



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 1, 2026 – 07:24 PM UTC

PDB ID : 2DKA / pdb_00002dka
Title : Crystal structure of N-acetylglucosamine-phosphate mutase, a member of the alpha-D-phosphohexomutase superfamily, in the apo-form
Authors : Nishitani, Y.; Maruyama, D.; Nonaka, T.; Kita, A.; Fukami, T.A.; Mio, T.; Yamada-Okabe, H.; Yamada-Okabe, T.; Miki, K.
Deposited on : 2006-04-07
Resolution : 1.93 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
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

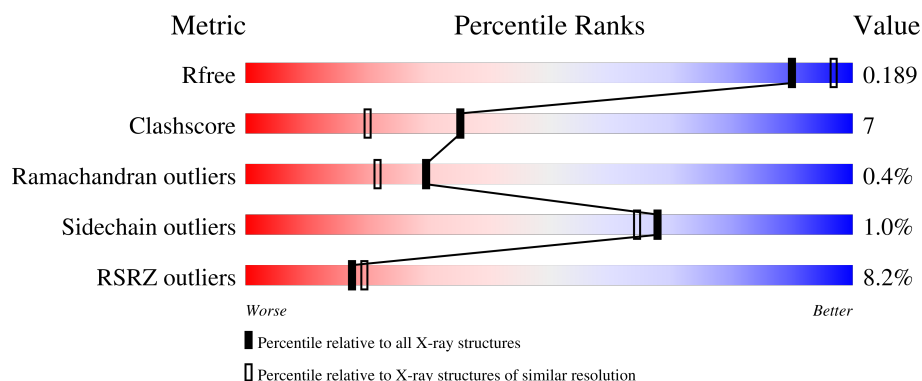
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.93 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	1452 (1.94-1.94)
Clashscore	190562	1494 (1.94-1.94)
Ramachandran outliers	187476	1479 (1.94-1.94)
Sidechain outliers	187428	1479 (1.94-1.94)
RSRZ outliers	180081	1453 (1.94-1.94)

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	544	8% 78% 17% • 5%
1	B	544	7% 69% 15% • 15%

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 8413 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 Phosphoacetylglucosamine mutase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	519	Total	C	N	O	S	0	0	0
			4027	2568	663	788	8			
1	B	461	Total	C	N	O	S	0	0	0
			3584	2290	586	701	7			

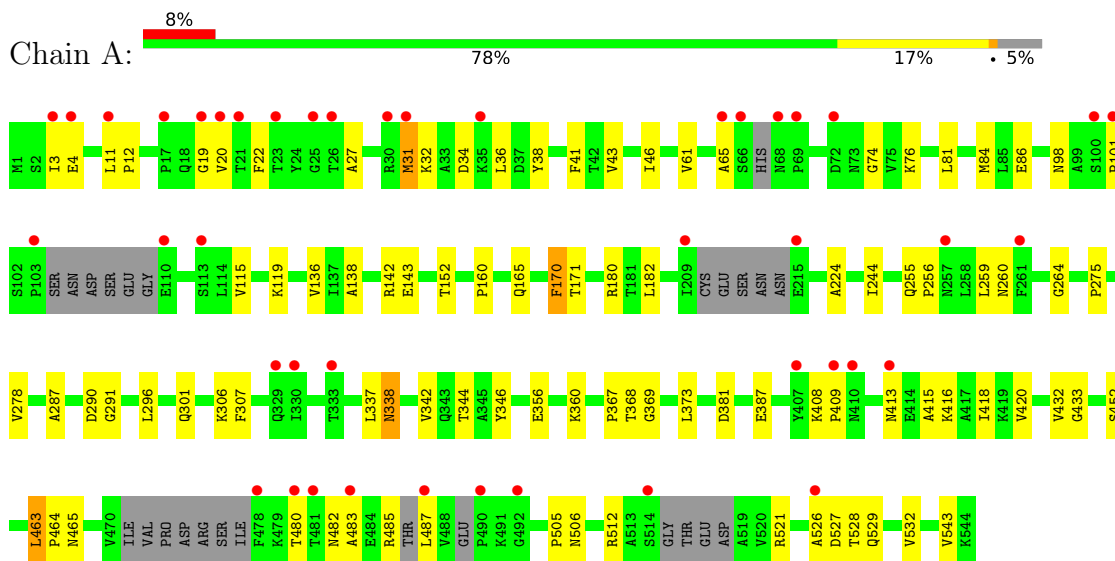
- Molecule 2 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	408	Total	O	0	0
			408	408		
2	B	394	Total	O	0	0
			394	394		

