



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 15, 2026 – 01:23 AM UTC

PDB ID : 7D97 / pdb_00007d97
Title : Crystal structure of N109P mutant of GATase subunit of Methanocaldococcus jannaschii GMP synthetase
Authors : Bellur, A.; Dongre, A.; Kavya, J.; Balaram, H.
Deposited on : 2020-10-12
Resolution : 1.89 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

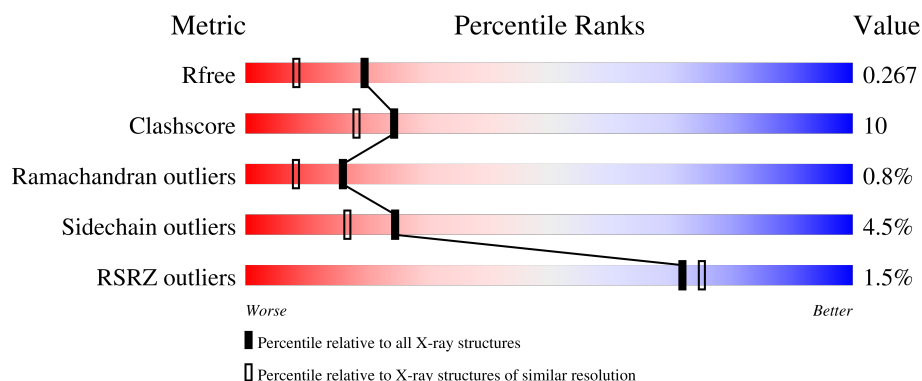
1 Overall quality at a glance ⓘ

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.89 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	7789 (1.90-1.90)
Clashscore	190562	8410 (1.90-1.90)
Ramachandran outliers	187476	8333 (1.90-1.90)
Sidechain outliers	187428	8333 (1.90-1.90)
RSRZ outliers	180081	7790 (1.90-1.90)

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 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	188	74% 24% ..
1	B	188	% 77% 19% .
1	C	188	4% 82% 15% ...
1	D	188	2% 77% 20% .

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 6253 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 GMP synthase [glutamine-hydrolyzing] subunit A.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	185	Total	C	N	O	S	0	0	0
			1423	919	236	261	7			
1	B	188	Total	C	N	O	S	0	0	0
			1414	908	235	264	7			
1	C	187	Total	C	N	O	S	0	0	0
			1399	898	232	262	7			
1	D	188	Total	C	N	O	S	0	0	0
			1432	921	235	269	7			

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	109	PRO	ASN	engineered mutation	UNP Q58970
B	109	PRO	ASN	engineered mutation	UNP Q58970
C	109	PRO	ASN	engineered mutation	UNP Q58970
D	109	PRO	ASN	engineered mutation	UNP Q58970

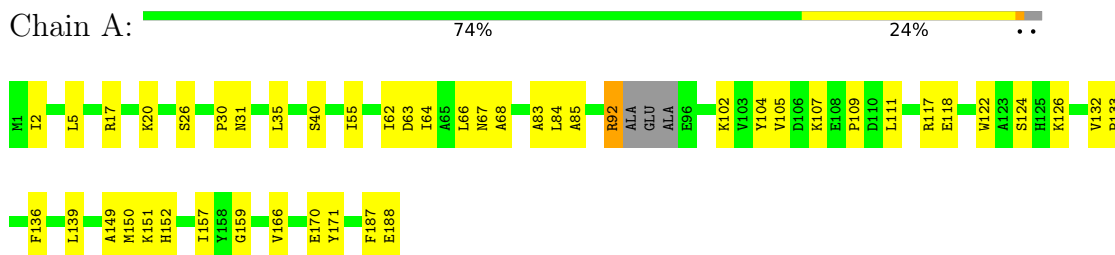
- Molecule 2 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	174	Total	O	0	0
			174	174		
2	B	154	Total	O	0	0
			154	154		
2	C	129	Total	O	0	0
			129	129		
2	D	128	Total	O	0	0
			128	128		

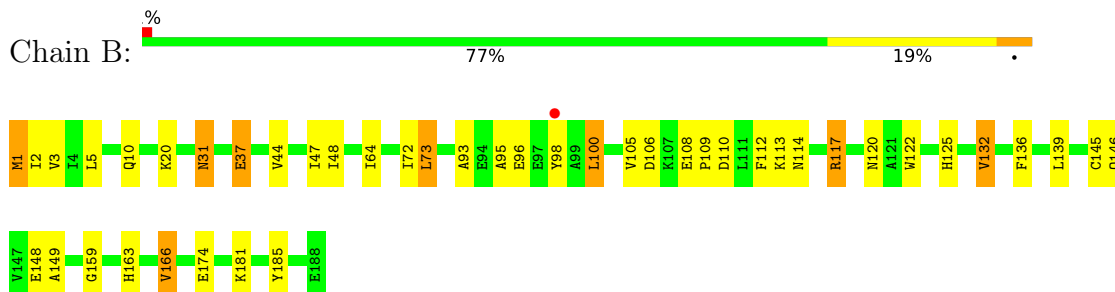
3 Residue-property plots [i](#)

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.

