



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 8, 2026 – 01:25 PM UTC

PDB ID : 4O9T / pdb_00004o9t
Title : Mechanism of transhydrogenase coupling proton translocation and hydride transfer
Authors : Leung, J.H.; Yamaguchi, M.; Moeller, A.; Schurig-Briccio, L.A.; Gennis, R.B.; Potter, C.S.; Carragher, B.; Stout, C.D.
Deposited on : 2014-01-02
Resolution : 3.08 Å(reported)

This is a wwPDB X-ray Structure Validation Summary 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

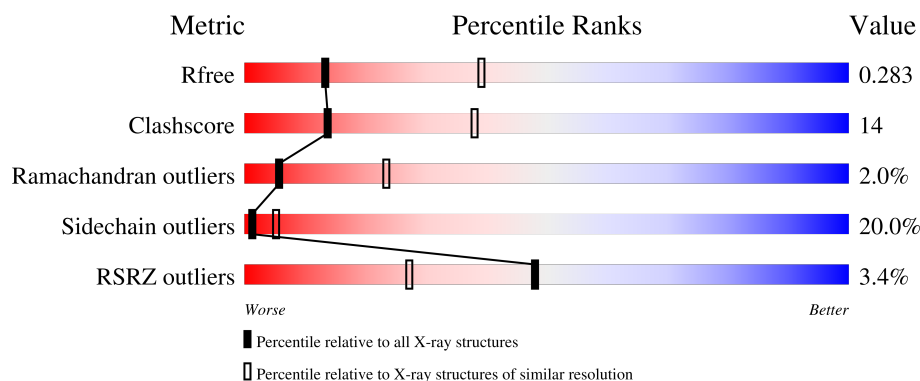
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.08 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	2010 (3.10-3.06)
Clashscore	190562	2102 (3.10-3.06)
Ramachandran outliers	187476	1982 (3.10-3.06)
Sidechain outliers	187428	1981 (3.10-3.06)
RSRZ outliers	180081	2010 (3.10-3.06)

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	100	
1	C	100	
1	E	100	
1	G	100	
2	B	283	

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Mol	Chain	Length	Quality of chain
2	D	283	5% 61% 24% 7% 8%
2	F	283	3% 61% 25% 7% 7%
2	H	283	4% 60% 26% 5% 8%

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 10352 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 NAD(P) transhydrogenase subunit alpha 2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	94	Total	C	N	O	S	0	0	0
			713	475	114	119	5			
1	C	89	Total	C	N	O	S	0	0	0
			666	444	105	112	5			
1	E	94	Total	C	N	O	S	0	0	0
			713	475	114	119	5			
1	G	89	Total	C	N	O	S	0	0	0
			666	444	105	112	5			

- Molecule 2 is a protein called NAD(P) transhydrogenase subunit beta.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	262	Total	C	N	O	S	0	0	0
			1904	1269	304	315	16			
2	D	260	Total	C	N	O	S	0	0	0
			1893	1262	302	313	16			
2	F	262	Total	C	N	O	S	0	0	0
			1904	1269	304	315	16			
2	H	260	Total	C	N	O	S	0	0	0
			1893	1262	302	313	16			

There are 32 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	276	HIS	-	expression tag	UNP Q72GS0
B	277	HIS	-	expression tag	UNP Q72GS0
B	278	HIS	-	expression tag	UNP Q72GS0
B	279	HIS	-	expression tag	UNP Q72GS0
B	280	HIS	-	expression tag	UNP Q72GS0
B	281	HIS	-	expression tag	UNP Q72GS0
B	282	HIS	-	expression tag	UNP Q72GS0
B	283	HIS	-	expression tag	UNP Q72GS0