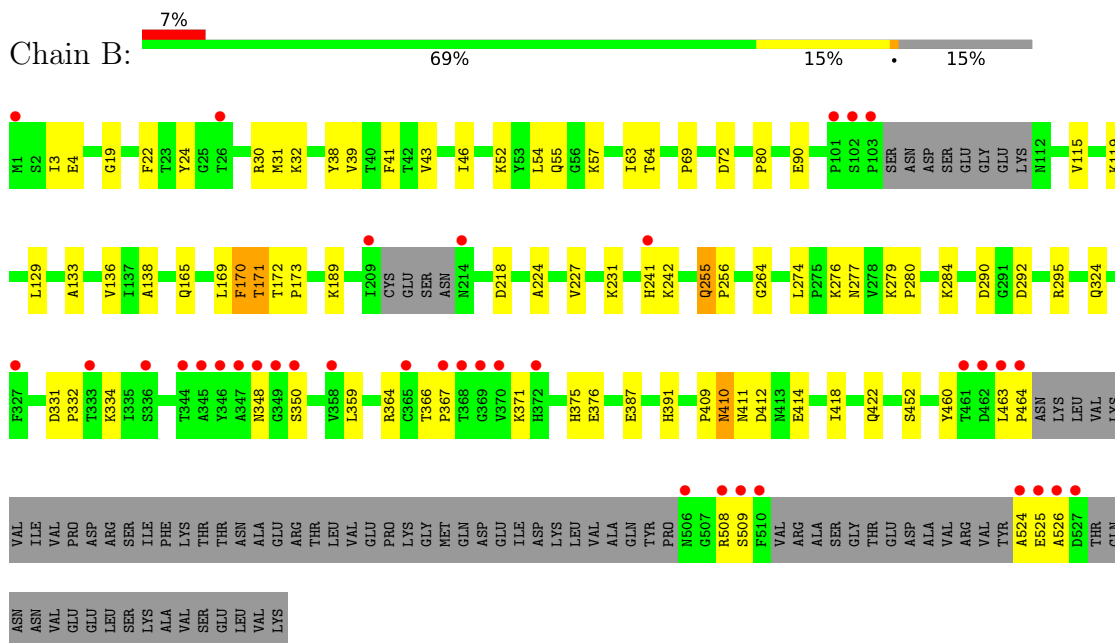
3 Residue-property plots

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: Phosphoacetylglucosamine mutase



• Molecule 1: Phosphoacetylglucosamine mutase



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	60.17Å 130.22Å 77.96Å 90.00° 106.68° 90.00°	Depositor
Resolution (Å)	29.56 – 1.93 29.56 – 1.93	Depositor EDS
% Data completeness (in resolution range)	99.6 (29.56-1.93) 99.6 (29.56-1.93)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.84 (at 1.93Å)	Xtriage
Refinement program	CNS 1.1	Depositor
R, R_{free}	0.192 , 0.222 0.193 , 0.189	Depositor DCC
R_{free} test set	4285 reflections (4.99%)	wwPDB-VP
Wilson B-factor (Å ²)	21.3	Xtriage
Anisotropy	0.271	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.37 , 53.7	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	8413	wwPDB-VP
Average B, all atoms (Å ²)	27.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.53% 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

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	0.35	0/4104	0.85	11/5572 (0.2%)
1	B	0.35	0/3659	0.86	9/4973 (0.2%)
All	All	0.35	0/7763	0.86	20/10545 (0.2%)

There are no bond length outliers.

