



Full wwPDB X-ray Structure Validation Report ⓘ

May 25, 2020 – 06:27 am BST

PDB ID : 5NZH
Title : Crystal structure of UDP-glucose pyrophosphorylase V402W mutant from *Leishmania major*
Authors : Cramer, J.T.; Fuehring, J.I.; Baruch, P.; Bruetting, C.; Hesse, R.; Knoelker, H.-J.; Gerardy-Schahn, R.; Fedorov, R.
Deposited on : 2017-05-14
Resolution : 2.90 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 following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity : 4.02b-467
Xtriage (Phenix) : 1.13
EDS : 2.11
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac : 5.8.0158
CCP4 : 7.0.044 (Gargrove)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.11

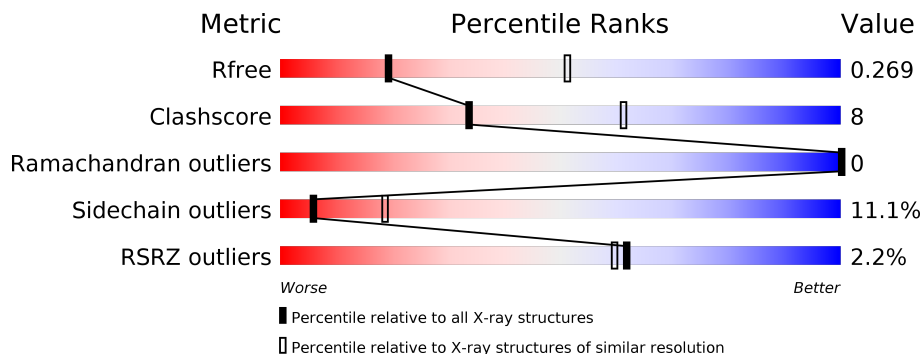
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.90 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}	130704	1957 (2.90-2.90)
Clashscore	141614	2172 (2.90-2.90)
Ramachandran outliers	138981	2115 (2.90-2.90)
Sidechain outliers	138945	2117 (2.90-2.90)
RSRZ outliers	127900	1906 (2.90-2.90)

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 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	505	 73% 18% • •
1	B	505	 4% 72% 19% • 5%

2 Entry composition i

There are 2 unique types of molecules in this entry. The entry contains 7820 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 UDP-glucose pyrophosphorylase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	483	3737	2357	637	717	26	0	0	0
1	B	482	3728	2351	635	716	26	0	0	0

There are 24 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	402	TRP	VAL	engineered mutation	UNP Q4QDU3
A	495	MET	-	expression tag	UNP Q4QDU3
A	496	ARG	-	expression tag	UNP Q4QDU3
A	497	PRO	-	expression tag	UNP Q4QDU3
A	498	LEU	-	expression tag	UNP Q4QDU3
A	499	GLU	-	expression tag	UNP Q4QDU3
A	500	HIS	-	expression tag	UNP Q4QDU3
A	501	HIS	-	expression tag	UNP Q4QDU3
A	502	HIS	-	expression tag	UNP Q4QDU3
A	503	HIS	-	expression tag	UNP Q4QDU3
A	504	HIS	-	expression tag	UNP Q4QDU3
A	505	HIS	-	expression tag	UNP Q4QDU3
B	402	TRP	VAL	engineered mutation	UNP Q4QDU3
B	495	MET	-	expression tag	UNP Q4QDU3
B	496	ARG	-	expression tag	UNP Q4QDU3
B	497	PRO	-	expression tag	UNP Q4QDU3
B	498	LEU	-	expression tag	UNP Q4QDU3
B	499	GLU	-	expression tag	UNP Q4QDU3
B	500	HIS	-	expression tag	UNP Q4QDU3
B	501	HIS	-	expression tag	UNP Q4QDU3
B	502	HIS	-	expression tag	UNP Q4QDU3
B	503	HIS	-	expression tag	UNP Q4QDU3
B	504	HIS	-	expression tag	UNP Q4QDU3
B	505	HIS	-	expression tag	UNP Q4QDU3

