



Full wwPDB X-ray Structure Validation Report ⓘ

Apr 24, 2026 – 09:36 PM EDT

PDB ID : 1DC3 / pdb_00001dc3
Title : STRUCTURAL ANALYSIS OF GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE FROM ESCHERICHIA COLI: DIRECT EVIDENCE FOR SUBSTRATE BINDING AND COFACTOR-INDUCED CONFORMATIONAL CHANGES
Authors : Yun, M.; Park, C.G.; Kim, J.Y.; Park, H.W.
Deposited on : 1999-11-04
Resolution : 2.50 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

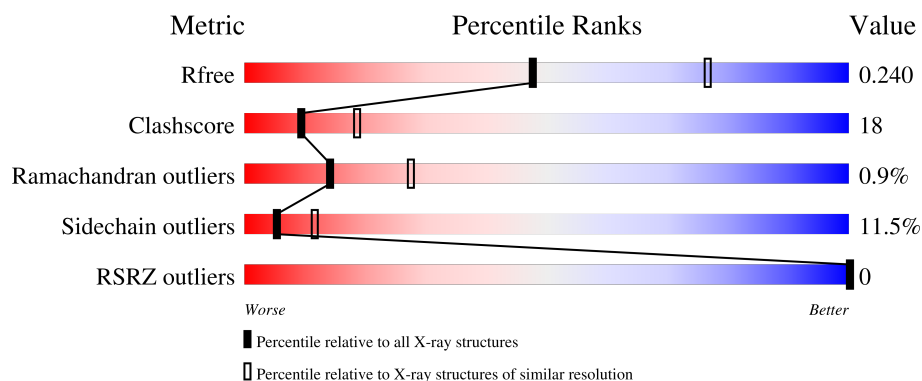
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.50 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	5829 (2.50-2.50)
Clashscore	190562	6492 (2.50-2.50)
Ramachandran outliers	187476	6378 (2.50-2.50)
Sidechain outliers	187428	6380 (2.50-2.50)
RSRZ outliers	180081	5833 (2.50-2.50)

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	330	 59% 36% 5%
1	B	330	 62% 32% 6%

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 5183 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 GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	330	Total	C	N	O	S	0	0	0
			2488	1563	431	484	10			
1	B	330	Total	C	N	O	S	0	0	0
			2488	1563	431	484	10			

- Molecule 2 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	103	Total	O	0	0
			103	103		
2	B	104	Total	O	0	0
			104	104		

4 Data and refinement statistics

Property	Value	Source
Space group	I 41	Depositor
Cell constants a, b, c, α , β , γ	119.57Å 119.57Å 158.55Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	20.00 – 2.50 20.00 – 2.50	Depositor EDS
% Data completeness (in resolution range)	(Not available) (20.00-2.50) 95.4 (20.00-2.50)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	7.94 (at 2.50Å)	Xtriage
Refinement program	X-PLOR	Depositor
R, R_{free}	0.189 , 0.241 0.189 , 0.240	Depositor DCC
R_{free} test set	1861 reflections (5.08%)	wwPDB-VP
Wilson B-factor (Å ²)	25.6	Xtriage
Anisotropy	0.180	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.37 , 18.3	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	0.490 for -h,k,-l	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	5183	wwPDB-VP
Average B, all atoms (Å ²)	26.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.60% 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	0.50	0/2527	0.98	7/3421 (0.2%)
1	B	0.52	0/2527	1.00	10/3421 (0.3%)
All	All	0.51	0/5054	0.99	17/6842 (0.2%)

There are no bond length outliers.