All (20) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	290	ASP	N-CA-C	-7.58	98.73	110.17
1	A	463	LEU	N-CA-C	-6.61	101.73	109.93
1	B	255	GLN	CA-C-N	6.45	127.90	119.84
1	B	255	GLN	C-N-CA	6.45	127.90	119.84
1	A	290	ASP	N-CA-C	-6.42	100.48	110.17
1	B	171	THR	N-CA-C	-6.32	102.02	110.55
1	A	255	GLN	CA-C-N	6.31	126.79	119.47
1	A	255	GLN	C-N-CA	6.31	126.79	119.47
1	A	291	GLY	N-CA-C	6.30	120.51	112.83
1	B	387	GLU	N-CA-C	-5.97	101.68	110.52
1	A	171	THR	N-CA-C	-5.74	102.80	110.55
1	A	387	GLU	N-CA-C	-5.68	101.62	110.42
1	B	69	PRO	CA-C-N	5.53	125.89	119.47
1	B	69	PRO	C-N-CA	5.53	125.89	119.47
1	B	452	SER	N-CA-C	-5.53	102.00	110.07
1	A	543	VAL	N-CA-C	5.49	118.91	113.53
1	A	452	SER	N-CA-C	-5.40	102.19	110.07
1	B	412	ASP	N-CA-C	5.29	117.04	111.28
1	A	344	THR	N-CA-C	-5.21	102.19	109.69
1	A	244	ILE	N-CA-C	5.01	115.93	108.46

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	4027	0	3949	63	0
1	B	3584	0	3519	49	0
2	A	408	0	0	8	0
2	B	394	0	0	2	0
All	All	8413	0	7468	111	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 7.

