



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 6, 2026 – 04:13 PM UTC

PDB ID : 5UGJ / pdb_00005ugj
Title : Crystal structure of HTPA Reductase from neisseria meningitidis
Authors : Keown, J.K.; Richards, E.W.; Pearce, F.G.; Goldstone, D.C.
Deposited on : 2017-01-08
Resolution : 2.70 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

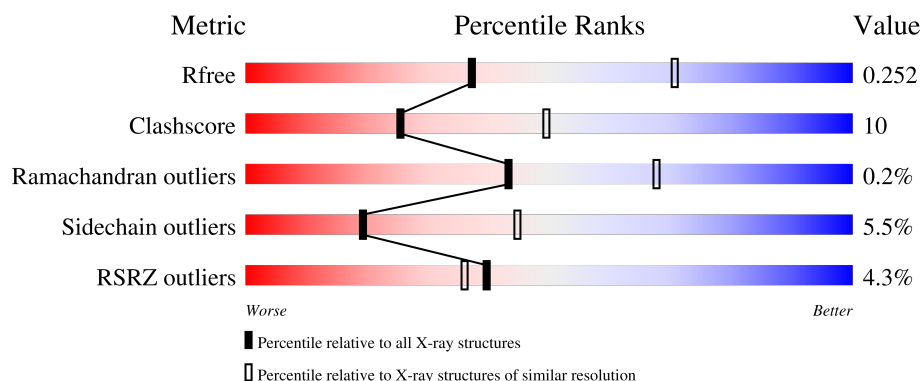
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.70 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	3538 (2.70-2.70)
Clashscore	190562	3843 (2.70-2.70)
Ramachandran outliers	187476	3778 (2.70-2.70)
Sidechain outliers	187428	3778 (2.70-2.70)
RSRZ outliers	180081	3538 (2.70-2.70)

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	302	8% 71% 14% • 13%
1	B	302	79% 7% • 12%
1	C	302	80% 8% • 12%
1	D	302	8% 70% 16% • 12%

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 7812 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 4-hydroxy-tetrahydrodipicolinate reductase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	263	Total	C	N	O	S	0	0	0
			1931	1207	345	373	6			
1	B	265	Total	C	N	O	S	0	0	0
			1941	1213	345	377	6			
1	C	266	Total	C	N	O	S	0	0	0
			1954	1220	349	379	6			
1	D	266	Total	C	N	O	S	0	0	0
			1950	1218	349	377	6			

There are 132 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-32	MET	-	initiating methionine	UNP Q9K1F1
A	-31	HIS	-	expression tag	UNP Q9K1F1
A	-30	HIS	-	expression tag	UNP Q9K1F1
A	-29	HIS	-	expression tag	UNP Q9K1F1
A	-28	HIS	-	expression tag	UNP Q9K1F1
A	-27	HIS	-	expression tag	UNP Q9K1F1
A	-26	HIS	-	expression tag	UNP Q9K1F1
A	-25	GLY	-	expression tag	UNP Q9K1F1
A	-24	LEU	-	expression tag	UNP Q9K1F1
A	-23	PRO	-	expression tag	UNP Q9K1F1
A	-22	ILE	-	expression tag	UNP Q9K1F1
A	-21	PRO	-	expression tag	UNP Q9K1F1
A	-20	ASN	-	expression tag	UNP Q9K1F1
A	-19	PRO	-	expression tag	UNP Q9K1F1
A	-18	LEU	-	expression tag	UNP Q9K1F1
A	-17	LEU	-	expression tag	UNP Q9K1F1
A	-16	GLY	-	expression tag	UNP Q9K1F1
A	-15	LEU	-	expression tag	UNP Q9K1F1
A	-14	ASP	-	expression tag	UNP Q9K1F1
A	-13	SER	-	expression tag	UNP Q9K1F1
A	-12	THR	-	expression tag	UNP Q9K1F1