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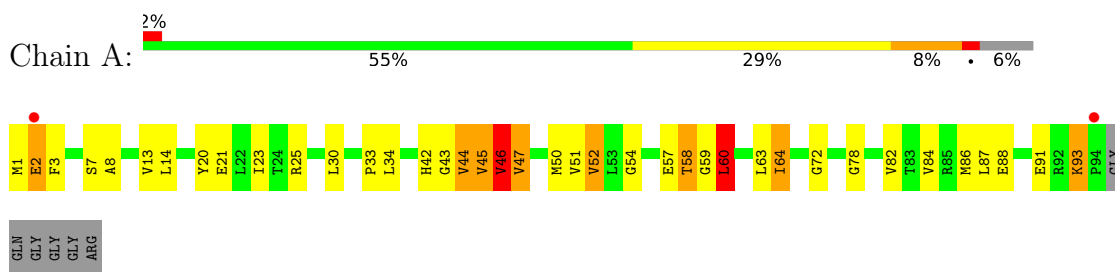
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Chain	Residue	Modelled	Actual	Comment	Reference
D	276	HIS	-	expression tag	UNP Q72GS0
D	277	HIS	-	expression tag	UNP Q72GS0
D	278	HIS	-	expression tag	UNP Q72GS0
D	279	HIS	-	expression tag	UNP Q72GS0
D	280	HIS	-	expression tag	UNP Q72GS0
D	281	HIS	-	expression tag	UNP Q72GS0
D	282	HIS	-	expression tag	UNP Q72GS0
D	283	HIS	-	expression tag	UNP Q72GS0
F	276	HIS	-	expression tag	UNP Q72GS0
F	277	HIS	-	expression tag	UNP Q72GS0
F	278	HIS	-	expression tag	UNP Q72GS0
F	279	HIS	-	expression tag	UNP Q72GS0
F	280	HIS	-	expression tag	UNP Q72GS0
F	281	HIS	-	expression tag	UNP Q72GS0
F	282	HIS	-	expression tag	UNP Q72GS0
F	283	HIS	-	expression tag	UNP Q72GS0
H	276	HIS	-	expression tag	UNP Q72GS0
H	277	HIS	-	expression tag	UNP Q72GS0
H	278	HIS	-	expression tag	UNP Q72GS0
H	279	HIS	-	expression tag	UNP Q72GS0
H	280	HIS	-	expression tag	UNP Q72GS0
H	281	HIS	-	expression tag	UNP Q72GS0
H	282	HIS	-	expression tag	UNP Q72GS0
H	283	HIS	-	expression tag	UNP Q72GS0

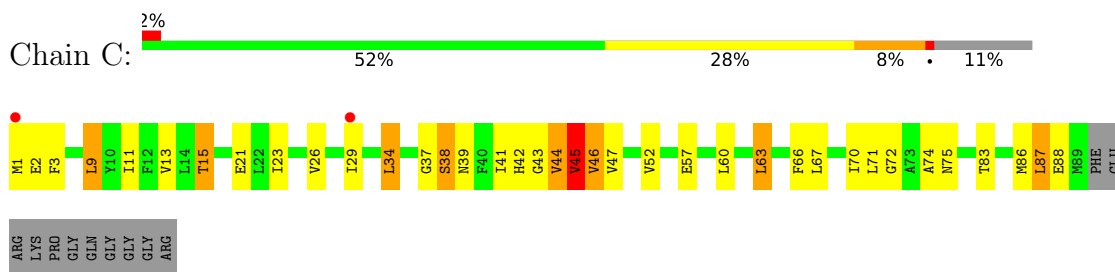
3 Residue-property plots [i](#)

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.

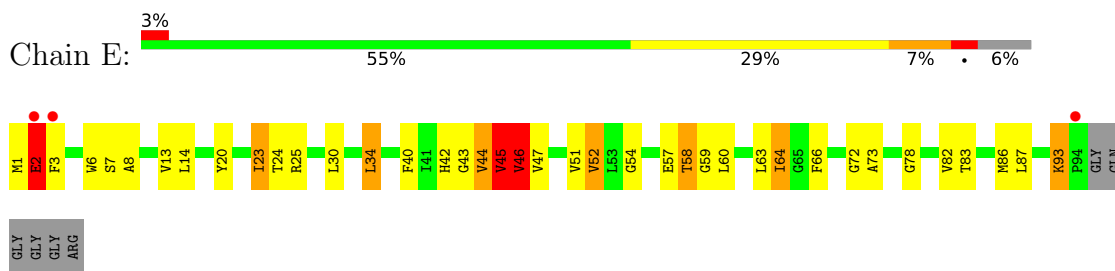
- Molecule 1: NAD(P) transhydrogenase subunit alpha 2



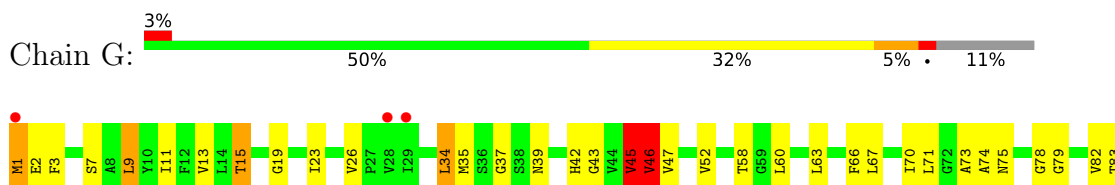
- Molecule 1: NAD(P) transhydrogenase subunit alpha 2