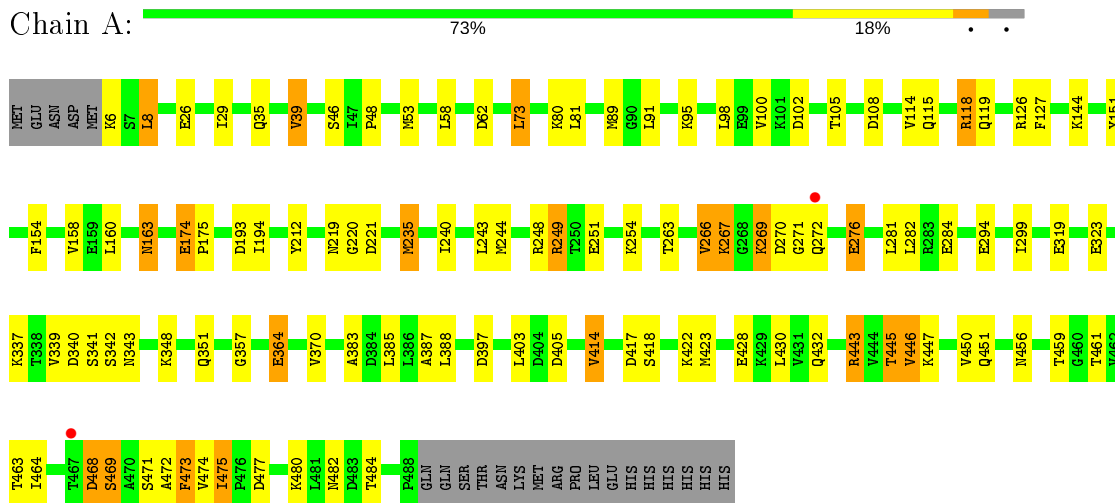
- Molecule 2 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	175	Total 175	O 175	0	0
2	B	180	Total 180	O 180	0	0

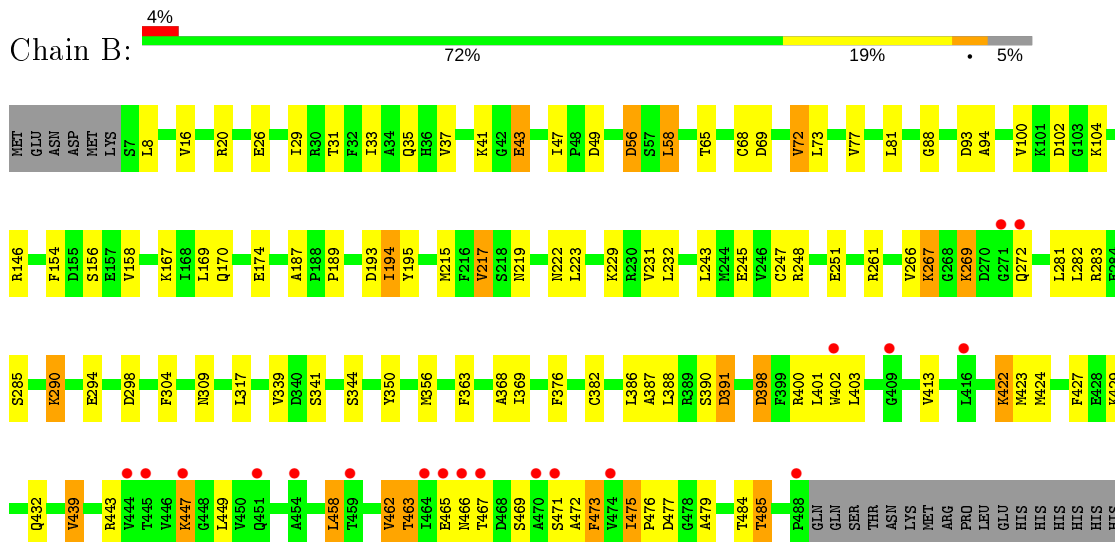
3 Residue-property plots

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of 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: UDP-glucose pyrophosphorylase