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Chain	Residue	Modelled	Actual	Comment	Reference
A	-11	GLU	-	expression tag	UNP Q9K1F1
A	-10	ASN	-	expression tag	UNP Q9K1F1
A	-9	LEU	-	expression tag	UNP Q9K1F1
A	-8	TYR	-	expression tag	UNP Q9K1F1
A	-7	PHE	-	expression tag	UNP Q9K1F1
A	-6	GLN	-	expression tag	UNP Q9K1F1
A	-5	GLY	-	expression tag	UNP Q9K1F1
A	-4	ILE	-	expression tag	UNP Q9K1F1
A	-3	ASP	-	expression tag	UNP Q9K1F1
A	-2	PRO	-	expression tag	UNP Q9K1F1
A	-1	PHE	-	expression tag	UNP Q9K1F1
A	0	THR	-	expression tag	UNP Q9K1F1
B	-32	MET	-	initiating methionine	UNP Q9K1F1
B	-31	HIS	-	expression tag	UNP Q9K1F1
B	-30	HIS	-	expression tag	UNP Q9K1F1
B	-29	HIS	-	expression tag	UNP Q9K1F1
B	-28	HIS	-	expression tag	UNP Q9K1F1
B	-27	HIS	-	expression tag	UNP Q9K1F1
B	-26	HIS	-	expression tag	UNP Q9K1F1
B	-25	GLY	-	expression tag	UNP Q9K1F1
B	-24	LEU	-	expression tag	UNP Q9K1F1
B	-23	PRO	-	expression tag	UNP Q9K1F1
B	-22	ILE	-	expression tag	UNP Q9K1F1
B	-21	PRO	-	expression tag	UNP Q9K1F1
B	-20	ASN	-	expression tag	UNP Q9K1F1
B	-19	PRO	-	expression tag	UNP Q9K1F1
B	-18	LEU	-	expression tag	UNP Q9K1F1
B	-17	LEU	-	expression tag	UNP Q9K1F1
B	-16	GLY	-	expression tag	UNP Q9K1F1
B	-15	LEU	-	expression tag	UNP Q9K1F1
B	-14	ASP	-	expression tag	UNP Q9K1F1
B	-13	SER	-	expression tag	UNP Q9K1F1
B	-12	THR	-	expression tag	UNP Q9K1F1
B	-11	GLU	-	expression tag	UNP Q9K1F1
B	-10	ASN	-	expression tag	UNP Q9K1F1
B	-9	LEU	-	expression tag	UNP Q9K1F1
B	-8	TYR	-	expression tag	UNP Q9K1F1
B	-7	PHE	-	expression tag	UNP Q9K1F1
B	-6	GLN	-	expression tag	UNP Q9K1F1
B	-5	GLY	-	expression tag	UNP Q9K1F1
B	-4	ILE	-	expression tag	UNP Q9K1F1
B	-3	ASP	-	expression tag	UNP Q9K1F1

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Chain	Residue	Modelled	Actual	Comment	Reference
B	-2	PRO	-	expression tag	UNP Q9K1F1
B	-1	PHE	-	expression tag	UNP Q9K1F1
B	0	THR	-	expression tag	UNP Q9K1F1
C	-32	MET	-	initiating methionine	UNP Q9K1F1
C	-31	HIS	-	expression tag	UNP Q9K1F1
C	-30	HIS	-	expression tag	UNP Q9K1F1
C	-29	HIS	-	expression tag	UNP Q9K1F1
C	-28	HIS	-	expression tag	UNP Q9K1F1
C	-27	HIS	-	expression tag	UNP Q9K1F1
C	-26	HIS	-	expression tag	UNP Q9K1F1
C	-25	GLY	-	expression tag	UNP Q9K1F1
C	-24	LEU	-	expression tag	UNP Q9K1F1
C	-23	PRO	-	expression tag	UNP Q9K1F1
C	-22	ILE	-	expression tag	UNP Q9K1F1
C	-21	PRO	-	expression tag	UNP Q9K1F1
C	-20	ASN	-	expression tag	UNP Q9K1F1
C	-19	PRO	-	expression tag	UNP Q9K1F1
C	-18	LEU	-	expression tag	UNP Q9K1F1
C	-17	LEU	-	expression tag	UNP Q9K1F1
C	-16	GLY	-	expression tag	UNP Q9K1F1
C	-15	LEU	-	expression tag	UNP Q9K1F1
C	-14	ASP	-	expression tag	UNP Q9K1F1
C	-13	SER	-	expression tag	UNP Q9K1F1
C	-12	THR	-	expression tag	UNP Q9K1F1
C	-11	GLU	-	expression tag	UNP Q9K1F1
C	-10	ASN	-	expression tag	UNP Q9K1F1
C	-9	LEU	-	expression tag	UNP Q9K1F1
C	-8	TYR	-	expression tag	UNP Q9K1F1
C	-7	PHE	-	expression tag	UNP Q9K1F1
C	-6	GLN	-	expression tag	UNP Q9K1F1
C	-5	GLY	-	expression tag	UNP Q9K1F1
C	-4	ILE	-	expression tag	UNP Q9K1F1
C	-3	ASP	-	expression tag	UNP Q9K1F1
C	-2	PRO	-	expression tag	UNP Q9K1F1
C	-1	PHE	-	expression tag	UNP Q9K1F1
C	0	THR	-	expression tag	UNP Q9K1F1
D	-32	MET	-	initiating methionine	UNP Q9K1F1
D	-31	HIS	-	expression tag	UNP Q9K1F1
D	-30	HIS	-	expression tag	UNP Q9K1F1
D	-29	HIS	-	expression tag	UNP Q9K1F1
D	-28	HIS	-	expression tag	UNP Q9K1F1
D	-27	HIS	-	expression tag	UNP Q9K1F1

