



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 20, 2026 – 12:15 AM UTC

PDB ID : 4DQX / pdb_00004dqx
Title : Crystal structure of a short chain dehydrogenase from Rhizobium etli CFN 42
Authors : Agarwal, R.; Chamala, S.; Evans, B.; Foti, R.; Gizzi, A.; Hillerich, B.; Kar, A.; LaFleur, J.; Siedel, R.; Villigas, G.; Zencheck, W.; Almo, S.C.; Swaminathan, S.; New York Structural Genomics Research Consortium (NYSGRG)
Deposited on : 2012-02-16
Resolution : 2.00 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
Mogul : 2022.3.0, CSD as543be (2022)
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

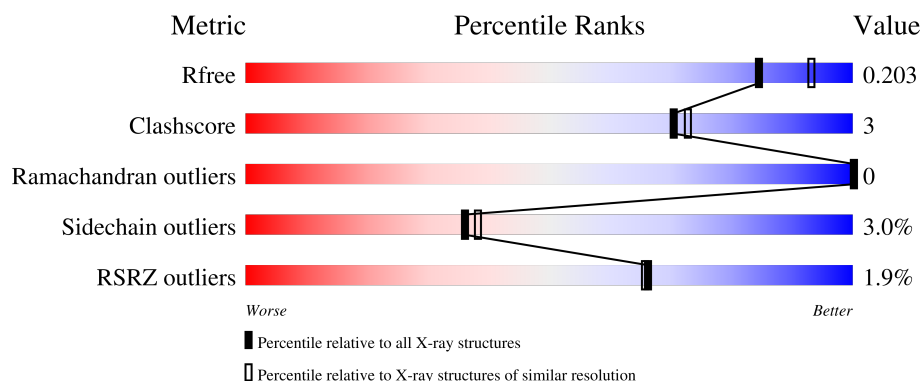
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.00 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	10052 (2.00-2.00)
Clashscore	190562	11152 (2.00-2.00)
Ramachandran outliers	187476	11031 (2.00-2.00)
Sidechain outliers	187428	11029 (2.00-2.00)
RSRZ outliers	180081	10067 (2.00-2.00)

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	277	0% 79% 12% 8%
1	B	277	0% 78% 10% 10%
1	C	277	2% 80% 10% 9%
1	D	277	2% 79% 10% 10%

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 8052 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 Probable oxidoreductase protein.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	255	Total	C	N	O	S	Se	0	0	0
			1879	1165	335	368	2	9			
1	B	250	Total	C	N	O	S	Se	0	0	0
			1838	1139	328	360	2	9			
1	C	251	Total	C	N	O	S	Se	0	0	0
			1837	1137	329	360	2	9			
1	D	250	Total	C	N	O	S	Se	0	0	0
			1845	1143	329	362	2	9			

There are 88 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	1	MSE	-	expression tag	UNP Q8KL31
A	2	HIS	-	expression tag	UNP Q8KL31
A	3	HIS	-	expression tag	UNP Q8KL31
A	4	HIS	-	expression tag	UNP Q8KL31
A	5	HIS	-	expression tag	UNP Q8KL31
A	6	HIS	-	expression tag	UNP Q8KL31
A	7	HIS	-	expression tag	UNP Q8KL31
A	8	SER	-	expression tag	UNP Q8KL31
A	9	SER	-	expression tag	UNP Q8KL31
A	10	GLY	-	expression tag	UNP Q8KL31
A	11	VAL	-	expression tag	UNP Q8KL31
A	12	ASP	-	expression tag	UNP Q8KL31
A	13	LEU	-	expression tag	UNP Q8KL31
A	14	GLY	-	expression tag	UNP Q8KL31
A	15	THR	-	expression tag	UNP Q8KL31
A	16	GLU	-	expression tag	UNP Q8KL31
A	17	ASN	-	expression tag	UNP Q8KL31
A	18	LEU	-	expression tag	UNP Q8KL31
A	19	TYR	-	expression tag	UNP Q8KL31
A	20	PHE	-	expression tag	UNP Q8KL31
A	21	GLN	-	expression tag	UNP Q8KL31