All (111) 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:338:ASN:HD21	1:A:381:ASP:H	1.22	0.87
1:A:27:ALA:HA	1:A:76:LYS:HE2	1.56	0.87
1:A:338:ASN:HD22	1:A:338:ASN:C	1.87	0.80
1:A:338:ASN:ND2	1:A:381:ASP:H	1.82	0.77
1:B:57:LYS:HE3	1:B:80:PRO:HG2	1.69	0.75
1:A:482:ASN:ND2	1:A:485:ARG:HH21	1.88	0.72
1:A:482:ASN:HD21	1:A:485:ARG:HH21	1.36	0.71
1:B:32:LYS:HD3	1:B:72:ASP:OD1	1.94	0.67
1:A:22:PHE:H	1:A:98:ASN:HD21	1.46	0.64
1:A:138:ALA:HB1	1:A:170:PHE:HB2	1.80	0.64
1:B:136:VAL:HG12	1:B:165:GLN:HB3	1.81	0.62
1:A:409:PRO:HG3	1:A:415:ALA:HA	1.82	0.61
1:B:189:LYS:HE3	2:B:582:HOH:O	2.01	0.60
1:A:464:PRO:HD2	1:A:526:ALA:O	2.03	0.59
1:A:338:ASN:C	1:A:338:ASN:ND2	2.61	0.59
1:B:54:LEU:HB3	1:B:57:LYS:HE2	1.86	0.57
1:B:464:PRO:HD2	1:B:526:ALA:O	2.05	0.57
1:A:11:LEU:HD11	1:A:101:PRO:HB3	1.87	0.57
1:A:3:ILE:HD12	1:A:160:PRO:HD3	1.88	0.55
1:A:76:LYS:HD3	2:A:685:HOH:O	2.06	0.55
1:A:65:ALA:HB3	1:A:142:ARG:CZ	2.36	0.55
1:B:169:LEU:HG	1:B:227:VAL:HG23	1.87	0.55
1:A:36:LEU:HD21	1:A:74:GLY:HA2	1.89	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:22:PHE:CD2	1:B:39:VAL:HG21	2.42	0.54
1:A:527:ASP:OD2	1:A:528:THR:HG23	2.08	0.54
1:A:84:MET:HE1	2:A:951:HOH:O	2.08	0.53
1:A:180:ARG:NE	2:A:874:HOH:O	2.42	0.53
1:B:409:PRO:HB3	1:B:414:GLU:HB3	1.90	0.53
1:A:342:VAL:HG12	1:A:373:LEU:HD23	1.91	0.53
1:B:138:ALA:HB1	1:B:170:PHE:HB2	1.91	0.52
1:B:331:ASP:CG	1:B:334:LYS:HD3	2.33	0.52
1:A:367:PRO:HG3	1:A:483:ALA:HA	1.89	0.52
1:A:306:LYS:HD2	1:A:307:PHE:N	2.24	0.52
1:A:259:LEU:CD1	1:A:260:ASN:ND2	2.73	0.52
1:A:180:ARG:HG3	1:A:180:ARG:HH11	1.76	0.51
1:B:24:TYR:CD2	1:B:90:GLU:HG2	2.45	0.51
1:B:418:ILE:O	1:B:422:GLN:HG3	2.11	0.51
1:B:115:VAL:HG22	1:B:119:LYS:HE3	1.92	0.50
1:B:218:ASP:OD2	1:B:284:LYS:NZ	2.44	0.50
1:A:11:LEU:HD11	1:A:101:PRO:CB	2.42	0.50
1:A:415:ALA:O	1:A:418:ILE:HG22	2.10	0.50
1:B:410:ASN:HD22	1:B:410:ASN:C	2.19	0.49
1:A:306:LYS:HD2	1:A:307:PHE:H	1.77	0.49
1:A:337:LEU:HA	1:A:381:ASP:OD1	2.12	0.49
1:A:338:ASN:HD21	1:A:381:ASP:N	2.03	0.49
1:A:529:GLN:O	1:A:532:VAL:HG12	2.11	0.49
1:A:306:LYS:HE3	1:A:307:PHE:O	2.13	0.48
1:B:31:MET:HB2	2:B:823:HOH:O	2.13	0.48
1:A:480:THR:HG22	1:A:487:LEU:HD13	1.95	0.48
1:A:256:PRO:HA	2:A:803:HOH:O	2.13	0.48
1:B:410:ASN:HD22	1:B:411:ASN:N	2.11	0.48
1:A:11:LEU:HB3	1:A:12:PRO:HD3	1.97	0.47
1:B:274:LEU:CD1	1:B:280:PRO:HB3	2.44	0.47
1:A:86:GLU:OE1	1:B:375:HIS:HE1	1.97	0.47
1:A:275:PRO:HG2	1:A:278:VAL:CG2	2.45	0.47
1:A:4:GLU:HG3	1:A:115:VAL:HG21	1.96	0.47
1:A:32:LYS:HB3	1:A:34:ASP:OD1	2.14	0.47