- Molecule 1: UDP-glucose pyrophosphorylase



4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	179.56Å 70.89Å 112.29Å 90.00° 123.54° 90.00°	Depositor
Resolution (Å)	47.85 – 2.90 47.85 – 2.90	Depositor EDS
% Data completeness (in resolution range)	99.7 (47.85-2.90) 99.7 (47.85-2.90)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.02	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.00 (at 2.91Å)	Xtrriage
Refinement program	PHENIX (1.11.1_2575: ???)	Depositor
R, R_{free}	0.226 , 0.269 0.225 , 0.269	Depositor DCC
R_{free} test set	1399 reflections (5.31%)	wwPDB-VP
Wilson B-factor (Å ²)	43.6	Xtrriage
Anisotropy	0.271	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 7.9	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
F_o, F_c correlation	0.89	EDS
Total number of atoms	7820	wwPDB-VP
Average B, all atoms (Å ²)	32.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.95% 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](#)

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	0.42	0/3809	0.57	1/5160 (0.0%)
1	B	0.43	0/3800	0.58	2/5149 (0.0%)
All	All	0.42	0/7609	0.57	3/10309 (0.0%)

There are no bond length outliers.

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	471	SER	N-CA-C	-8.39	88.35	111.00
1	A	272	GLN	N-CA-C	6.78	129.30	111.00
1	B	8	LEU	CA-CB-CG	5.09	127.01	115.30

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

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	3737	0	3720	65	3
1	B	3728	0	3707	62	0
2	A	175	0	0	5	0
2	B	180	0	0	5	0
All	All	7820	0	7427	126	3

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 8.