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Chain	Residue	Modelled	Actual	Comment	Reference
A	22	SER	-	expression tag	UNP Q8KL31
B	1	MSE	-	expression tag	UNP Q8KL31
B	2	HIS	-	expression tag	UNP Q8KL31
B	3	HIS	-	expression tag	UNP Q8KL31
B	4	HIS	-	expression tag	UNP Q8KL31
B	5	HIS	-	expression tag	UNP Q8KL31
B	6	HIS	-	expression tag	UNP Q8KL31
B	7	HIS	-	expression tag	UNP Q8KL31
B	8	SER	-	expression tag	UNP Q8KL31
B	9	SER	-	expression tag	UNP Q8KL31
B	10	GLY	-	expression tag	UNP Q8KL31
B	11	VAL	-	expression tag	UNP Q8KL31
B	12	ASP	-	expression tag	UNP Q8KL31
B	13	LEU	-	expression tag	UNP Q8KL31
B	14	GLY	-	expression tag	UNP Q8KL31
B	15	THR	-	expression tag	UNP Q8KL31
B	16	GLU	-	expression tag	UNP Q8KL31
B	17	ASN	-	expression tag	UNP Q8KL31
B	18	LEU	-	expression tag	UNP Q8KL31
B	19	TYR	-	expression tag	UNP Q8KL31
B	20	PHE	-	expression tag	UNP Q8KL31
B	21	GLN	-	expression tag	UNP Q8KL31
B	22	SER	-	expression tag	UNP Q8KL31
C	1	MSE	-	expression tag	UNP Q8KL31
C	2	HIS	-	expression tag	UNP Q8KL31
C	3	HIS	-	expression tag	UNP Q8KL31
C	4	HIS	-	expression tag	UNP Q8KL31
C	5	HIS	-	expression tag	UNP Q8KL31
C	6	HIS	-	expression tag	UNP Q8KL31
C	7	HIS	-	expression tag	UNP Q8KL31
C	8	SER	-	expression tag	UNP Q8KL31
C	9	SER	-	expression tag	UNP Q8KL31
C	10	GLY	-	expression tag	UNP Q8KL31
C	11	VAL	-	expression tag	UNP Q8KL31
C	12	ASP	-	expression tag	UNP Q8KL31
C	13	LEU	-	expression tag	UNP Q8KL31
C	14	GLY	-	expression tag	UNP Q8KL31
C	15	THR	-	expression tag	UNP Q8KL31
C	16	GLU	-	expression tag	UNP Q8KL31
C	17	ASN	-	expression tag	UNP Q8KL31
C	18	LEU	-	expression tag	UNP Q8KL31
C	19	TYR	-	expression tag	UNP Q8KL31

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Chain	Residue	Modelled	Actual	Comment	Reference
C	20	PHE	-	expression tag	UNP Q8KL31
C	21	GLN	-	expression tag	UNP Q8KL31
C	22	SER	-	expression tag	UNP Q8KL31
D	1	MSE	-	expression tag	UNP Q8KL31
D	2	HIS	-	expression tag	UNP Q8KL31
D	3	HIS	-	expression tag	UNP Q8KL31
D	4	HIS	-	expression tag	UNP Q8KL31
D	5	HIS	-	expression tag	UNP Q8KL31
D	6	HIS	-	expression tag	UNP Q8KL31
D	7	HIS	-	expression tag	UNP Q8KL31
D	8	SER	-	expression tag	UNP Q8KL31
D	9	SER	-	expression tag	UNP Q8KL31
D	10	GLY	-	expression tag	UNP Q8KL31
D	11	VAL	-	expression tag	UNP Q8KL31
D	12	ASP	-	expression tag	UNP Q8KL31
D	13	LEU	-	expression tag	UNP Q8KL31
D	14	GLY	-	expression tag	UNP Q8KL31
D	15	THR	-	expression tag	UNP Q8KL31
D	16	GLU	-	expression tag	UNP Q8KL31
D	17	ASN	-	expression tag	UNP Q8KL31
D	18	LEU	-	expression tag	UNP Q8KL31
D	19	TYR	-	expression tag	UNP Q8KL31
D	20	PHE	-	expression tag	UNP Q8KL31
D	21	GLN	-	expression tag	UNP Q8KL31
D	22	SER	-	expression tag	UNP Q8KL31