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Chain	Residue	Modelled	Actual	Comment	Reference
D	-26	HIS	-	expression tag	UNP Q9K1F1
D	-25	GLY	-	expression tag	UNP Q9K1F1
D	-24	LEU	-	expression tag	UNP Q9K1F1
D	-23	PRO	-	expression tag	UNP Q9K1F1
D	-22	ILE	-	expression tag	UNP Q9K1F1
D	-21	PRO	-	expression tag	UNP Q9K1F1
D	-20	ASN	-	expression tag	UNP Q9K1F1
D	-19	PRO	-	expression tag	UNP Q9K1F1
D	-18	LEU	-	expression tag	UNP Q9K1F1
D	-17	LEU	-	expression tag	UNP Q9K1F1
D	-16	GLY	-	expression tag	UNP Q9K1F1
D	-15	LEU	-	expression tag	UNP Q9K1F1
D	-14	ASP	-	expression tag	UNP Q9K1F1
D	-13	SER	-	expression tag	UNP Q9K1F1
D	-12	THR	-	expression tag	UNP Q9K1F1
D	-11	GLU	-	expression tag	UNP Q9K1F1
D	-10	ASN	-	expression tag	UNP Q9K1F1
D	-9	LEU	-	expression tag	UNP Q9K1F1
D	-8	TYR	-	expression tag	UNP Q9K1F1
D	-7	PHE	-	expression tag	UNP Q9K1F1
D	-6	GLN	-	expression tag	UNP Q9K1F1
D	-5	GLY	-	expression tag	UNP Q9K1F1
D	-4	ILE	-	expression tag	UNP Q9K1F1
D	-3	ASP	-	expression tag	UNP Q9K1F1
D	-2	PRO	-	expression tag	UNP Q9K1F1
D	-1	PHE	-	expression tag	UNP Q9K1F1
D	0	THR	-	expression tag	UNP Q9K1F1

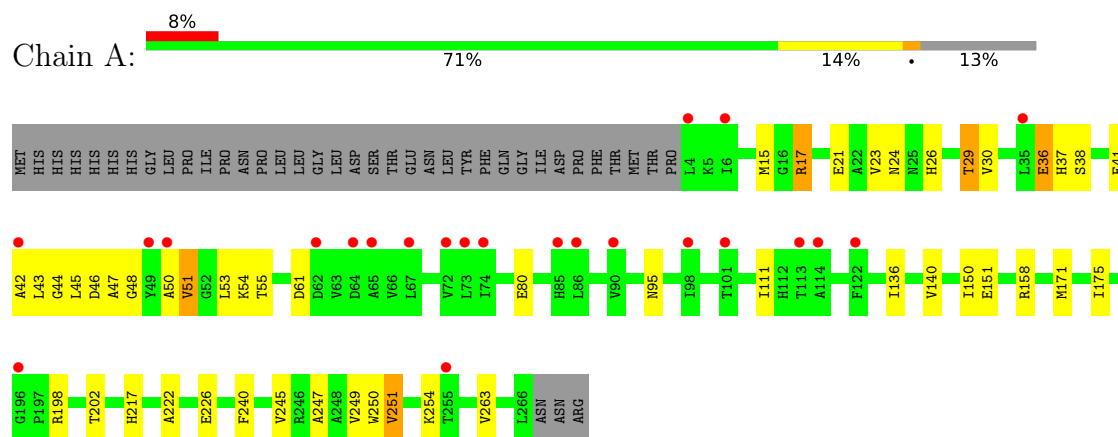
- Molecule 2 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	2	Total O 2 2	0	0
2	B	12	Total O 12 12	0	0
2	C	19	Total O 19 19	0	0
2	D	3	Total O 3 3	0	0

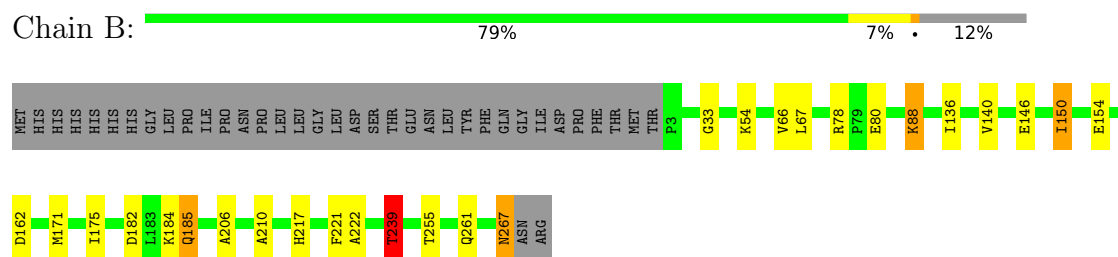
3 Residue-property plots [i](#)

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.