All (126) 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:449:LEU:HB3	1:B:472:ALA:HB2	1.41	1.02
1:A:417:ASP:OD2	1:A:447:LYS:O	1.78	1.02
1:B:465:GLU:O	1:B:466:ASN:OD1	1.77	1.01
1:B:449:LEU:HD22	1:B:472:ALA:H	1.33	0.93
1:A:451:GLN:HG3	1:A:474:VAL:HG12	1.55	0.87
1:A:235:MET:SD	2:A:718:HOH:O	2.38	0.81
1:A:267:LYS:N	1:A:267:LYS:HE3	2.00	0.77
1:A:81:LEU:HB2	1:A:219:ASN:HA	1.67	0.76
1:A:383:ALA:HB1	1:A:414:VAL:HB	1.68	0.74
1:B:189:PRO:HG2	1:B:193:ASP:HB2	1.69	0.73
1:A:468:ASP:OD2	1:A:468:ASP:N	2.21	0.73
1:B:391:ASP:HB3	1:B:439:VAL:HG13	1.71	0.71
1:B:68:CYS:O	1:B:229:LYS:NZ	2.24	0.71
1:B:449:LEU:CB	1:B:472:ALA:HB2	2.17	0.70
1:A:115:GLN:HA	1:A:118:ARG:HB2	1.73	0.69
1:B:41:LYS:HE2	1:B:43:GLU:HG3	1.74	0.69
1:B:424:MET:SD	2:B:724:HOH:O	2.52	0.67
1:A:443:ARG:HB3	1:A:461:THR:HG23	1.78	0.66
1:B:382:CYS:SG	2:B:724:HOH:O	2.53	0.66
1:A:95:LYS:NZ	2:A:603:HOH:O	2.31	0.63
1:A:450:VAL:HG22	1:A:473:PHE:HB3	1.84	0.60
1:A:8:LEU:HA	2:A:668:HOH:O	2.02	0.59
1:A:469:SER:O	1:A:469:SER:OG	2.20	0.59
1:A:418:SER:HA	1:A:422:LYS:HD3	1.83	0.59
1:B:398:ASP:HB2	1:B:400:ARG:HG3	1.84	0.59
1:B:290:LYS:H	1:B:290:LYS:HE2	1.67	0.58
1:A:174:GLU:HG3	1:A:175:PRO:HD2	1.86	0.58
1:A:417:ASP:OD2	1:A:447:LYS:C	2.41	0.57
1:A:337:LYS:HD2	1:A:351:GLN:HE22	1.69	0.57
1:B:102:ASP:HB3	1:B:104:LYS:HE2	1.87	0.57
1:A:91:LEU:HD22	1:A:98:LEU:HD11	1.87	0.56
1:B:465:GLU:C	1:B:466:ASN:OD1	2.42	0.56
1:B:49:ASP:OD1	1:B:283:ARG:NH2	2.39	0.55
1:B:29:ILE:O	1:B:33:ILE:HG12	2.06	0.55
1:A:8:LEU:H	1:A:8:LEU:HD23	1.72	0.54
1:B:463:THR:HG23	1:B:485:THR:HG23	1.89	0.54
1:B:58:LEU:HD22	1:B:368:ALA:HB3	1.89	0.54
1:A:267:LYS:HE3	1:A:267:LYS:H	1.71	0.53
1:A:8:LEU:HD23	1:A:8:LEU:N	2.23	0.53
1:B:223:LEU:HD13	1:B:401:LEU:HD22	1.90	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:215:MET:HG2	1:B:217:VAL:HG22	1.90	0.53
1:A:267:LYS:HG2	1:A:267:LYS:O	2.07	0.53
1:A:267:LYS:H	1:A:267:LYS:CE	2.21	0.53
1:A:8:LEU:CD2	1:A:8:LEU:N	2.72	0.52
1:A:263:THR:HG22	1:A:276:GLU:HB2	1.91	0.52
1:A:269:LYS:HG3	1:A:269:LYS:O	2.09	0.52
1:A:459:THR:HB	1:A:482:ASN:HB3	1.90	0.52
1:A:81:LEU:HD21	1:A:194:ILE:HD12	1.91	0.52
1:B:387:ALA:O	1:B:390:SER:OG	2.25	0.52
1:A:219:ASN:ND2	1:A:221:ASP:OD1	2.44	0.51
1:A:430:LEU:HD12	1:A:451:GLN:HA	1.93	0.51
1:B:251:GLU:H	1:B:251:GLU:CD	2.12	0.51
1:B:458:LEU:HD21	1:B:462:VAL:HB	1.93	0.50
1:B:167:LYS:HE2	1:B:187:ALA:HB2	1.92	0.50
1:B:93:ASP:OD1	1:B:94:ALA:N	2.39	0.50
1:A:473:PHE:C	1:A:473:PHE:CD1	2.85	0.50
1:A:473:PHE:C	1:A:473:PHE:HD1	2.14	0.50
1:A:114:VAL:HG21	1:A:127:PHE:CD1	2.48	0.49
1:A:115:GLN:O	1:A:119:GLN:HG2	2.13	0.49
1:B:245:GLU:HB2	1:B:309:ASN:HB2	1.95	0.48
1:B:31:THR:O	1:B:35:GLN:HG3	2.14	0.48
1:A:126:ARG:NH1	1:A:212:TYR:OH	2.44	0.47
1:B:290:LYS:H	1:B:290:LYS:CE	2.26	0.47