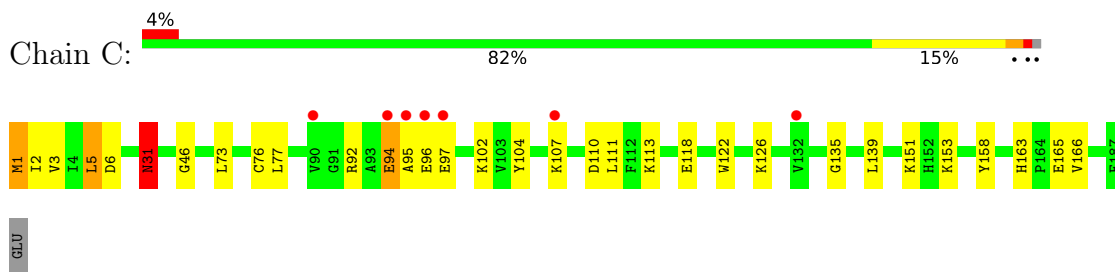
- Molecule 1: GMP synthase [glutamine-hydrolyzing] subunit A



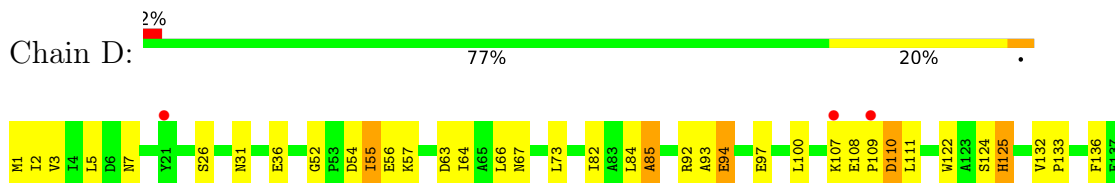
- Molecule 1: GMP synthase [glutamine-hydrolyzing] subunit A



- Molecule 1: GMP synthase [glutamine-hydrolyzing] subunit A



- Molecule 1: GMP synthase [glutamine-hydrolyzing] subunit A





4 Data and refinement statistics

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α , β , γ	35.50Å 68.05Å 75.35Å 90.95° 90.47° 91.45°	Depositor
Resolution (Å)	35.49 – 1.89 35.49 – 1.89	Depositor EDS
% Data completeness (in resolution range)	85.3 (35.49-1.89) 94.0 (35.49-1.89)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.28 (at 1.89Å)	Xtriage
Refinement program	REFMAC 5.8.0238	Depositor
R, R_{free}	0.204 , 0.264 0.210 , 0.267	Depositor DCC
R_{free} test set	2597 reflections (4.59%)	wwPDB-VP
Wilson B-factor (Å ²)	12.4	Xtriage
Anisotropy	0.058	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 37.4	EDS
L-test for twinning ²	$\langle L \rangle = 0.52$, $\langle L^2 \rangle = 0.37$	Xtriage
Estimated twinning fraction	0.035 for h,-k,-l 0.047 for -h,k,-l 0.055 for -h,-k,l	Xtriage
Reported twinning fraction	0.773 for H, K, L 0.089 for -h,-k,l 0.059 for h,-k,-l 0.080 for -H, K, -L	Depositor
Outliers	0 of 53050 reflections	Xtriage
F_o, F_c correlation	0.91	EDS
Total number of atoms	6253	wwPDB-VP
Average B, all atoms (Å ²)	14.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.00% 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	1.12	0/1454	1.42	2/1969 (0.1%)
1	B	1.17	0/1443	1.52	4/1961 (0.2%)
1	C	1.13	0/1430	1.41	2/1946 (0.1%)
1	D	1.10	0/1463	1.46	3/1985 (0.2%)
All	All	1.13	0/5790	1.45	11/7861 (0.1%)

There are no bond length outliers.