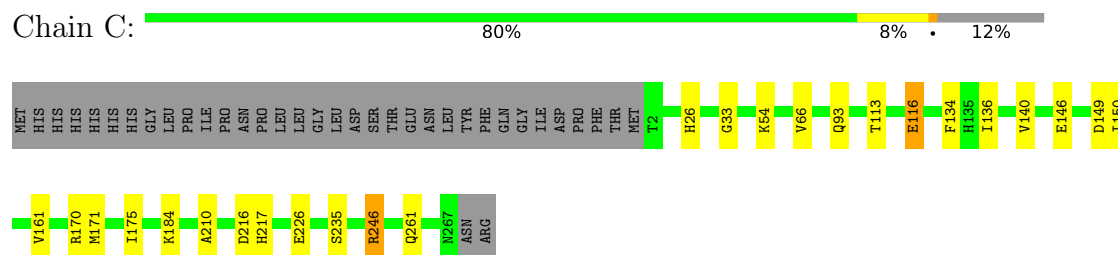
- Molecule 1: 4-hydroxy-tetrahydrodipicolinate reductase



- Molecule 1: 4-hydroxy-tetrahydrodipicolinate reductase

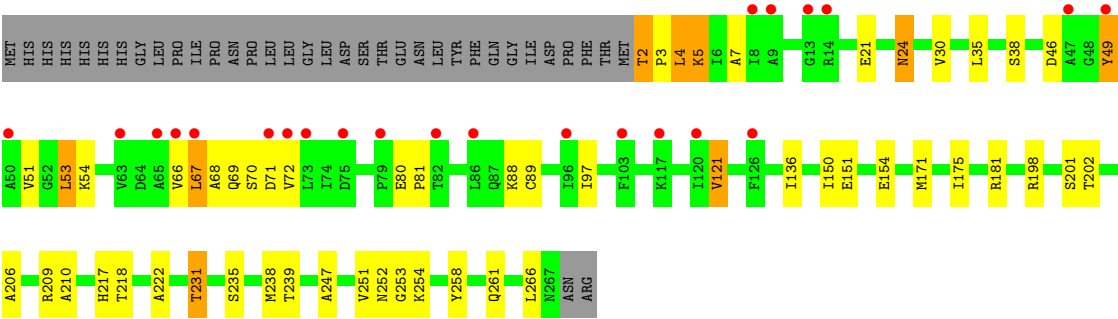


- Molecule 1: 4-hydroxy-tetrahydrodipicolinate reductase



- Molecule 1: 4-hydroxy-tetrahydrodipicolinate reductase





4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	69.87Å 66.75Å 133.53Å 90.00° 105.12° 90.00°	Depositor
Resolution (Å)	47.44 – 2.70 47.44 – 2.70	Depositor EDS
% Data completeness (in resolution range)	91.5 (47.44-2.70) 91.5 (47.44-2.70)	Depositor EDS
R_{merge}	0.09	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.28 (at 2.69Å)	Xtriage
Refinement program	REFMAC	Depositor
R, R_{free}	0.206 , 0.250 0.207 , 0.252	Depositor DCC
R_{free} test set	1592 reflections (4.83%)	wwPDB-VP
Wilson B-factor (Å ²)	41.8	Xtriage
Anisotropy	0.313	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.31 , 38.4	EDS
L-test for twinning ²	$\langle L \rangle = 0.46$, $\langle L^2 \rangle = 0.29$	Xtriage
Estimated twinning fraction	0.038 for h,-k,-h-l	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	7812	wwPDB-VP
Average B, all atoms (Å ²)	62.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.31% 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	0.97	0/1961	1.15	3/2662 (0.1%)
1	B	0.93	0/1972	1.09	1/2678 (0.0%)
1	C	0.97	1/1985 (0.1%)	1.10	4/2696 (0.1%)
1	D	0.89	0/1981	1.15	3/2691 (0.1%)
All	All	0.94	1/7899 (0.0%)	1.12	11/10727 (0.1%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	C	216	ASP	C-O	-5.05	1.18	1.24