1:A:364:GLU:H	1:A:364:GLU:CD	2.17	0.47
1:A:58:LEU:HB2	1:A:370:VAL:HG23	1.95	0.47
1:B:33:ILE:O	1:B:37:VAL:HG23	2.14	0.47
1:B:247:CYS:O	1:B:304:PHE:HA	2.15	0.47
1:B:413:VAL:HB	1:B:443:ARG:HG2	1.95	0.47
1:B:69:ASP:HB3	2:B:712:HOH:O	2.14	0.47
1:B:69:ASP:O	1:B:72:VAL:HG13	2.15	0.46
1:A:80:LYS:HG3	1:A:220:GLY:HA2	1.98	0.46
1:B:100:VAL:HB	1:B:388:LEU:HD21	1.96	0.46
1:A:473:PHE:O	1:A:473:PHE:CD1	2.69	0.46
1:B:195:TYR:OH	1:B:356:MET:O	2.24	0.46
1:B:243:LEU:HD11	1:B:369:ILE:HB	1.98	0.46
1:B:229:LYS:HA	1:B:232:LEU:HD12	1.98	0.46
1:B:194:ILE:HD12	1:B:217:VAL:HG11	1.98	0.46
1:B:267:LYS:NZ	1:B:267:LYS:H	2.14	0.45
1:A:387:ALA:HB2	1:A:414:VAL:HG21	1.97	0.45
1:A:73:LEU:HD12	1:A:73:LEU:HA	1.72	0.45
1:B:449:LEU:HD23	1:B:472:ALA:HB3	1.98	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:476:PRO:HB2	1:B:479:ALA:HB2	1.98	0.45
1:B:169:LEU:HD12	1:B:174:GLU:HB2	1.98	0.45
1:A:46:SER:O	1:A:48:PRO:HD3	2.16	0.45
1:B:269:LYS:HD2	1:B:269:LYS:HA	1.40	0.45
1:A:456:ASN:CG	1:A:475:ILE:HD11	2.37	0.45
1:A:154:PHE:HA	1:A:158:VAL:HB	1.99	0.45
1:A:475:ILE:O	1:A:475:ILE:HG13	2.17	0.45
1:B:154:PHE:HA	1:B:158:VAL:HB	1.99	0.45
1:B:422:LYS:HB3	1:B:423:MET:HE2	1.98	0.45
1:B:56:ASP:OD2	1:B:261:ARG:NH1	2.50	0.44
1:A:340:ASP:HB3	1:A:343:ASN:HB3	1.99	0.44
1:A:451:GLN:O	1:A:474:VAL:HA	2.18	0.44
1:B:473:PHE:CD2	1:B:475:ILE:HG12	2.52	0.44
1:A:243:LEU:HD22	2:A:733:HOH:O	2.17	0.44
1:B:222:ASN:HD21	1:B:376:PHE:HA	1.83	0.44
1:A:144:LYS:HB2	1:A:151:TYR:CD1	2.53	0.43
1:B:77:VAL:HB	1:B:215:MET:HE2	2.00	0.43
1:A:263:THR:CG2	1:A:276:GLU:HB2	2.49	0.43
1:A:282:LEU:HD21	1:A:357:GLY:HA3	1.99	0.43
1:B:73:LEU:HD12	1:B:73:LEU:HA	1.85	0.43
1:A:126:ARG:HD3	2:A:707:HOH:O	2.19	0.43
1:A:249:ARG:O	1:A:299:ILE:HG23	2.18	0.43
1:A:446:VAL:HG12	1:A:464:ILE:HB	2.00	0.42
1:B:294:GLU:HG2	2:B:608:HOH:O	2.18	0.42
1:B:16:VAL:HG23	1:B:33:ILE:HD11	2.00	0.42
1:B:266:VAL:HG22	1:B:266:VAL:O	2.20	0.42
1:A:26:GLU:OE1	1:A:29:ILE:HD12	2.19	0.42
1:A:423:MET:HE3	1:B:88:GLY:HA2	2.01	0.42
1:A:35:GLN:O	1:A:39:VAL:HG23	2.20	0.42
1:B:317:LEU:HD12	1:B:363:PHE:HZ	1.84	0.42
1:B:298:ASP:HA	2:B:672:HOH:O	2.19	0.42
1:B:170:GLN:HG2	1:B:350:TYR:CZ	2.55	0.42
1:A:114:VAL:HG11	1:A:127:PHE:HB2	2.02	0.41
1:A:235:MET:HG3	1:A:240:ILE:HB	2.01	0.41
1:B:81:LEU:HB2	1:B:219:ASN:HA	2.01	0.41
1:B:231:VAL:HG13	1:B:243:LEU:HD23	2.01	0.41
1:B:386:LEU:HB2	1:B:427:PHE:CE2	2.55	0.41
1:B:447:LYS:HE2	1:B:447:LYS:HB2	1.90	0.41
1:A:163:ASN:ND2	1:A:193:ASP:OD1	2.52	0.41
1:B:47:ILE:O	1:B:283:ARG:NH1	2.52	0.41
1:A:105:THR:H	1:A:108:ASP:HB2	1.86	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:471:SER:O	1:A:472:ALA:C	2.59	0.41
1:A:348:LYS:HB2	1:A:348:LYS:HE2	1.91	0.40
1:A:445:THR:HB	1:A:463:THR:HG23	2.02	0.40
1:A:266:VAL:HA	1:A:267:LYS:NZ	2.36	0.40