1:A:115:VAL:O	1:A:119:LYS:HG3	2.15	0.47
1:B:63:ILE:O	1:B:64:THR:HB	2.14	0.47
1:A:76:LYS:NZ	2:A:683:HOH:O	2.47	0.46
1:B:22:PHE:CE2	1:B:39:VAL:HG21	2.50	0.46
1:A:38:TYR:O	1:A:41:PHE:HB3	2.16	0.45
1:A:505:PRO:O	1:A:506:ASN:HB2	2.16	0.45
1:A:43:VAL:O	1:A:46:ILE:HG22	2.16	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:416:LYS:O	1:A:420:VAL:HG23	2.16	0.45
1:B:276:LYS:O	1:B:277:ASN:HB2	2.17	0.45
1:A:287:ALA:HB1	1:A:296:LEU:HD11	1.98	0.45
1:A:136:VAL:HG12	1:A:165:GLN:HB3	1.98	0.45
1:B:350:SER:OG	1:B:463:LEU:HG	2.18	0.44
1:A:463:LEU:O	1:A:464:PRO:C	2.58	0.44
1:B:171:THR:HG23	1:B:231:LYS:HG3	1.99	0.44
1:B:43:VAL:O	1:B:46:ILE:HG22	2.17	0.44
1:B:366:THR:HB	1:B:367:PRO:HD2	1.99	0.44
1:A:3:ILE:HG23	1:A:4:GLU:N	2.33	0.44
1:B:364:ARG:HH11	1:B:364:ARG:HG3	1.82	0.43
1:A:224:ALA:HB2	1:A:264:GLY:HA2	1.99	0.43
1:B:255:GLN:HA	1:B:256:PRO:HD2	1.75	0.43
1:B:324:GLN:NE2	1:B:359:LEU:HA	2.33	0.43
1:B:348:ASN:ND2	1:B:350:SER:H	2.16	0.43
2:A:627:HOH:O	1:B:55:GLN:HG2	2.19	0.43
1:A:301:GLN:NE2	2:A:832:HOH:O	2.47	0.42
1:A:432:VAL:HG22	1:A:433:GLY:N	2.34	0.42
1:B:64:THR:OG1	1:B:292:ASP:OD1	2.32	0.42
1:B:224:ALA:HB2	1:B:264:GLY:HA2	2.00	0.42
1:B:172:THR:HB	1:B:173:PRO:HD3	2.02	0.42
1:A:76:LYS:NZ	1:A:76:LYS:HB3	2.35	0.42
1:A:275:PRO:HG2	1:A:278:VAL:HG23	2.02	0.42
1:B:508:ARG:O	1:B:525:GLU:O	2.38	0.42
1:B:509:SER:HA	1:B:524:ALA:HB1	2.02	0.42
1:A:346:TYR:OH	1:A:512:ARG:HD3	2.20	0.42
1:B:460:TYR:CD1	1:B:460:TYR:C	2.97	0.42
2:A:626:HOH:O	1:B:57:LYS:HE2	2.19	0.42
1:B:38:TYR:O	1:B:41:PHE:HB3	2.20	0.41
1:B:241:HIS:CE1	1:B:242:LYS:HG3	2.54	0.41
1:B:295:ARG:HG2	1:B:391:HIS:HB2	2.02	0.41
1:A:31:MET:CG	1:A:36:LEU:HD13	2.50	0.41
1:A:368:THR:HG22	1:A:369:GLY:N	2.35	0.41
1:A:465:ASN:HA	1:A:532:VAL:HG21	2.02	0.41
1:A:408:LYS:HA	1:A:409:PRO:HD2	1.96	0.41
1:B:30:ARG:O	1:B:31:MET:HB3	2.21	0.41
1:B:52:LYS:HD3	1:B:129:LEU:HA	2.03	0.41
1:B:52:LYS:HG3	1:B:133:ALA:HB2	2.03	0.41
1:A:61:VAL:HG11	1:A:152:THR:HG21	2.02	0.41
1:A:136:VAL:HG11	1:A:182:LEU:CD1	2.51	0.41
1:A:259:LEU:HD13	1:A:260:ASN:ND2	2.36	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:279:LYS:HA	1:B:280:PRO:HD2	1.87	0.41
1:B:331:ASP:HA	1:B:332:PRO:HD2	1.97	0.41
1:B:364:ARG:HG3	1:B:376:GLU:OE1	2.20	0.40
1:B:3:ILE:HG23	1:B:4:GLU:N	2.36	0.40
1:A:356:GLU:O	1:A:360:LYS:HA	2.21	0.40
1:A:521:ARG:HG2	1:A:521:ARG:HH11	1.84	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	503/544 (92%)	487 (97%)	13 (3%)	3 (1%)	21	11
1	B	451/544 (83%)	432 (96%)	18 (4%)	1 (0%)	43	37
All	All	954/1088 (88%)	919 (96%)	31 (3%)	4 (0%)	30	22