All (11) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	106	ASP	CB-CA-C	5.68	119.76	110.95
1	B	146	GLN	CB-CG-CD	-5.67	102.97	112.60
1	C	31	ASN	CA-CB-CG	5.63	118.23	112.60
1	A	30	PRO	CA-C-O	-5.50	115.18	121.56
1	B	73	LEU	CA-C-N	5.42	127.35	122.20
1	B	73	LEU	C-N-CA	5.42	127.35	122.20
1	A	62	ILE	CA-C-O	-5.40	115.06	121.05
1	D	125	HIS	CB-CA-C	5.28	120.49	111.46
1	C	110	ASP	CA-CB-CG	5.20	117.80	112.60
1	D	166	VAL	CA-C-N	5.09	127.10	120.28
1	D	166	VAL	C-N-CA	5.09	127.10	120.28

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	1423	0	1399	26	0
1	B	1414	0	1362	32	0
1	C	1399	0	1341	25	0
1	D	1432	0	1396	31	0
2	A	174	0	0	1	0
2	B	154	0	0	1	0
2	C	129	0	0	1	0
2	D	128	0	0	0	0
All	All	6253	0	5498	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 10.

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:B:10:GLN:OE1	1:B:10:GLN:CB	2.25	0.84
1:D:107:LYS:O	1:D:109:PRO:CD	2.30	0.80
1:B:108:GLU:HG3	2:B:227:HOH:O	1.84	0.77
1:D:109:PRO:O	1:D:110:ASP:HB2	1.86	0.76
1:D:107:LYS:O	1:D:109:PRO:N	2.22	0.71
1:B:31:ASN:HD22	1:B:31:ASN:C	1.98	0.71
1:D:93:ALA:HB3	1:D:125:HIS:O	1.92	0.69
1:B:10:GLN:OE1	1:B:10:GLN:NE2	2.26	0.69
1:D:107:LYS:O	1:D:109:PRO:HD3	1.93	0.68
1:C:163:HIS:ND1	1:C:165:GLU:OE2	2.26	0.68
1:C:113:LYS:CB	2:C:241:HOH:O	2.43	0.67
1:B:100:LEU:HD22	1:B:120:ASN:HB3	1.77	0.67
1:B:98:TYR:HB3	1:B:122:TRP:CZ2	2.30	0.66
1:A:122:TRP:CD1	1:A:166:VAL:HG21	2.33	0.64
1:D:55:ILE:HD11	1:D:84:LEU:HD12	1.81	0.63
1:C:5:LEU:HD23	1:C:31:ASN:HA	1.82	0.62
1:B:5:LEU:HD21	1:B:64:ILE:CD1	2.30	0.61
1:B:1:MET:HE3	1:B:2:ILE:C	2.25	0.61
1:B:110:ASP:O	1:B:113:LYS:CG	2.49	0.60
1:C:151:LYS:HD2	1:C:158:TYR:CE2	2.36	0.59
1:A:20:LYS:NZ	1:D:94:GLU:OE1	2.35	0.59
1:A:132:VAL:HG12	1:A:136:PHE:HB2	1.85	0.59
1:B:163:HIS:HB3	1:B:166:VAL:HG13	1.84	0.58
1:A:40:SER:OG	2:A:201:HOH:O	2.09	0.58
1:B:93:ALA:HB3	1:B:125:HIS:O	2.05	0.56
1:A:122:TRP:CG	1:A:166:VAL:HG21	2.42	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:5:LEU:HD21	1:B:64:ILE:HD13	1.89	0.55
1:D:1:MET:HE3	1:D:2:ILE:O	2.08	0.53
1:B:109:PRO:HB3	1:B:139:LEU:HD22	1.89	0.53
1:D:133:PRO:HB2	1:D:136:PHE:CD1	2.44	0.53
1:D:55:ILE:HD11	1:D:84:LEU:CD1	2.38	0.53
1:D:1:MET:HE1	1:D:3:VAL:HG23	1.90	0.52
1:B:122:TRP:CD1	1:B:166:VAL:HG21	2.45	0.52
1:C:92:ARG:HD2	1:C:126:LYS:O	2.09	0.52
1:B:95:ALA:HB3	1:B:125:HIS:HB2	1.90	0.52
1:D:1:MET:HE3	1:D:2:ILE:C	2.34	0.52
1:A:83:ALA:HB2	1:A:150:MET:HE1	1.91	0.52
1:A:105:VAL:HG11	1:A:117:ARG:HH11	1.74	0.52
1:B:1:MET:HE1	1:B:3:VAL:HG23	1.92	0.52
1:C:1:MET:HE3	1:C:2:ILE:O	2.10	0.51
1:D:63:ASP:OD1	1:D:67:ASN:ND2	2.34	0.51
1:A:149:ALA:HA	1:A:159:GLY:O	2.10	0.51
1:D:5:LEU:HD21	1:D:64:ILE:CD1	2.41	0.51
1:C:1:MET:HE1	1:C:3:VAL:CG2	2.41	0.50
1:B:105:VAL:HG11	1:B:117:ARG:HH21	1.76	0.50
1:C:163:HIS:O	1:C:166:VAL:HG22	2.12	0.50
1:D:139:LEU:HD21	1:D:151:LYS:HG2	1.92	0.50
1:B:31:ASN:C	1:B:31:ASN:ND2	2.68	0.49
1:A:5:LEU:HD21	1:A:64:ILE:CD1	2.43	0.49