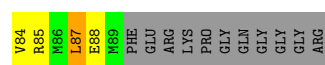


- Molecule 1: NAD(P) transhydrogenase subunit alpha 2

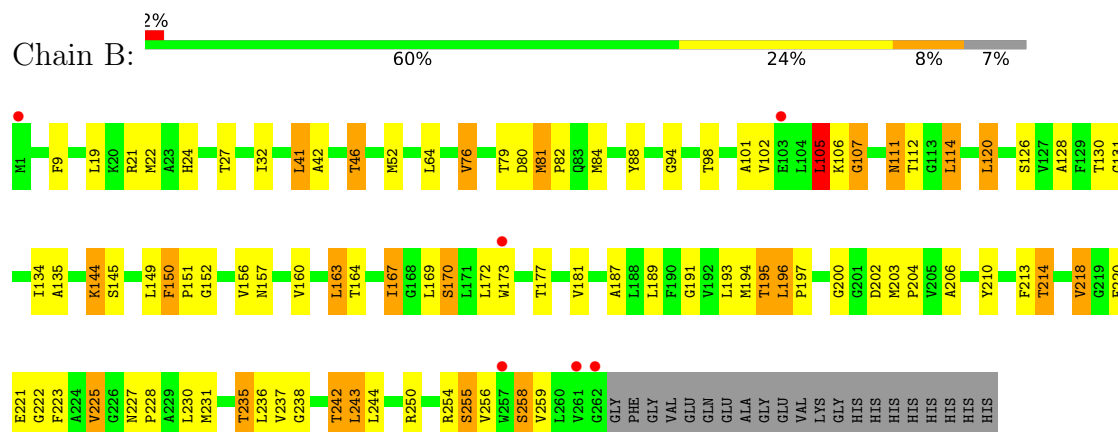


- Molecule 1: NAD(P) transhydrogenase subunit alpha 2

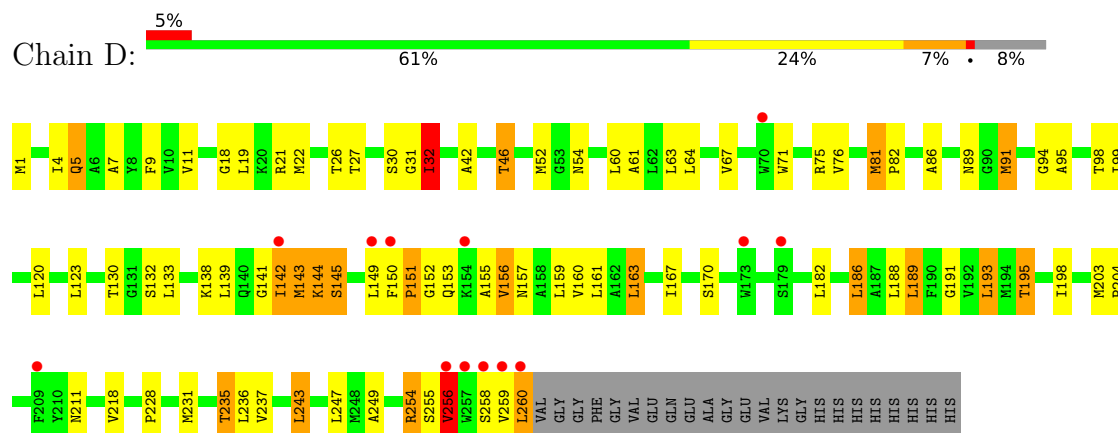




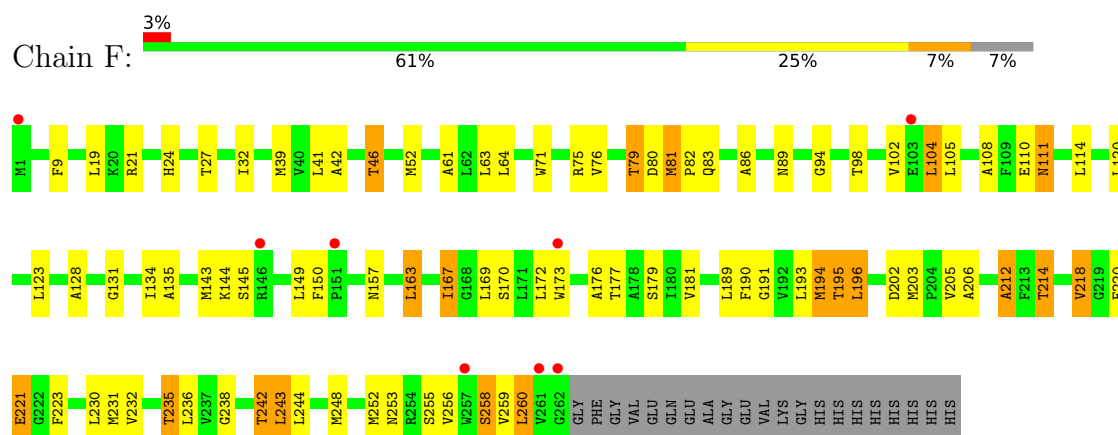
• Molecule 2: NAD(P) transhydrogenase subunit beta



• Molecule 2: NAD(P) transhydrogenase subunit beta

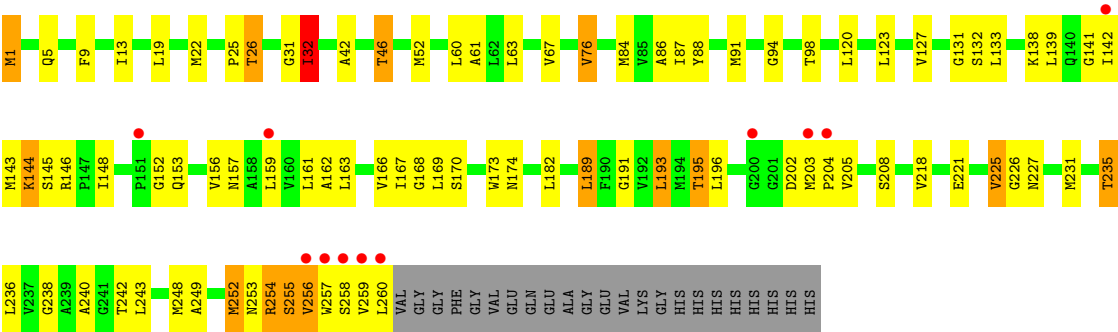


• Molecule 2: NAD(P) transhydrogenase subunit beta



• Molecule 2: NAD(P) transhydrogenase subunit beta





4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	97.22Å 86.39Å 125.15Å 90.00° 93.99° 90.00°	Depositor
Resolution (Å)	46.30 – 3.08 46.30 – 3.08	Depositor EDS
% Data completeness (in resolution range)	98.5 (46.30-3.08) 98.5 (46.30-3.08)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.26 (at 3.06Å)	Xtriage
Refinement program	REFMAC 5.8.0049	Depositor
R, R_{free}	0.219 , 0.280 0.233 , 0.283	Depositor DCC
R_{free} test set	1899 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å ²)	83.5	Xtriage
Anisotropy	0.232	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.29 , 51.4	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	10352	wwPDB-VP