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	20	VAL
1	A	19	GLY
1	A	31	MET
1	B	19	GLY

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	442/480 (92%)	437 (99%)	5 (1%)	65	60
1	B	396/480 (82%)	393 (99%)	3 (1%)	73	71
All	All	838/960 (87%)	830 (99%)	8 (1%)	68	64

All (8) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	81	LEU
1	A	143	GLU
1	A	170	PHE
1	A	338	ASN
1	A	413	ASN
1	B	170	PHE
1	B	371	LYS
1	B	410	ASN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (26) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	98	ASN
1	A	120	ASN
1	A	134	ASN
1	A	260	ASN
1	A	282	ASN
1	A	324	GLN
1	A	325	GLN
1	A	338	ASN
1	A	343	GLN
1	A	482	ASN
1	A	494	GLN
1	A	503	GLN
1	A	506	ASN
1	A	529	GLN
1	A	531	ASN
1	B	5	GLN
1	B	55	GLN
1	B	134	ASN
1	B	161	ASN
1	B	204	GLN

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Mol	Chain	Res	Type
1	B	255	GLN
1	B	277	ASN
1	B	343	GLN
1	B	348	ASN
1	B	375	HIS
1	B	410	ASN

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](#)

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	519/544 (95%)	0.33	43 (8%)	17 19	12, 25, 50, 60	0
1	B	461/544 (84%)	0.19	37 (8%)	18 20	12, 23, 47, 60	0
All	All	980/1088 (90%)	0.26	80 (8%)	17 19	12, 24, 50, 60	0

All (80) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	490	PRO	5.5
1	B	510	PHE	5.0
1	B	463	LEU	4.9
1	B	527	ASP	4.8
1	B	524	ALA	4.4
1	B	464	PRO	4.2
1	B	370	VAL	4.0
1	A	68	ASN	4.0
1	A	103	PRO	3.7
1	B	526	ALA	3.7
1	A	20	VAL	3.7
1	B	346	TYR	3.5
1	B	209	ILE	3.4
1	B	368	THR	3.2
1	B	348	ASN	3.2
1	B	369	GLY	3.2
1	A	333	THR	3.1
1	B	372	HIS	3.1
1	A	17	PRO	3.1
1	B	345	ALA	3.0
1	B	462	ASP	3.0
1	B	103	PRO	2.8
1	B	347	ALA	2.8
1	A	483	ALA	2.8

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Mol	Chain	Res	Type	RSRZ
1	A	330	ILE	2.8
1	A	480	THR	2.8
1	B	367	PRO	2.8
1	A	407	TYR	2.7
1	A	413	ASN	2.7
1	A	215	GLU	2.7
1	A	66	SER	2.7
1	B	327	PHE	2.7
1	A	481	THR	2.7
1	A	30	ARG	2.7
1	B	350	SER	2.7
1	A	25	GLY	2.6
1	A	329	GLN	2.6
1	A	209	ILE	2.6
1	A	26	THR	2.6
1	A	257	ASN	2.6
1	B	506	ASN	2.6
1	A	19	GLY	2.5
1	B	365	CYS	2.5
1	B	461	THR	2.5
1	A	31	MET	2.5
1	A	487	LEU	2.5
1	B	509	SER	2.5
1	A	65	ALA	2.5
1	A	409	PRO	2.5
1	A	492	GLY	2.4
1	B	349	GLY	2.4
1	A	69	PRO	2.4
1	B	358	VAL	2.4
1	A	113	SER	2.4
1	A	261	PHE	2.3
1	B	344	THR	2.3
1	A	100	SER	2.3
1	A	478	PHE	2.2
1	B	214	ASN	2.2
1	B	1	MET	2.2
1	B	508	ARG	2.2
1	B	525	GLU	2.2
1	B	336	SER	2.2
1	A	35	LYS	2.2
1	A	110	GLU	2.1
1	A	101	PRO	2.1

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Mol	Chain	Res	Type	RSRZ
1	B	241	HIS	2.1
1	A	11	LEU	2.1
1	A	410	ASN	2.1
1	A	526	ALA	2.1
1	A	72	ASP	2.1
1	A	23	THR	2.0
1	B	101	PRO	2.0
1	A	4	GLU	2.0
1	A	514	SER	2.0
1	B	102	SER	2.0
1	A	3	ILE	2.0
1	A	21	THR	2.0
1	B	26	THR	2.0
1	B	333	THR	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 oligosaccharides 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.