1:D:109:PRO:O	1:D:110:ASP:CB	2.59	0.49
1:C:102:LYS:HE3	1:C:118:GLU:OE1	2.13	0.48
1:A:92:ARG:CD	1:A:126:LYS:O	2.61	0.48
1:C:1:MET:CE	1:C:2:ILE:C	2.87	0.48
1:A:92:ARG:HD2	1:A:126:LYS:O	2.14	0.48
1:D:56:GLU:OE2	1:D:56:GLU:HA	2.14	0.48
1:D:7:ASN:O	1:D:52:GLY:HA3	2.14	0.48
1:D:163:HIS:O	1:D:166:VAL:HG22	2.15	0.47
1:A:122:TRP:CB	1:A:166:VAL:HG21	2.45	0.47
1:D:1:MET:CE	1:D:2:ILE:C	2.88	0.47
1:B:105:VAL:HG11	1:B:117:ARG:NH2	2.30	0.46
1:A:107:LYS:C	1:A:109:PRO:HD3	2.40	0.46
1:B:149:ALA:HA	1:B:159:GLY:O	2.16	0.46
1:A:66:LEU:HD21	1:A:85:ALA:O	2.16	0.46
1:C:1:MET:HE1	1:C:3:VAL:HG22	1.98	0.46
1:C:73:LEU:HA	1:C:158:TYR:O	2.16	0.46
1:D:109:PRO:HB3	1:D:139:LEU:HD22	1.97	0.46
1:B:48:ILE:HA	1:B:73:LEU:O	2.16	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:104:TYR:CD1	1:A:118:GLU:HG2	2.52	0.45
1:A:139:LEU:HD11	1:A:151:LYS:CB	2.47	0.45
1:D:82:ILE:O	1:D:85:ALA:HB3	2.17	0.45
1:B:20:LYS:NZ	1:C:94:GLU:HA	2.32	0.44
1:C:102:LYS:HE3	1:C:118:GLU:CD	2.42	0.44
1:D:2:ILE:O	1:D:26:SER:HB2	2.18	0.44
1:D:66:LEU:HD23	1:D:66:LEU:HA	1.85	0.44
1:C:1:MET:HE2	1:C:2:ILE:C	2.42	0.44
1:A:2:ILE:O	1:A:26:SER:HA	2.17	0.44
1:B:117:ARG:HD3	1:B:117:ARG:HA	1.48	0.43
1:C:6:ASP:O	1:C:31:ASN:HB3	2.18	0.43
1:C:102:LYS:HD3	1:C:104:TYR:OH	2.18	0.43
1:A:35:LEU:HD11	1:A:68:ALA:HA	2.00	0.43
1:A:133:PRO:HB2	1:A:136:PHE:CD1	2.53	0.43
1:B:37:GLU:HG2	1:D:100:LEU:HG	2.01	0.43
1:C:139:LEU:HD11	1:C:151:LYS:HB2	2.01	0.43
1:B:1:MET:HE3	1:B:2:ILE:N	2.34	0.43
1:C:95:ALA:C	1:C:97:GLU:H	2.27	0.43
1:C:135:GLY:O	1:C:153:LYS:HB2	2.19	0.43
1:C:95:ALA:HB1	1:C:97:GLU:HG2	2.00	0.42
1:A:139:LEU:HD11	1:A:151:LYS:HB2	2.01	0.42
1:B:1:MET:HE1	1:B:44:VAL:HG22	2.00	0.42
1:B:114:ASN:HB2	1:B:174:GLU:HG2	2.01	0.42
1:A:187:PHE:O	1:A:188:GLU:C	2.63	0.42
1:A:5:LEU:HD21	1:A:64:ILE:HD13	2.01	0.42
1:B:181:LYS:HA	1:B:185:TYR:O	2.20	0.42
1:A:151:LYS:HA	1:A:157:ILE:O	2.20	0.42
1:D:54:ASP:OD2	1:D:57:LYS:HG2	2.20	0.42
1:D:122:TRP:CD1	1:D:166:VAL:HG21	2.55	0.41
1:C:2:ILE:HA	1:C:46:GLY:O	2.21	0.41
1:C:76:CYS:O	1:C:77:LEU:C	2.64	0.41
1:D:132:VAL:HG21	1:D:138:ILE:HG12	2.02	0.41
1:B:47:ILE:O	1:B:72:ILE:HA	2.20	0.41
1:B:145:CYS:HB3	1:B:148:GLU:OE2	2.21	0.41
1:D:97:GLU:O	1:D:124:SER:HA	2.21	0.41
1:A:151:LYS:HG2	1:A:152:HIS:O	2.21	0.41
1:B:109:PRO:HG2	1:B:112:PHE:HB2	2.01	0.41
1:B:132:VAL:HG13	1:B:136:PHE:HB2	2.03	0.40
1:C:122:TRP:CD1	1:C:166:VAL:HG21	2.56	0.40
1:D:1:MET:HE1	1:D:3:VAL:CG2	2.50	0.40
1:A:170:GLU:HB3	1:A:171:TYR:CD2	2.56	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:63:ASP:OD1	1:A:67:ASN:ND2	2.54	0.40
1:C:122:TRP:HB3	1:C:166:VAL:HG21	2.04	0.40
1:D:73:LEU:HA	1:D:158:TYR:O	2.22	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	181/188 (96%)	175 (97%)	6 (3%)	0	100	100
1	B	186/188 (99%)	179 (96%)	7 (4%)	0	100	100
1	C	185/188 (98%)	176 (95%)	6 (3%)	3 (2%)	7	2
1	D	186/188 (99%)	175 (94%)	8 (4%)	3 (2%)	7	2
All	All	738/752 (98%)	705 (96%)	27 (4%)	6 (1%)	16	8