All (17) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	203	ILE	N-CA-C	-10.65	91.61	107.37
1	B	203	ILE	N-CA-C	-10.12	92.40	107.37
1	B	278	VAL	N-CA-C	7.99	118.75	110.05
1	B	15	VAL	N-CA-C	-7.63	103.01	110.72
1	A	15	VAL	N-CA-C	-7.52	103.12	110.72
1	B	204	ILE	N-CA-C	7.38	114.86	107.55
1	A	109	ILE	N-CA-C	-6.92	104.02	110.53
1	A	202	ASN	N-CA-C	6.84	119.81	109.41
1	B	202	ASN	N-CA-C	6.68	119.56	109.41
1	B	82	LEU	N-CA-C	6.65	121.40	113.16
1	A	204	ILE	N-CA-C	6.48	114.53	107.60
1	B	109	ILE	N-CA-C	-6.37	104.55	110.53
1	A	168	ILE	N-CA-C	-6.13	104.77	110.53
1	B	190	HIS	N-CA-C	6.08	118.68	111.33
1	B	280	SER	N-CA-C	5.87	118.43	111.33
1	A	280	SER	N-CA-C	5.82	117.62	111.28
1	B	112	GLY	N-CA-C	5.03	122.25	115.00

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	2488	0	2506	93	0
1	B	2488	0	2506	91	0
2	A	103	0	0	6	0
2	B	104	0	0	2	0
All	All	5183	0	5012	180	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 18.