Average B, all atoms (Å ²)	74.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 55.04 % of the origin peak, indicating pseudo-translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo-translational symmetry is equal to 3.3471e-05. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

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	0.75	0/730	1.11	4/990 (0.4%)
1	C	0.71	0/681	1.09	1/925 (0.1%)
1	E	0.80	0/730	1.20	4/990 (0.4%)
1	G	0.79	0/681	1.08	2/925 (0.2%)
2	B	0.84	0/1945	1.06	3/2650 (0.1%)
2	D	0.72	0/1934	1.08	3/2635 (0.1%)
2	F	0.81	1/1945 (0.1%)	1.07	1/2650 (0.0%)
2	H	0.78	0/1934	1.08	5/2635 (0.2%)
All	All	0.78	1/10580 (0.0%)	1.08	23/14400 (0.2%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
2	B	0	1
2	D	0	1
2	H	0	1
All	All	0	3

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	F	150	PHE	N-CA	5.03	1.49	1.46

The worst 5 of 23 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	41	LEU	N-CA-C	-6.85	103.74	111.07
1	E	58	THR	N-CA-C	6.80	125.28	110.80
2	H	31	GLY	N-CA-C	6.45	120.29	112.49
1	E	2	GLU	N-CA-C	6.39	119.60	109.50

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Mol	Chain	Res	Type	Atoms	Z	Observed($^{\circ}$)	Ideal($^{\circ}$)
2	D	4	ILE	N-CA-C	-6.26	104.53	110.42

There are no chirality outliers.