All (6) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	D	108	GLU
1	D	110	ASP
1	C	94	GLU
1	C	107	LYS
1	D	85	ALA
1	C	96	GLU

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	147/160 (92%)	139 (95%)	8 (5%)	20	12
1	B	143/160 (89%)	135 (94%)	8 (6%)	19	11
1	C	142/160 (89%)	138 (97%)	4 (3%)	38	32
1	D	148/160 (92%)	142 (96%)	6 (4%)	27	19
All	All	580/640 (91%)	554 (96%)	26 (4%)	24	17

All (26) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	17	ARG
1	A	31	ASN
1	A	55	ILE
1	A	84	LEU
1	A	92	ARG
1	A	102	LYS
1	A	111	LEU
1	A	124	SER
1	B	1	MET
1	B	31	ASN
1	B	37	GLU
1	B	96	GLU
1	B	100	LEU
1	B	117	ARG
1	B	132	VAL
1	B	166	VAL
1	C	1	MET
1	C	5	LEU
1	C	31	ASN
1	C	111	LEU
1	D	31	ASN
1	D	36	GLU
1	D	55	ILE
1	D	92	ARG
1	D	94	GLU
1	D	111	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (12) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	7	ASN
1	A	80	GLN
1	A	114	ASN
1	A	161	GLN
1	B	31	ASN
1	B	168	HIS
1	C	16	HIS
1	C	31	ASN
1	C	114	ASN
1	D	13	HIS
1	D	31	ASN
1	D	114	ASN

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 ⓘ

There are no oligosaccharides 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 [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	185/188 (98%)	0.07	0 100 100	7, 11, 19, 26	0
1	B	188/188 (100%)	0.14	1 (0%) 87 89	6, 11, 20, 26	0
1	C	187/188 (99%)	0.41	7 (3%) 45 48	7, 15, 24, 44	0
1	D	188/188 (100%)	0.26	3 (1%) 70 74	7, 14, 22, 35	0
All	All	748/752 (99%)	0.22	11 (1%) 72 75	6, 13, 22, 44	0

All (11) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	95	ALA	6.0
1	D	107	LYS	3.4
1	C	94	GLU	3.1
1	C	96	GLU	2.7
1	D	21	TYR	2.6
1	D	109	PRO	2.6
1	C	107	LYS	2.5
1	B	98	TYR	2.4
1	C	97	GLU	2.4
1	C	90	VAL	2.3
1	C	132	VAL	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 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.