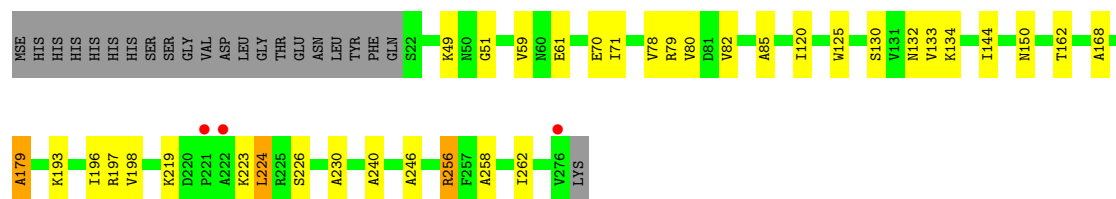
- Molecule 2 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	179	Total O 179 179	0	0
2	B	169	Total O 169 169	0	0
2	C	154	Total O 154 154	0	0
2	D	151	Total O 151 151	0	0

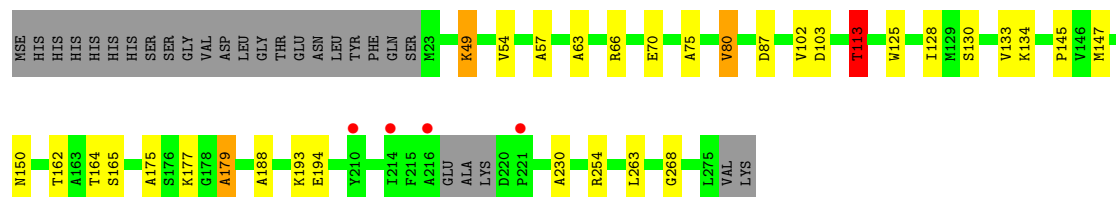
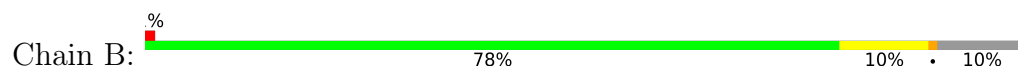
3 Residue-property plots [i](#)

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.

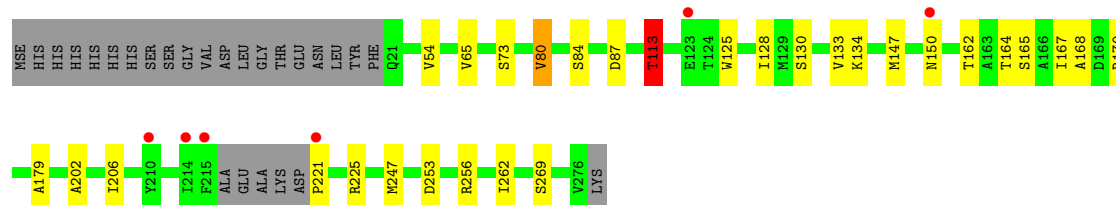
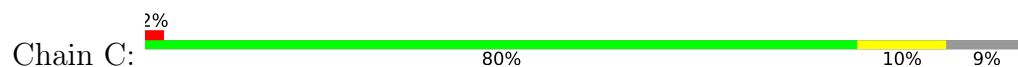
- Molecule 1: Probable oxidoreductase protein



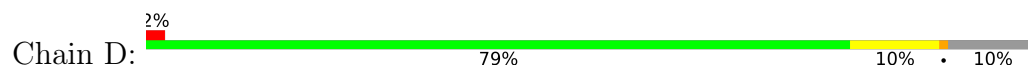
- Molecule 1: Probable oxidoreductase protein