All (180) 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:77:ARG:HH11	1:B:77:ARG:HB3	1.19	1.03
1:B:115:LYS:HG2	1:B:142:ASP:HA	1.48	0.95
1:B:83:LYS:HB3	1:B:86:GLU:HG3	1.51	0.92
1:A:83:LYS:HB3	1:A:86:GLU:HG3	1.64	0.79
1:B:41:ALA:O	1:B:45:LYS:HG3	1.83	0.78
1:B:77:ARG:HB3	1:B:77:ARG:NH1	1.99	0.73
1:A:87:VAL:HG13	1:A:89:VAL:HG23	1.69	0.72
1:A:11:ILE:HD11	2:A:2205:HOH:O	1.89	0.72
1:A:245:ARG:HD2	1:B:245:ARG:HD2	1.71	0.71
1:B:169:GLU:OE2	1:B:245:ARG:HD3	1.93	0.68
1:B:104:THR:O	1:B:107:LYS:HG3	1.92	0.67
1:A:131:GLY:O	1:A:267:MET:HE2	1.93	0.67
1:A:245:ARG:CD	1:B:245:ARG:HD2	2.25	0.67
1:B:155:ALA:HB3	1:B:156:PRO:HD3	1.76	0.67
1:A:122:SER:OG	1:A:125:THR:HB	1.94	0.67
1:B:266:GLU:HG2	1:B:267:MET:HG3	1.77	0.66
1:A:60:LYS:HD2	1:A:65:ILE:HG13	1.77	0.65
1:B:109:ILE:HD13	1:B:114:LYS:O	1.96	0.65
1:B:267:MET:CE	1:B:271:LEU:HD22	2.27	0.65
1:B:87:VAL:HG13	1:B:89:VAL:HG23	1.79	0.64
1:B:64:LEU:C	1:B:65:ILE:HD13	2.23	0.64
1:B:79:PRO:O	1:B:82:LEU:HD12	1.97	0.64
1:B:77:ARG:HH11	1:B:77:ARG:CB	2.03	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:83:LYS:HA	2:B:2135:HOH:O	1.98	0.62
1:A:83:LYS:HD2	1:A:86:GLU:OE2	2.00	0.62
1:B:130:LYS:HD2	1:B:270:VAL:CG2	2.31	0.61
1:A:172:MET:HE1	1:A:208:THR:HG21	1.82	0.61
1:B:83:LYS:HB3	1:B:86:GLU:CG	2.28	0.60
1:A:74:THR:HG23	2:A:2059:HOH:O	2.01	0.60
1:A:200:SER:HA	1:A:233:PRO:HB3	1.82	0.60
1:B:146:ASN:HD22	1:B:324:LEU:HD22	1.66	0.60
1:A:9:GLY:O	1:A:13:ARG:HG3	2.01	0.60
1:A:58:GLU:OE1	1:A:60:LYS:HE3	2.02	0.59
1:B:107:LYS:HA	1:B:110:THR:HB	1.84	0.59
1:B:10:ARG:HH11	1:B:13:ARG:NH2	2.00	0.58
1:B:267:MET:HE3	1:B:271:LEU:HB2	1.84	0.58
1:A:38:ASP:HA	1:A:59:VAL:HG21	1.85	0.58
1:A:78:ASP:HB3	1:A:81:ASN:HD21	1.69	0.58
1:A:299:ALA:CB	1:A:305:VAL:HG12	2.34	0.57
1:A:146:ASN:HD22	1:A:324:LEU:HD22	1.68	0.57
1:A:275:GLU:O	1:A:295:LYS:HD2	2.04	0.57
1:B:72:ARG:HD3	1:B:74:THR:HG23	1.84	0.57
1:B:176:HIS:HA	1:B:238:SER:HB3	1.85	0.57
1:B:64:LEU:O	1:B:65:ILE:HD13	2.05	0.57
1:B:200:SER:HA	1:B:233:PRO:HB3	1.87	0.57
1:A:154:LEU:HG	1:A:214:VAL:HG21	1.87	0.56
1:B:9:GLY:O	1:B:13:ARG:HG3	2.06	0.55
1:A:87:VAL:HG22	1:A:87:VAL:O	2.07	0.55
1:A:100:LEU:HB2	1:A:122(A):LYS:HG3	1.89	0.55
1:A:137:TYR:CE2	1:A:328:ILE:HA	2.42	0.55
1:B:189:SER:HB3	1:B:192:ASP:O	2.05	0.55
1:A:82:LEU:HD13	1:A:84:TRP:CZ2	2.41	0.55
1:A:125:THR:HG21	1:A:143:ILE:HG22	1.88	0.54
1:A:169:GLU:OE2	1:A:245:ARG:HD3	2.07	0.54
1:B:58:GLU:HG2	1:B:65:ILE:HB	1.90	0.54
1:B:262:ALA:HB1	1:B:267:MET:HE2	1.90	0.54
1:B:87:VAL:HG22	1:B:87:VAL:O	2.07	0.54
1:A:176:HIS:HB3	1:A:231:ARG:HD3	1.88	0.54
1:B:1:ILE:HD12	1:B:24:ASP:O	2.07	0.54
1:B:125:THR:CG2	1:B:143:ILE:HG22	2.37	0.54
1:A:232:VAL:HG11	1:B:232:VAL:HG11	1.90	0.54