All (11) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	2	THR	CA-C-N	7.41	127.44	119.89
1	D	2	THR	C-N-CA	7.41	127.44	119.89
1	A	26	HIS	CA-C-N	6.77	126.01	118.97
1	A	26	HIS	C-N-CA	6.77	126.01	118.97
1	A	111	ILE	CB-CG1-CD1	-6.13	100.92	113.80
1	B	239	THR	CB-CA-C	-5.84	101.46	110.81
1	D	54	LYS	CA-CB-CG	5.60	125.30	114.10
1	C	246	ARG	CB-CG-CD	-5.17	99.40	111.30
1	C	161	VAL	N-CA-C	5.15	116.62	111.00
1	C	26	HIS	CA-C-N	5.06	124.67	119.05
1	C	26	HIS	C-N-CA	5.06	124.67	119.05

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	1931	0	1912	52	0
1	B	1941	0	1919	19	0
1	C	1954	0	1936	12	0
1	D	1950	0	1932	81	0
2	A	2	0	0	0	0
2	B	12	0	0	0	0
2	C	19	0	0	0	0
2	D	3	0	0	0	0
All	All	7812	0	7699	149	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 (149) 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:48:GLY:H	1:A:55:THR:CG2	1.15	1.55
1:D:35:LEU:CD2	1:D:66:VAL:HG21	1.36	1.53
1:D:5:LYS:HD3	1:D:71:ASP:CG	1.44	1.41
1:A:48:GLY:N	1:A:55:THR:CG2	1.78	1.38
1:A:48:GLY:N	1:A:55:THR:HG21	1.31	1.33
1:D:35:LEU:CD2	1:D:66:VAL:CG2	2.09	1.29
1:D:5:LYS:CD	1:D:71:ASP:CG	2.11	1.23
1:D:97:ILE:CD1	1:D:121:VAL:HG21	1.72	1.19
1:D:35:LEU:CG	1:D:66:VAL:HG21	1.72	1.17
1:D:5:LYS:CD	1:D:71:ASP:OD2	1.93	1.16
1:A:48:GLY:H	1:A:55:THR:HG23	1.14	1.13
1:D:35:LEU:HD21	1:D:66:VAL:CG2	1.76	1.10
1:D:35:LEU:HD23	1:D:66:VAL:HG21	1.30	1.09
1:D:181:ARG:NH1	1:D:201:SER:O	1.84	1.09
1:D:97:ILE:CD1	1:D:121:VAL:CG2	2.31	1.09
1:D:97:ILE:HD12	1:D:121:VAL:HG21	1.07	1.02
1:D:97:ILE:HD12	1:D:121:VAL:CG2	1.92	1.00
1:D:97:ILE:HD13	1:D:121:VAL:CG2	1.92	0.99
1:D:35:LEU:HG	1:D:66:VAL:HG21	1.44	0.97