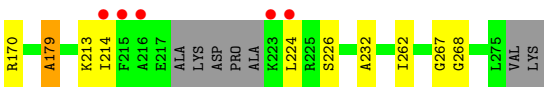


- Molecule 1: Probable oxidoreductase protein



- Molecule 1: Probable oxidoreductase protein





4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	81.25Å 64.59Å 113.35Å 90.00° 96.72° 90.00°	Depositor
Resolution (Å)	44.81 – 2.00 44.81 – 2.00	Depositor EDS
% Data completeness (in resolution range)	98.5 (44.81-2.00) 98.5 (44.81-2.00)	Depositor EDS
R_{merge}	0.09	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.28 (at 2.00Å)	Xtriage
Refinement program	REFMAC 5.5.0109	Depositor
R, R_{free}	0.159 , 0.198 0.168 , 0.203	Depositor DCC
R_{free} test set	3965 reflections (5.03%)	wwPDB-VP
Wilson B-factor (Å ²)	20.7	Xtriage
Anisotropy	0.130	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.32 , 31.4	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	8052	wwPDB-VP
Average B, all atoms (Å ²)	22.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.94% 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	1.56	15/1894 (0.8%)	1.24	4/2546 (0.2%)
1	B	1.50	9/1853 (0.5%)	1.21	2/2493 (0.1%)
1	C	1.45	5/1849 (0.3%)	1.23	9/2486 (0.4%)
1	D	1.56	7/1858 (0.4%)	1.29	9/2496 (0.4%)
All	All	1.52	36/7454 (0.5%)	1.25	24/10021 (0.2%)

All (36) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	C	202	ALA	CA-CB	7.85	1.63	1.53
1	B	63	ALA	CA-CB	6.80	1.64	1.53
1	D	267	GLY	C-O	-6.46	1.15	1.24
1	B	66	ARG	C-O	-6.44	1.16	1.24
1	C	168	ALA	CA-CB	6.25	1.63	1.53
1	A	196	ILE	C-O	-6.10	1.17	1.24
1	A	120	ILE	CA-CB	6.07	1.61	1.54
1	B	179	ALA	CA-CB	6.05	1.62	1.53
1	B	230	ALA	CA-CB	6.04	1.64	1.53
1	B	145	PRO	C-O	-5.97	1.16	1.24
1	A	240	ALA	CA-CB	5.79	1.62	1.53
1	A	82	VAL	CA-CB	5.77	1.62	1.54
1	B	268	GLY	C-O	-5.77	1.16	1.23
1	A	246	ALA	CA-CB	5.68	1.62	1.53
1	D	268	GLY	C-O	-5.65	1.16	1.23
1	A	224	LEU	C-O	-5.64	1.17	1.24
1	C	65	VAL	C-O	-5.63	1.17	1.24
1	C	262	ILE	CA-CB	5.54	1.61	1.54
1	A	179	ALA	CA-CB	5.41	1.61	1.53
1	D	164	THR	CA-CB	5.38	1.62	1.53
1	D	32	VAL	CA-CB	5.37	1.60	1.53
1	A	162	THR	CA-CB	5.32	1.62	1.53
1	B	175	ALA	CA-C	5.32	1.59	1.52
1	B	263	LEU	CA-C	5.29	1.59	1.52

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	168	ALA	CA-CB	5.29	1.61	1.53
1	A	144	ILE	CA-C	5.28	1.58	1.52
1	B	87	ASP	N-CA	5.24	1.52	1.46
1	A	85	ALA	CA-CB	5.23	1.61	1.53
1	D	179	ALA	CA-CB	5.19	1.61	1.53
1	A	198	VAL	C-O	-5.16	1.18	1.24
1	A	59	VAL	CA-CB	5.15	1.62	1.54
1	A	230	ALA	CA-CB	5.13	1.62	1.53
1	D	232	ALA	CA-CB	5.11	1.61	1.53
1	A	51	GLY	N-CA	5.08	1.52	1.45
1	C	206	ILE	CA-CB	5.07	1.60	1.54
1	D	163	ALA	CA-CB	5.02	1.61	1.53