1:A:251:THR:OG1	1:A:254:GLN:HG3	2.09	0.53
1:A:79:PRO:HA	1:A:82:LEU:CD1	2.39	0.53
1:A:123:ASP:CG	1:A:124:ASN:H	2.17	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:115:LYS:HG2	1:A:142:ASP:HA	1.90	0.53
1:A:102:ASP:O	1:A:106:ARG:HB2	2.09	0.52
1:A:245:ARG:NE	1:B:245:ARG:HD2	2.23	0.52
1:B:115:LYS:HG2	1:B:142:ASP:CA	2.31	0.52
1:A:72:ARG:HD3	1:A:74:THR:CG2	2.39	0.52
1:A:84:TRP:HB3	1:A:89:VAL:HB	1.91	0.52
1:A:5:ILE:HD11	1:A:27:ILE:HD12	1.92	0.52
1:B:125:THR:HG21	1:B:143:ILE:HG22	1.90	0.52
1:B:172:MET:HE1	1:B:208:THR:HG21	1.92	0.51
1:B:118:MET:HE3	1:B:125:THR:HG21	1.92	0.51
1:A:171:LEU:HA	1:A:226:THR:O	2.10	0.51
1:A:209:GLY:O	1:A:210:ALA:C	2.53	0.51
1:A:172:MET:CE	1:A:208:THR:HG21	2.40	0.50
1:A:298:ILE:HG13	1:A:299:ALA:N	2.25	0.50
1:B:134:PHE:O	1:B:327:HIS:HE1	1.93	0.50
1:A:169:GLU:OE2	1:A:245:ARG:NH1	2.42	0.50
1:B:72:ARG:NH2	1:B:83:LYS:O	2.44	0.50
1:B:109:ILE:HA	1:B:113:ALA:O	2.10	0.50
1:A:10:ARG:HH11	1:A:13:ARG:NH2	2.10	0.50
1:A:133:ASN:HB2	1:A:136:LYS:HG3	1.94	0.50
1:B:95:ALA:HA	1:B:119:THR:OG1	2.11	0.50
1:B:137:TYR:CE2	1:B:328:ILE:HA	2.47	0.49
1:A:162:ASN:HB2	1:A:167:ILE:HD12	1.95	0.49
1:B:0:THR:HG22	1:B:23:SER:O	2.13	0.49
1:B:80:ALA:HB2	1:B:107:LYS:HE2	1.93	0.49
1:B:109:ILE:HG23	1:B:113:ALA:O	2.12	0.49
1:A:41:ALA:O	1:A:45:LYS:HG3	2.13	0.49
1:A:217:VAL:HG23	1:A:218:LEU:HG	1.95	0.49
1:B:289:THR:HG23	1:B:320:LYS:HD3	1.95	0.48
1:B:176:HIS:HB3	1:B:231:ARG:HD3	1.96	0.48
1:A:118:MET:HE3	1:A:125:THR:HG21	1.96	0.48
1:A:182:GLN:HB3	2:A:2002:HOH:O	2.13	0.48
1:A:126:PRO:HB2	1:A:128:PHE:CE2	2.48	0.48
1:A:289:THR:HG23	1:A:320:LYS:HD3	1.96	0.47
1:A:72:ARG:NH2	1:A:83:LYS:O	2.47	0.47
1:A:106:ARG:NH1	1:A:106:ARG:HG3	2.29	0.47
1:A:219:PRO:O	1:A:222:ASN:HB2	2.14	0.47
1:B:259:VAL:HG11	1:B:292:PHE:CG	2.50	0.47
1:A:245:ARG:HA	1:A:303:ASN:O	2.14	0.47
1:B:237:VAL:HG22	1:B:312:ASP:HA	1.97	0.47
1:A:169:GLU:CG	1:A:245:ARG:HD3	2.44	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:115:LYS:CG	1:A:142:ASP:HA	2.44	0.47
1:B:267:MET:HE2	1:B:271:LEU:HD22	1.96	0.47
1:B:3:VAL:HB	1:B:27:ILE:HD13	1.97	0.47
1:B:267:MET:HE3	1:B:271:LEU:CB	2.44	0.47
1:B:25:ILE:HG23	1:B:26:GLU:N	2.30	0.47
1:A:124:ASN:HB2	2:A:2073:HOH:O	2.14	0.46
1:A:123:ASP:CG	1:A:124:ASN:N	2.74	0.46
1:A:134:PHE:O	1:A:327:HIS:HE1	1.99	0.46
1:B:171:LEU:HD23	1:B:226:THR:HG22	1.98	0.46
1:A:58:GLU:HG2	1:A:65:ILE:HB	1.97	0.46
1:B:115:LYS:HE2	1:B:137:TYR:OH	2.15	0.46
1:B:7:GLY:HA3	1:B:96:THR:HG22	1.98	0.45
1:A:211:ALA:CB	1:A:226:THR:HA	2.46	0.45
1:B:217:VAL:HG23	1:B:218:LEU:HG	1.98	0.45
1:A:106:ARG:HG3	1:A:106:ARG:HH11	1.82	0.45
1:A:134:PHE:O	1:A:327:HIS:CE1	2.69	0.45
1:B:215:GLY:O	1:B:219:PRO:HA	2.17	0.45