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:48:GLY:CA	1:A:55:THR:CG2	2.45	0.94
1:D:5:LYS:HD2	1:D:71:ASP:OD2	1.67	0.92
1:D:35:LEU:HG	1:D:66:VAL:HG11	1.51	0.90
1:A:36:GLU:OE2	1:A:42:ALA:CB	2.20	0.90
1:D:35:LEU:HD21	1:D:66:VAL:HG23	1.51	0.89
1:A:48:GLY:H	1:A:55:THR:HG21	0.85	0.88
1:D:5:LYS:HD3	1:D:71:ASP:OD2	1.63	0.86
1:D:5:LYS:HD2	1:D:71:ASP:CG	2.01	0.85
1:A:198:ARG:NH2	1:A:202:THR:O	2.09	0.85
1:D:35:LEU:HD23	1:D:66:VAL:CG2	1.90	0.84
1:A:47:ALA:C	1:A:55:THR:HG21	2.02	0.83
1:D:46:ASP:O	1:D:49:TYR:HB3	1.78	0.83
1:D:218:THR:HG1	1:D:231:THR:HG1	1.16	0.83
1:D:5:LYS:HE2	1:D:70:SER:C	2.08	0.79
1:D:67:LEU:HD11	1:D:88:LYS:C	2.08	0.79
1:D:198:ARG:NH2	1:D:202:THR:O	2.18	0.76
1:A:250:TRP:CD2	1:A:263:VAL:HG22	2.21	0.76
1:A:36:GLU:OE2	1:A:42:ALA:HB2	1.88	0.74
1:B:261:GLN:OE1	1:B:267:ASN:ND2	2.20	0.73
1:C:226:GLU:OE1	1:D:239:THR:HG23	1.89	0.72
1:D:97:ILE:HA	1:D:121:VAL:HG23	1.70	0.72
1:A:48:GLY:HA3	1:A:55:THR:HG22	1.70	0.72
1:D:154:GLU:OE2	1:D:209:ARG:NH1	2.18	0.72
1:D:5:LYS:HD3	1:D:71:ASP:CB	2.18	0.71
1:A:48:GLY:HA3	1:A:55:THR:CG2	2.19	0.71
1:A:250:TRP:CE3	1:A:263:VAL:HG22	2.27	0.70
1:A:36:GLU:OE2	1:A:42:ALA:HB1	1.91	0.69
1:A:17:ARG:CD	1:A:50:ALA:CB	2.71	0.69
1:B:150:ILE:HD13	1:B:221:PHE:CD2	2.28	0.69
1:D:5:LYS:CG	1:D:71:ASP:OD2	2.40	0.68
1:A:48:GLY:CA	1:A:55:THR:HG22	2.22	0.68
1:D:35:LEU:HG	1:D:66:VAL:CG2	2.21	0.68
1:A:48:GLY:N	1:A:55:THR:HG23	1.82	0.65
1:A:43:LEU:HD21	1:A:61:ASP:HB3	1.79	0.64
1:D:254:LYS:HG2	1:D:258:TYR:OH	1.96	0.64
1:D:67:LEU:HG	1:D:88:LYS:HG2	1.79	0.64
1:D:53:LEU:HD12	1:D:53:LEU:N	2.12	0.64
1:D:35:LEU:HG	1:D:66:VAL:CG1	2.25	0.62
1:D:5:LYS:CD	1:D:71:ASP:OD1	2.46	0.62
1:A:48:GLY:N	1:A:55:THR:HG22	2.05	0.62
1:A:48:GLY:CA	1:A:55:THR:HG23	2.25	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:247:ALA:O	1:D:251:VAL:HG23	2.01	0.60
1:B:171:MET:HE1	1:B:217:HIS:HB3	1.84	0.60
1:D:68:ALA:O	1:D:69:GLN:C	2.46	0.59
1:A:251:VAL:HA	1:A:254:LYS:HD2	1.84	0.59
1:A:17:ARG:HD3	1:A:50:ALA:CB	2.32	0.59
1:D:97:ILE:HD13	1:D:121:VAL:HG23	1.81	0.59
1:A:226:GLU:HB3	1:B:239:THR:HG23	1.85	0.58
1:D:35:LEU:CD2	1:D:66:VAL:HG23	2.12	0.58
1:A:17:ARG:HD2	1:A:50:ALA:CB	2.35	0.57
1:D:5:LYS:HG3	1:D:71:ASP:OD2	2.05	0.57
1:D:151:GLU:OE2	1:D:198:ARG:NH1	2.38	0.57
1:D:4:LEU:O	1:D:30:VAL:HG22	2.05	0.56
1:D:5:LYS:HE2	1:D:70:SER:CA	2.35	0.56
1:A:95:ASN:HD22	1:A:251:VAL:HB	1.70	0.56
1:A:44:GLY:O	1:A:45:LEU:HD23	2.06	0.56
1:A:47:ALA:CA	1:A:55:THR:HG21	2.36	0.55
1:A:226:GLU:OE1	1:B:239:THR:HG22	2.07	0.55
1:D:53:LEU:HD12	1:D:53:LEU:H	1.72	0.54
1:D:171:MET:HE1	1:D:217:HIS:HB3	1.90	0.53
1:D:7:ALA:HB1	1:D:66:VAL:CG1	2.38	0.53
1:D:67:LEU:CD1	1:D:88:LYS:O	2.56	0.53
1:D:97:ILE:CD1	1:D:121:VAL:HG23	2.33	0.53
1:D:4:LEU:HD21	1:D:72:VAL:HG23	1.92	0.52
1:D:181:ARG:NH1	1:D:201:SER:C	2.63	0.52
1:A:46:ASP:OD2	1:A:55:THR:N	2.40	0.52
1:A:251:VAL:HG12	1:A:254:LYS:HB2	1.92	0.52
1:D:80:GLU:HG2	1:D:81:PRO:HD3	1.92	0.52
1:C:113:THR:O	1:C:116:GLU:HG2	2.10	0.51