All (24) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	221	PRO	N-CA-CB	7.56	111.32	103.00
1	C	113	THR	N-CA-CB	-7.25	99.07	111.69
1	D	226	SER	N-CA-C	-6.77	103.98	111.36
1	C	80	VAL	N-CA-C	6.26	117.31	108.17
1	C	54	VAL	N-CA-C	5.90	116.37	108.11
1	B	113	THR	N-CA-CB	-5.74	102.07	111.66
1	D	42	ALA	N-CA-C	-5.65	105.27	111.82
1	D	133	VAL	CB-CA-C	-5.53	106.18	111.44
1	D	132	ASN	CA-C-N	-5.51	117.51	123.08
1	D	132	ASN	C-N-CA	-5.51	117.51	123.08
1	A	132	ASN	CA-C-N	-5.44	117.58	123.08
1	A	132	ASN	C-N-CA	-5.44	117.58	123.08
1	D	262	ILE	CB-CA-C	-5.42	102.61	110.63
1	A	71	ILE	N-CA-C	5.36	115.56	110.42
1	D	113	THR	N-CA-CB	-5.31	102.79	111.66
1	A	262	ILE	N-CA-C	-5.28	100.05	107.75
1	B	188	ALA	N-CA-C	-5.26	105.62	111.36
1	C	73	SER	N-CA-C	5.21	118.74	112.38
1	C	113	THR	OG1-CB-CG2	5.19	119.69	109.30
1	D	214	ILE	N-CA-C	5.10	115.83	110.62
1	D	143	VAL	N-CA-C	5.09	115.86	110.72
1	C	269	SER	N-CA-C	-5.04	107.29	113.50
1	C	225	ARG	N-CA-C	-5.03	105.80	111.28
1	C	247	MSE	N-CA-C	-5.02	105.88	111.36

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	1879	0	1880	16	0
1	B	1838	0	1828	16	0
1	C	1837	0	1827	12	0
1	D	1845	0	1840	12	0
2	A	179	0	0	1	0
2	B	169	0	0	3	0
2	C	154	0	0	2	0
2	D	151	0	0	1	0
All	All	8052	0	7375	50	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 3.

All (50) 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:256:ARG:CG	1:A:256:ARG:HH11	1.84	0.89
1:A:256:ARG:HH11	1:A:256:ARG:HG2	1.42	0.84
1:D:167:ILE:HD12	1:D:170:ARG:HD3	1.59	0.82
1:D:167:ILE:CD1	1:D:170:ARG:HD3	2.11	0.79
1:C:253:ASP:OD2	1:C:256:ARG:NH1	2.24	0.70
1:D:61:GLU:HB2	1:D:79:ARG:HB2	1.77	0.66
1:C:133:VAL:HG12	1:D:125:TRP:HZ2	1.61	0.65
1:A:223:LYS:C	1:A:223:LYS:HD3	2.26	0.61
1:D:113:THR:HB	1:D:128:ILE:HD11	1.84	0.59
1:B:113:THR:HG23	2:B:340:HOH:O	2.03	0.58
1:C:130:SER:O	1:C:134:LYS:HB3	2.04	0.58
1:C:113:THR:HB	1:C:128:ILE:HD11	1.86	0.56
1:C:113:THR:HG23	2:C:357:HOH:O	2.05	0.56
1:B:103:ASP:C	1:B:147:MSE:HE2	2.32	0.54
1:B:57:ALA:HB1	1:B:80:VAL:HG13	1.90	0.54
1:A:61:GLU:HB2	1:A:79:ARG:HB2	1.90	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:113:THR:HG22	2:C:309:HOH:O	2.08	0.53
1:A:256:ARG:HG2	1:A:256:ARG:NH1	2.14	0.53
1:D:167:ILE:HD11	1:D:170:ARG:HD3	1.89	0.52
1:A:197:ARG:HD2	1:A:258:ALA:O	2.10	0.52
1:C:167:ILE:HD12	1:C:170:ARG:HD3	1.92	0.51
1:B:102:VAL:H	1:B:150:ASN:HD21	1.57	0.51
1:A:193:LYS:HG2	2:A:388:HOH:O	2.12	0.50
1:B:113:THR:HB	1:B:128:ILE:HD11	1.92	0.50
1:A:256:ARG:CG	1:A:256:ARG:NH1	2.57	0.49
1:B:113:THR:CG2	2:B:340:HOH:O	2.59	0.49
1:C:162:THR:HA	1:C:165:SER:O	2.13	0.48
1:B:193:LYS:HG3	1:B:194:GLU:HG3	1.95	0.47
1:C:125:TRP:HZ2	1:D:133:VAL:HG12	1.80	0.47
1:B:49:LYS:HE2	1:B:49:LYS:HB3	1.39	0.46
1:A:133:VAL:HG12	1:B:125:TRP:HZ2	1.81	0.46
1:C:80:VAL:HG13	1:C:87:ASP:HB3	1.99	0.45
1:A:49:LYS:HB3	1:A:49:LYS:HE2	1.70	0.45
1:B:162:THR:HA	1:B:165:SER:O	2.17	0.45
1:A:179:ALA:HB2	1:B:179:ALA:HB2	1.98	0.45
1:D:162:THR:HA	1:D:165:SER:O	2.17	0.45
1:B:54:VAL:O	1:B:75:ALA:HA	2.17	0.44
1:D:33:THR:O	1:D:108:ASN:HB3	2.18	0.44
1:A:223:LYS:C	1:A:223:LYS:CD	2.90	0.44
1:C:147:MSE:HA	1:C:150:ASN:ND2	2.33	0.44
1:D:113:THR:HG22	2:D:320:HOH:O	2.16	0.44
1:A:130:SER:O	1:A:134:LYS:HB3	2.19	0.43
1:A:224:LEU:HD12	1:A:224:LEU:HA	1.87	0.43
1:A:223:LYS:HD3	1:A:223:LYS:O	2.18	0.42
1:B:177:LYS:HA	1:B:177:LYS:HD3	1.92	0.42
1:B:130:SER:O	1:B:134:LYS:HB3	2.20	0.41
1:D:224:LEU:HD12	1:D:224:LEU:HA	1.65	0.41
1:C:179:ALA:HB2	1:D:179:ALA:HB2	2.03	0.41
1:A:125:TRP:HZ2	1:B:133:VAL:HG12	1.85	0.41
1:B:254:ARG:NH2	2:B:394:HOH:O	2.49	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	253/277 (91%)	249 (98%)	4 (2%)	0	100	100
1	B	246/277 (89%)	238 (97%)	8 (3%)	0	100	100
1	C	247/277 (89%)	241 (98%)	6 (2%)	0	100	100
1	D	246/277 (89%)	243 (99%)	3 (1%)	0	100	100
All	All	992/1108 (90%)	971 (98%)	21 (2%)	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	196/207 (95%)	189 (96%)	7 (4%)	31	31
1	B	191/207 (92%)	186 (97%)	5 (3%)	40	44
1	C	191/207 (92%)	188 (98%)	3 (2%)	55	62
1	D	193/207 (93%)	185 (96%)	8 (4%)	27	26
All	All	771/828 (93%)	748 (97%)	23 (3%)	36	38