1:B:38:ASP:HA	1:B:59:VAL:HG21	1.98	0.45
1:B:154:LEU:CD2	1:B:214:VAL:HG21	2.47	0.44
1:A:155:ALA:HB3	1:A:156:PRO:HD3	1.99	0.44
1:B:25:ILE:HD11	1:B:325:ILE:CG2	2.48	0.44
1:B:0:THR:O	1:B:2:LYS:HE3	2.18	0.44
1:B:327:HIS:O	1:B:330:LYS:HB2	2.18	0.44
1:B:56:THR:OG1	1:B:67:ASN:HA	2.17	0.44
1:B:102:ASP:CG	1:B:106:ARG:HH21	2.25	0.44
1:B:0:THR:OG1	1:B:2:LYS:HE2	2.18	0.44
1:A:283:PHE:CE1	1:A:291:VAL:HG11	2.53	0.44
1:A:109:ILE:HA	1:A:113:ALA:O	2.17	0.43
1:A:253:GLU:OE2	1:A:256:LYS:HE2	2.17	0.43
1:B:190:HIS:CD2	1:B:190:HIS:H	2.35	0.43
1:B:10:ARG:HH11	1:B:13:ARG:HH21	1.64	0.43
1:B:79:PRO:HA	1:B:82:LEU:CD1	2.48	0.43
1:A:130:LYS:HG2	1:A:270:VAL:CG2	2.49	0.43
1:A:253:GLU:CD	1:A:256:LYS:HE2	2.44	0.43
1:B:91:VAL:HA	1:B:115:LYS:O	2.18	0.43
1:A:259:VAL:HG11	1:A:292:PHE:CB	2.48	0.43
1:B:83:LYS:HD3	1:B:86:GLU:OE1	2.17	0.43
1:B:44:LEU:O	1:B:53:PHE:HB2	2.19	0.43
1:A:63:HIS:HA	1:A:73:VAL:HG23	2.00	0.43
1:B:85:ASP:OD2	1:B:86:GLU:N	2.51	0.43
1:A:215:GLY:O	1:A:219:PRO:HA	2.19	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:25:ILE:HD11	1:B:325:ILE:HG22	1.99	0.43
1:B:211:ALA:CB	1:B:226:THR:HA	2.49	0.42
1:B:135:ASP:OD1	1:B:135:ASP:N	2.50	0.42
1:B:82:LEU:O	1:B:83:LYS:C	2.62	0.42
1:A:63:HIS:CE1	2:A:2188:HOH:O	2.72	0.42
1:A:78:ASP:HA	1:A:79:PRO:HD2	1.85	0.42
1:A:83:LYS:CB	1:A:86:GLU:HG3	2.44	0.42
1:B:107:LYS:HE2	1:B:107:LYS:HB3	1.79	0.42
1:B:122:SER:OG	1:B:125:THR:HB	2.19	0.42
1:A:125:THR:CG2	1:A:143:ILE:HG22	2.49	0.42
1:B:2:LYS:HA	1:B:2:LYS:HD3	1.78	0.42
1:B:312:ASP:C	1:B:314:GLU:H	2.28	0.42
1:B:7:GLY:CA	1:B:96:THR:HG22	2.49	0.42
1:B:266:GLU:HG2	1:B:267:MET:N	2.33	0.42
1:A:41:ALA:HB2	1:A:64:LEU:HD11	2.01	0.41
1:A:320:LYS:HA	1:A:323:ASP:HB2	2.02	0.41
1:B:102:ASP:OD1	1:B:106:ARG:NH2	2.54	0.41
1:A:78:ASP:HB3	1:A:81:ASN:ND2	2.33	0.41
1:A:96:THR:OG1	1:A:98:LEU:HB2	2.21	0.41
1:A:165:PHE:CD1	1:A:250:ALA:HB2	2.55	0.41
1:A:213:ALA:O	1:A:217:VAL:HG13	2.20	0.41
1:A:245:ARG:HB3	2:A:2076:HOH:O	2.21	0.41
1:A:299:ALA:HB1	1:A:305:VAL:HG12	2.02	0.41
1:B:198:GLY:O	1:B:202:ASN:ND2	2.48	0.41
1:A:91:VAL:HG11	1:A:325:ILE:HG12	2.03	0.41
1:A:61:ASP:C	1:A:63:HIS:N	2.79	0.40
1:A:221:LEU:O	1:A:224:LYS:HB2	2.21	0.40
1:A:238:SER:HB2	1:A:311:TYR:CZ	2.56	0.40
1:B:11:ILE:O	1:B:15:VAL:HG23	2.21	0.40
1:B:78:ASP:HB3	2:B:2170:HOH:O	2.21	0.40
1:A:109:ILE:H	1:A:109:ILE:HG12	1.75	0.40
1:A:259:VAL:HG11	1:A:292:PHE:CG	2.57	0.40
1:A:44:LEU:O	1:A:53:PHE:HB2	2.21	0.40
1:A:330:LYS:NZ	1:A:330:LYS:CB	2.85	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	328/330 (99%)	298 (91%)	27 (8%)	3 (1%)	14	27
1	B	328/330 (99%)	298 (91%)	27 (8%)	3 (1%)	14	27
All	All	656/660 (99%)	596 (91%)	54 (8%)	6 (1%)	14	27

