:ASN:HB2	2:A:871:HOH:O	2.17	0.43
1:A:606:LYS:HG3	1:A:608:GLU:H	1.84	0.42
1:B:436:ASN:HD22	1:B:437:CYS:N	2.17	0.42
1:A:606:LYS:HZ2	1:A:607:LYS:NZ	2.15	0.42
1:A:102:GLN:HA	1:A:102:GLN:HE21	1.84	0.42
1:B:252:TYR:CB	1:B:613:PRO:HB2	2.49	0.42
1:A:436:ASN:C	1:A:436:ASN:HD22	2.21	0.42
1:A:46:SER:HB2	1:A:56:LYS:HG2	2.02	0.42
1:A:469:PRO:HB2	1:A:470:GLN:NE2	2.33	0.42
1:B:56:LYS:HB3	1:B:57:TRP:CE2	2.55	0.42
1:B:102:GLN:O	1:B:189:MET:HA	2.19	0.42
1:B:301:LEU:HD11	1:B:491:TRP:HA	2.02	0.42
1:A:142:LYS:HG3	1:A:164:GLU:OE1	2.19	0.42
1:A:182:ASP:N	1:A:182:ASP:OD1	2.50	0.42
1:A:48:ILE:O	1:A:49:ASP:HB2	2.20	0.41
1:B:300:ARG:HH22	1:B:482:PRO:HG3	1.85	0.41
1:A:393:ASN:HD21	1:A:414:ARG:HH21	1.68	0.41
1:A:498:LYS:CE	1:A:533:LYS:HD3	2.50	0.41
1:B:153:SER:O	1:B:154:PRO:C	2.58	0.41
1:B:528:THR:HG21	1:B:569:GLN:HB2	2.02	0.41
1:A:606:LYS:HG3	1:A:607:LYS:N	2.35	0.41
1:A:230:LYS:HB2	1:A:230:LYS:HE3	1.72	0.41
1:A:393:ASN:HA	1:A:393:ASN:HD22	1.65	0.41
1:A:329:TYR:HE1	1:A:573:LEU:CD2	2.30	0.41
1:B:281:VAL:HG22	1:B:503:ILE:HD13	2.01	0.41
1:A:218:ASN:C	1:A:218:ASN:OD1	2.59	0.41
1:B:476:ILE:O	1:B:476:ILE:HG13	2.20	0.41
1:A:291:PHE:CD1	1:A:291:PHE:N	2.89	0.41
1:A:245:ILE:CG2	1:A:246:ASN:N	2.84	0.40
1:B:201:GLN:HA	1:B:202:PRO:HD3	2.00	0.40
1:A:264:ILE:HG12	1:A:592:TYR:CD2	2.57	0.40
1:A:165:LEU:HD23	1:A:179:THR:HG23	2.03	0.40
1:B:316:ARG:HD3	1:B:584:CYS:CB	2.39	0.40
1:B:374:LYS:CE	2:B:1158:HOH:O	2.70	0.40

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:346:LEU:HD22	1:A:613:PRO:HA	2.02	0.40
1:A:201:GLN:HA	1:A:202:PRO:HD3	1.84	0.40
1:B:346:LEU:HD23	1:B:346:LEU:HA	1.78	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	565/619 (91%)	539 (95%)	21 (4%)	5 (1%)	25	21
1	B	576/619 (93%)	548 (95%)	25 (4%)	3 (0%)	38	38
All	All	1141/1238 (92%)	1087 (95%)	46 (4%)	8 (1%)	30	28

All (8) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	13	GLY
1	A	31	SER
1	A	32	SER
1	A	127	LYS
1	B	127	LYS
1	B	32	SER
1	A	35	PRO
1	B	38	TYR

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	490/530 (92%)	470 (96%)	20 (4%)	41	49
1	B	500/530 (94%)	479 (96%)	21 (4%)	40	48
All	All	990/1060 (93%)	949 (96%)	41 (4%)	41	49