All (3) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
2	B	105	LEU	Peptide
2	D	152	GLY	Peptide
2	H	152	GLY	Peptide

5.2 Too-close contacts [i](#)

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	713	0	739	28	0
1	C	666	0	691	35	0
1	E	713	0	739	25	0
1	G	666	0	691	31	0
2	B	1904	0	2018	66	0
2	D	1893	0	2006	73	0
2	F	1904	0	2018	55	0
2	H	1893	0	2006	64	0
All	All	10352	0	10908	308	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 14.

The worst 5 of 308 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)
2:H:255:SER:OG	2:H:258:SER:OG	1.74	1.03
2:H:202:ASP:OD1	2:H:254:ARG:NH1	1.98	0.96
2:D:260:LEU:HD12	2:D:260:LEU:H	1.30	0.94
2:D:42:ALA:O	2:D:46:THR:HG23	1.67	0.94
2:D:254:ARG:HG3	2:D:254:ARG:HH11	1.36	0.89

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	92/100 (92%)	81 (88%)	7 (8%)	4 (4%)	2	11
1	C	87/100 (87%)	81 (93%)	4 (5%)	2 (2%)	5	21
1	E	92/100 (92%)	83 (90%)	5 (5%)	4 (4%)	2	11
1	G	87/100 (87%)	78 (90%)	6 (7%)	3 (3%)	3	14
2	B	260/283 (92%)	244 (94%)	15 (6%)	1 (0%)	30	58
2	D	258/283 (91%)	234 (91%)	18 (7%)	6 (2%)	5	21
2	F	260/283 (92%)	237 (91%)	20 (8%)	3 (1%)	10	34
2	H	258/283 (91%)	233 (90%)	20 (8%)	5 (2%)	6	24
All	All	1394/1532 (91%)	1271 (91%)	95 (7%)	28 (2%)	6	23

5 of 28 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	58	THR
2	D	145	SER
2	D	256	VAL
1	E	58	THR
2	H	26	THR

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	73/75 (97%)	58 (80%)	15 (20%)	1	5
1	C	68/75 (91%)	54 (79%)	14 (21%)	1	5
1	E	73/75 (97%)	58 (80%)	15 (20%)	1	5
1	G	68/75 (91%)	54 (79%)	14 (21%)	1	5
2	B	188/204 (92%)	147 (78%)	41 (22%)	1	4
2	D	187/204 (92%)	153 (82%)	34 (18%)	2	7
2	F	188/204 (92%)	146 (78%)	42 (22%)	1	4
2	H	187/204 (92%)	156 (83%)	31 (17%)	2	9
All	All	1032/1116 (92%)	826 (80%)	206 (20%)	1	5

5 of 206 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	E	63	LEU
2	F	181	VAL
2	H	235	THR
2	F	19	LEU
2	F	111	ASN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 12 such sidechains are listed below:

Mol	Chain	Res	Type
2	F	89	ASN
2	F	111	ASN
2	H	227	ASN
1	G	39	ASN
2	D	5	GLN

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	94/100 (94%)	-0.26	2 (2%) 63 41	42, 61, 105, 132	0
1	C	89/100 (89%)	0.17	2 (2%) 62 40	51, 74, 123, 148	0
1	E	94/100 (94%)	-0.31	3 (3%) 50 28	42, 60, 102, 141	0
1	G	89/100 (89%)	-0.01	3 (3%) 48 27	49, 71, 115, 140	0
2	B	262/283 (92%)	-0.16	6 (2%) 61 38	30, 63, 91, 127	0
2	D	260/283 (91%)	0.16	13 (5%) 34 17	52, 80, 119, 139	0
2	F	262/283 (92%)	-0.24	8 (3%) 51 29	30, 60, 87, 119	0
2	H	260/283 (91%)	0.17	11 (4%) 40 22	51, 79, 123, 163	0
All	All	1410/1532 (92%)	-0.04	48 (3%) 48 27	30, 69, 113, 163	0

The worst 5 of 48 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	29	ILE	4.6
2	H	260	LEU	4.6
2	H	259	VAL	4.5
2	H	204	PRO	4.0
2	D	257	TRP	3.9

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.