1:A:17:ARG:CD	1:A:50:ALA:HB3	2.40	0.51
1:A:151:GLU:OE2	1:A:198:ARG:NH1	2.44	0.51
1:A:21:GLU:CD	1:A:51:VAL:HG11	2.36	0.50
1:A:21:GLU:HG3	1:A:51:VAL:HG11	1.93	0.50
1:D:21:GLU:HB3	1:D:238:MET:HE1	1.93	0.50
1:A:140:VAL:HG22	1:B:136:ILE:HD11	1.94	0.50
1:B:206:ALA:HB1	1:D:206:ALA:HB1	1.94	0.49
1:A:21:GLU:CG	1:A:51:VAL:HG11	2.42	0.49
1:D:67:LEU:HD11	1:D:89:CYS:N	2.26	0.49
1:B:182:ASP:HB3	1:B:185:GLN:HG3	1.94	0.48
1:C:140:VAL:HG22	1:D:136:ILE:HD11	1.96	0.48
1:A:136:ILE:HD11	1:B:140:VAL:HG22	1.95	0.48
1:A:247:ALA:O	1:A:251:VAL:HG22	2.13	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:226:GLU:OE1	1:D:239:THR:CG2	2.59	0.47
1:D:5:LYS:HD2	1:D:71:ASP:OD1	2.13	0.47
1:D:2:THR:N	1:D:3:PRO:HD2	2.28	0.47
1:D:24:ASN:ND2	1:D:24:ASN:C	2.72	0.47
1:B:222:ALA:HB3	1:D:210:ALA:HB1	1.95	0.47
1:A:222:ALA:HB3	1:C:210:ALA:HB1	1.97	0.47
1:C:171:MET:HE1	1:C:217:HIS:HB3	1.95	0.47
1:B:150:ILE:CD1	1:B:221:PHE:CE2	2.98	0.47
1:A:17:ARG:HD2	1:A:50:ALA:HB3	1.96	0.46
1:D:67:LEU:CD1	1:D:88:LYS:C	2.85	0.46
1:D:49:TYR:CD2	1:D:49:TYR:C	2.93	0.46
1:B:150:ILE:CD1	1:B:221:PHE:CD2	2.99	0.46
1:C:140:VAL:CG2	1:D:136:ILE:HD11	2.46	0.45
1:D:5:LYS:NZ	1:D:71:ASP:OD1	2.40	0.45
1:D:7:ALA:HB1	1:D:66:VAL:HG12	1.98	0.45
1:D:261:GLN:HG2	1:D:266:LEU:O	2.15	0.45
1:D:3:PRO:HB2	1:D:30:VAL:HG13	1.99	0.45
1:A:23:VAL:HG13	1:A:29:THR:OG1	2.16	0.45
1:B:171:MET:HE1	1:B:217:HIS:CB	2.46	0.45
1:D:5:LYS:HE2	1:D:71:ASP:N	2.32	0.45
1:A:158:ARG:HH11	1:C:149:ASP:CG	2.25	0.44
1:D:67:LEU:HD12	1:D:88:LYS:O	2.17	0.44
1:D:67:LEU:HD11	1:D:88:LYS:O	2.15	0.44
1:D:80:GLU:CG	1:D:81:PRO:HD3	2.47	0.44
1:D:35:LEU:CG	1:D:66:VAL:CG2	2.64	0.44
1:D:68:ALA:O	1:D:70:SER:N	2.51	0.43
1:B:267:ASN:HD22	1:B:267:ASN:HA	1.66	0.43
1:C:150:ILE:HG21	1:C:175:ILE:HG21	2.01	0.43
1:A:24:ASN:ND2	1:A:53:LEU:HD13	2.34	0.42
1:B:33:GLY:HA3	1:B:66:VAL:HG13	2.02	0.42
1:D:35:LEU:HG	1:D:66:VAL:CB	2.49	0.42
1:D:5:LYS:HG3	1:D:5:LYS:H	1.62	0.42
1:A:95:ASN:ND2	1:A:251:VAL:HB	2.33	0.42
1:D:150:ILE:HG21	1:D:175:ILE:HG21	2.01	0.42
1:A:226:GLU:HB3	1:B:239:THR:CG2	2.49	0.42
1:A:54:LYS:HD3	1:A:54:LYS:HA	1.77	0.42
1:A:15:MET:HE1	1:A:240:PHE:HB2	2.02	0.41
1:A:171:MET:HE1	1:A:217:HIS:HB3	2.01	0.41
1:B:210:ALA:HB1	1:D:222:ALA:HB3	2.02	0.41
1:B:88:LYS:HB3	1:B:88:LYS:HE3	1.45	0.41
1:D:171:MET:HE1	1:D:217:HIS:CB	2.51	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:150:ILE:HG21	1:A:175:ILE:HG21	2.03	0.41
1:A:245:VAL:O	1:A:249:VAL:HG23	2.21	0.41
1:B:150:ILE:HG21	1:B:175:ILE:HG21	2.03	0.41
1:A:250:TRP:CG	1:A:263:VAL:HG22	2.55	0.40
1:C:134:PHE:CZ	1:C:170:ARG:HG2	2.56	0.40
1:C:33:GLY:HA3	1:C:66:VAL:HG13	2.03	0.40
1:C:226:GLU:HB3	1:D:239:THR:HG23	2.04	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	261/302 (86%)	252 (97%)	9 (3%)	0	100	100
1	B	263/302 (87%)	258 (98%)	5 (2%)	0	100	100
1	C	264/302 (87%)	260 (98%)	4 (2%)	0	100	100
1	D	264/302 (87%)	249 (94%)	13 (5%)	2 (1%)	16	37
All	All	1052/1208 (87%)	1019 (97%)	31 (3%)	2 (0%)	43	68