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

Mol	Chain	Res	Type
1	A	30	TYR
1	A	34	ASP
1	A	91	ARG
1	A	154	PRO
1	A	283	LYS
1	A	300	ARG
1	A	306	GLN
1	A	324	ARG
1	A	328	VAL
1	A	351	GLU
1	A	360	ASN
1	A	389	ASP
1	A	416	LEU
1	A	431	GLU
1	A	436	ASN
1	A	469	PRO
1	A	471	ASN
1	A	493	VAL
1	A	608	GLU
1	A	610	ASP
1	B	38	TYR
1	B	95	ASN
1	B	127	LYS
1	B	128	ASP
1	B	153	SER
1	B	154	PRO
1	B	171	ASN
1	B	215	ARG
1	B	246	ASN
1	B	303	LEU
1	B	307	ARG
1	B	326	LEU
1	B	328	VAL
1	B	332	ASN
1	B	352	GLN

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Mol	Chain	Res	Type
1	B	379	ARG
1	B	436	ASN
1	B	469	PRO
1	B	471	ASN
1	B	480	LEU
1	B	603	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (32) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	58	GLN
1	A	97	ASN
1	A	102	GLN
1	A	149	ASN
1	A	171	ASN
1	A	201	GLN
1	A	268	ASN
1	A	360	ASN
1	A	386	GLN
1	A	393	ASN
1	A	395	HIS
1	A	436	ASN
1	A	470	GLN
1	A	471	ASN
1	A	569	GLN
1	B	70	ASN
1	B	95	ASN
1	B	131	HIS
1	B	171	ASN
1	B	201	GLN
1	B	246	ASN
1	B	261	GLN
1	B	268	ASN
1	B	332	ASN
1	B	339	HIS
1	B	352	GLN
1	B	367	ASN
1	B	401	GLN
1	B	405	GLN
1	B	436	ASN
1	B	471	ASN
1	B	565	ASN

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 ⓘ

There are no ligands in this entry.

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	571/619 (92%)	-0.17	18 (3%)	45 46	18, 33, 69, 106	0
1	B	582/619 (94%)	-0.17	21 (3%)	41 41	17, 32, 67, 104	0
All	All	1153/1238 (93%)	-0.17	39 (3%)	43 43	17, 33, 69, 106	0

All (39) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	38	TYR	9.3
1	A	32	SER	5.5
1	B	545	LEU	5.2
1	B	543	ILE	5.1
1	A	530	TYR	5.0
1	A	33	LEU	4.8
1	A	521	VAL	4.5
1	A	38	TYR	4.2
1	A	564	LYS	4.0
1	A	30	TYR	4.0
1	B	520	THR	3.6
1	B	519	PHE	3.5
1	B	525	LEU	3.2
1	B	527	LYS	3.1
1	A	12	PHE	3.1
1	B	30	TYR	3.1
1	B	528	THR	3.0
1	B	469	PRO	3.0
1	A	520	THR	2.7
1	B	41	ASP	2.7
1	A	469	PRO	2.7
1	B	524	GLU	2.6
1	B	567	TYR	2.6
1	A	565	ASN	2.5

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Mol	Chain	Res	Type	RSRZ
1	B	565	ASN	2.5
1	B	522	ASN	2.5
1	A	41	ASP	2.4
1	B	535	ILE	2.3
1	A	567	TYR	2.3
1	B	546	VAL	2.3
1	A	522	ASN	2.3
1	A	44	PHE	2.2
1	A	531	ALA	2.2
1	B	32	SER	2.1
1	B	35	PRO	2.1
1	A	519	PHE	2.1
1	B	29	ASP	2.1
1	B	223	ASP	2.0
1	A	470	GLN	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 ⓘ

There are no ligands in this entry.

6.5 Other polymers ⓘ

There are no such residues in this entry.