All (23) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	70	GLU
1	A	78	VAL

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Mol	Chain	Res	Type
1	A	80	VAL
1	A	150	ASN
1	A	219	LYS
1	A	226	SER
1	A	256	ARG
1	B	49	LYS
1	B	70	GLU
1	B	80	VAL
1	B	113	THR
1	B	164	THR
1	C	84	SER
1	C	113	THR
1	C	164	THR
1	D	49	LYS
1	D	70	GLU
1	D	74	LYS
1	D	80	VAL
1	D	113	THR
1	D	150	ASN
1	D	164	THR
1	D	213	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (6) such sidechains are listed below:

Mol	Chain	Res	Type
1	B	150	ASN
1	C	21	GLN
1	C	107	ASN
1	C	150	ASN
1	C	157	ASN
1	D	108	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 [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	246/277 (88%)	-0.63	3 (1%) 76 76	11, 18, 32, 51	0
1	B	241/277 (87%)	-0.45	4 (1%) 69 68	13, 18, 40, 65	0
1	C	242/277 (87%)	-0.40	6 (2%) 58 58	13, 20, 37, 56	0
1	D	241/277 (87%)	-0.49	5 (2%) 63 63	11, 18, 33, 51	0
All	All	970/1108 (87%)	-0.50	18 (1%) 66 66	11, 18, 36, 65	0

All (18) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	221	PRO	4.7
1	D	223	LYS	4.3
1	B	214	ILE	4.0
1	C	150	ASN	3.7
1	B	216	ALA	3.6
1	C	123	GLU	3.1
1	D	216	ALA	2.9
1	D	214	ILE	2.6
1	C	215	PHE	2.5
1	A	222	ALA	2.5
1	D	224	LEU	2.5
1	A	276	VAL	2.5
1	C	210	TYR	2.4
1	D	215	PHE	2.4
1	B	210	TYR	2.2
1	B	221	PRO	2.2
1	C	214	ILE	2.1
1	A	221	PRO	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.