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	D	253	GLY
1	D	38	SER

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	196/235 (83%)	186 (95%)	10 (5%)	21	48
1	B	198/235 (84%)	184 (93%)	14 (7%)	13	33
1	C	200/235 (85%)	191 (96%)	9 (4%)	24	52
1	D	199/235 (85%)	188 (94%)	11 (6%)	19	45
All	All	793/940 (84%)	749 (94%)	44 (6%)	19	45

All (44) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	17	ARG
1	A	29	THR
1	A	30	VAL
1	A	36	GLU
1	A	37	HIS
1	A	38	SER
1	A	41	GLU
1	A	51	VAL
1	A	80	GLU
1	A	251	VAL
1	B	54	LYS
1	B	67	LEU
1	B	78	ARG
1	B	80	GLU
1	B	88	LYS
1	B	146	GLU
1	B	150	ILE
1	B	154	GLU
1	B	162	ASP
1	B	184	LYS
1	B	185	GLN
1	B	239	THR
1	B	255	THR
1	B	267	ASN
1	C	54	LYS
1	C	93	GLN
1	C	116	GLU
1	C	136	ILE
1	C	146	GLU
1	C	184	LYS

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Mol	Chain	Res	Type
1	C	235	SER
1	C	246	ARG
1	C	261	GLN
1	D	4	LEU
1	D	5	LYS
1	D	24	ASN
1	D	49	TYR
1	D	51	VAL
1	D	53	LEU
1	D	67	LEU
1	D	121	VAL
1	D	231	THR
1	D	235	SER
1	D	252	ASN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (15) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	24	ASN
1	A	125	ASN
1	A	131	ASN
1	A	252	ASN
1	B	12	ASN
1	B	185	GLN
1	B	252	ASN
1	B	267	ASN
1	C	12	ASN
1	C	26	HIS
1	C	261	GLN
1	D	12	ASN
1	D	24	ASN
1	D	69	GLN
1	D	252	ASN

5.3.3 RNA ⓘ

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 [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	263/302 (87%)	0.55	23 (8%) 16 13	24, 84, 160, 195	0
1	B	265/302 (87%)	-0.30	0 100 100	19, 40, 71, 93	0
1	C	266/302 (88%)	-0.40	0 100 100	18, 32, 60, 80	0
1	D	266/302 (88%)	0.58	23 (8%) 16 13	28, 80, 147, 196	0
All	All	1060/1208 (87%)	0.11	46 (4%) 40 36	18, 47, 146, 196	0

All (46) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	47	ALA	5.4
1	D	66	VAL	4.2
1	D	67	LEU	4.1
1	A	74	ILE	3.5
1	A	65	ALA	3.5
1	A	90	VAL	3.3
1	A	49	TYR	3.2
1	A	67	LEU	3.2
1	D	82	THR	3.0
1	A	86	LEU	3.0
1	A	72	VAL	2.9
1	A	196	GLY	2.8
1	D	13	GLY	2.8
1	D	49	TYR	2.7
1	A	85	HIS	2.7
1	D	65	ALA	2.6
1	A	4	LEU	2.6
1	D	120	ILE	2.6
1	D	73	LEU	2.6
1	D	72	VAL	2.6
1	D	63	VAL	2.5

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Mol	Chain	Res	Type	RSRZ
1	A	6	ILE	2.4
1	A	64	ASP	2.4
1	D	79	PRO	2.4
1	A	98	ILE	2.4
1	D	75	ASP	2.4
1	A	50	ALA	2.4
1	A	101	THR	2.3
1	D	117	LYS	2.3
1	A	35	LEU	2.3
1	A	42	ALA	2.2
1	D	86	LEU	2.2
1	D	103	PHE	2.2
1	A	114	ALA	2.2
1	A	122	PHE	2.2
1	D	9	ALA	2.1
1	A	113	THR	2.1
1	D	8	ILE	2.1
1	D	71	ASP	2.1
1	A	62	ASP	2.1
1	D	126	PHE	2.1
1	A	255	THR	2.1
1	D	50	ALA	2.0
1	D	96	ILE	2.0
1	D	14	ARG	2.0
1	A	73	LEU	2.0

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.