All (6) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	210	ALA
1	A	237	VAL
1	B	186	ASP
1	B	237	VAL
1	A	186	ASP
1	B	313	ASN

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	265/265 (100%)	234 (88%)	31 (12%)	5	11
1	B	265/265 (100%)	235 (89%)	30 (11%)	5	12
All	All	530/530 (100%)	469 (88%)	61 (12%)	5	11

All (61) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	2	LYS
1	A	3	VAL
1	A	21	LYS
1	A	22	ARG
1	A	25	ILE
1	A	45	LYS
1	A	57	VAL
1	A	64	LEU
1	A	69	LYS
1	A	70	LYS
1	A	81	ASN
1	A	83	LYS
1	A	98	LEU
1	A	106	ARG
1	A	109	ILE
1	A	115	LYS
1	A	134	PHE
1	A	159	LYS
1	A	172	MET
1	A	181	THR
1	A	207	SER
1	A	217	VAL
1	A	240	VAL
1	A	244	VAL
1	A	248	LYS
1	A	256	LYS
1	A	266	GLU
1	A	289	THR
1	A	298	ILE
1	A	325	ILE
1	A	330	LYS
1	B	2	LYS
1	B	21	LYS
1	B	23	SER
1	B	25	ILE
1	B	26	GLU
1	B	34	LEU
1	B	45	LYS
1	B	57	VAL
1	B	58	GLU
1	B	61	ASP
1	B	69	LYS
1	B	70	LYS

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Mol	Chain	Res	Type
1	B	71	ILE
1	B	72	ARG
1	B	77	ARG
1	B	109	ILE
1	B	110	THR
1	B	130	LYS
1	B	172	MET
1	B	181	THR
1	B	189	SER
1	B	207	SER
1	B	216	LYS
1	B	224	LYS
1	B	225	LEU
1	B	247	GLU
1	B	248	LYS
1	B	266	GLU
1	B	289	THR
1	B	298	ILE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (9) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	81	ASN
1	A	146	ASN
1	A	236	ASN
1	A	303	ASN
1	A	327	HIS
1	B	81	ASN
1	B	146	ASN
1	B	303	ASN
1	B	327	HIS

5.3.3 RNA ⓘ

There are no RNA molecules 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 [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 [i](#)

6.1 Protein, DNA and RNA chains [i](#)

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	330/330 (100%)	-1.84	0 100 100	13, 24, 40, 48	0
1	B	330/330 (100%)	-1.84	0 100 100	12, 25, 39, 47	0
All	All	660/660 (100%)	-1.84	0 100 100	12, 25, 40, 48	0

There are no RSRZ outliers to report.

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 oligosaccharides 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.