All (3) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:271:GLY:CA	1:A:405:ASP:OD2[4_758]	1.83	0.37
1:A:271:GLY:N	1:A:405:ASP:OD2[4_758]	1.96	0.24
1:A:271:GLY:C	1:A:405:ASP:OD2[4_758]	2.04	0.16

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	481/505 (95%)	466 (97%)	15 (3%)	0	100	100
1	B	480/505 (95%)	455 (95%)	25 (5%)	0	100	100
All	All	961/1010 (95%)	921 (96%)	40 (4%)	0	100	100

There are no Ramachandran outliers to report.

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	410/432 (95%)	360 (88%)	50 (12%)	5	15
1	B	409/432 (95%)	368 (90%)	41 (10%)	7	23
All	All	819/864 (95%)	728 (89%)	91 (11%)	6	19

All (91) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	6	LYS
1	A	8	LEU
1	A	39	VAL
1	A	53	MET
1	A	62	ASP
1	A	73	LEU
1	A	89	MET
1	A	100	VAL
1	A	102	ASP
1	A	118	ARG
1	A	160	LEU
1	A	163	ASN
1	A	174	GLU
1	A	235	MET
1	A	244	MET
1	A	248	ARG
1	A	249	ARG
1	A	251	GLU
1	A	254	LYS
1	A	266	VAL
1	A	267	LYS
1	A	269	LYS
1	A	270	ASP
1	A	276	GLU
1	A	281	LEU
1	A	284	GLU
1	A	294	GLU
1	A	319	GLU
1	A	323	GLU
1	A	339	VAL
1	A	341	SER
1	A	342	SER
1	A	364	GLU
1	A	385	LEU
1	A	388	LEU

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Mol	Chain	Res	Type
1	A	397	ASP
1	A	403	LEU
1	A	414	VAL
1	A	428	GLU
1	A	432	GLN
1	A	443	ARG
1	A	445	THR
1	A	446	VAL
1	A	468	ASP
1	A	469	SER
1	A	473	PHE
1	A	475	ILE
1	A	477	ASP
1	A	480	LYS
1	A	484	THR
1	B	20	ARG
1	B	26	GLU
1	B	43	GLU
1	B	56	ASP
1	B	58	LEU
1	B	65	THR
1	B	72	VAL
1	B	146	ARG
1	B	156	SER
1	B	194	ILE
1	B	217	VAL
1	B	248	ARG
1	B	267	LYS
1	B	269	LYS
1	B	272	GLN
1	B	281	LEU
1	B	282	LEU
1	B	285	SER
1	B	290	LYS
1	B	339	VAL
1	B	341	SER
1	B	344	SER
1	B	391	ASP
1	B	398	ASP
1	B	402	TRP
1	B	403	LEU
1	B	422	LYS

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Mol	Chain	Res	Type
1	B	429	LYS
1	B	432	GLN
1	B	439	VAL
1	B	447	LYS
1	B	458	LEU
1	B	462	VAL
1	B	463	THR
1	B	467	THR
1	B	469	SER
1	B	473	PHE
1	B	475	ILE
1	B	477	ASP
1	B	484	THR
1	B	485	THR

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (1) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	272	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 carbohydrates in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

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

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	483/505 (95%)	-0.27	2 (0%) 92 93	10, 26, 64, 115	0
1	B	482/505 (95%)	-0.12	19 (3%) 39 35	10, 27, 85, 120	0
All	All	965/1010 (95%)	-0.19	21 (2%) 62 59	10, 26, 79, 120	0

All (21) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	464	ILE	4.1
1	B	454	ALA	3.9
1	B	465	GLU	3.6
1	B	471	SER	3.6
1	B	445	THR	3.5
1	B	467	THR	3.3
1	B	271	GLY	3.2
1	B	474	VAL	3.2
1	A	272	GLN	3.1
1	B	488	PRO	2.7
1	B	444	VAL	2.6
1	B	272	GLN	2.6
1	B	459	THR	2.5
1	B	416	LEU	2.4
1	B	466	ASN	2.3
1	B	470	ALA	2.3
1	B	451	GLN	2.3
1	B	409	GLY	2.2
1	B	447	LYS	2.1
1	A	467	THR	2.1
1	B	402	TRP	2.1

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 carbohydrates in this entry.

6.4 Ligands [i](#)

There are no ligands in this entry.

6.5 Other polymers [i](#)

There are no such residues in this entry.