



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 8, 2026 – 06:04 AM UTC

PDB ID : 5ZOJ / pdb_00005zoj
Title : Crystal structure of human SMAD2-MAN1 complex
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Deposited on : 2018-04-13
Resolution : 2.79 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

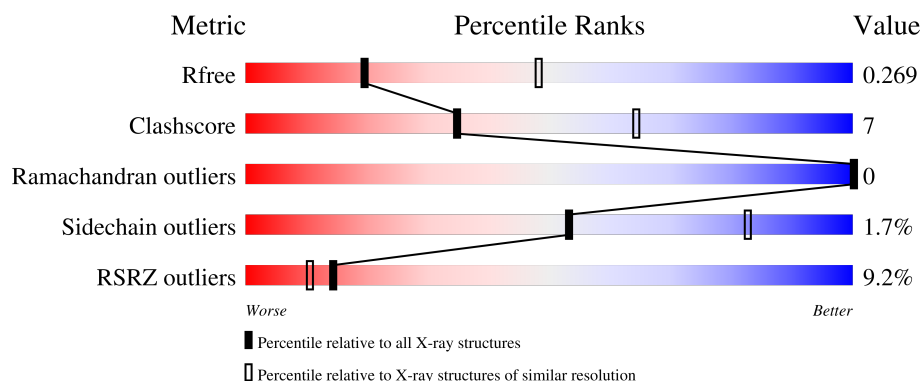
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.79 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	3866 (2.80-2.80)
Clashscore	190562	4276 (2.80-2.80)
Ramachandran outliers	187476	4196 (2.80-2.80)
Sidechain outliers	187428	4198 (2.80-2.80)
RSRZ outliers	180081	3869 (2.80-2.80)

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	200	5% 79% 14% 6%
1	B	200	4% 76% 16% 8%
1	C	200	15% 78% 16% 7%
2	D	132	7% 78% 17% .
2	E	132	14% 65% 23% 12%

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 6383 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 Mothers against decapentaplegic homolog 2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	187	Total	C	N	O	S	0	0	0
			1492	946	263	271	12			
1	B	185	Total	C	N	O	S	0	0	0
			1476	936	261	267	12			
1	C	186	Total	C	N	O	S	0	0	0
			1483	941	262	268	12			

There are 9 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	259	GLY	-	expression tag	UNP Q15796
A	260	PRO	-	expression tag	UNP Q15796
A	261	GLY	-	expression tag	UNP Q15796
B	259	GLY	-	expression tag	UNP Q15796
B	260	PRO	-	expression tag	UNP Q15796
B	261	GLY	-	expression tag	UNP Q15796
C	259	GLY	-	expression tag	UNP Q15796
C	260	PRO	-	expression tag	UNP Q15796
C	261	GLY	-	expression tag	UNP Q15796

- Molecule 2 is a protein called Inner nuclear membrane protein Man1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	D	127	Total	C	N	O	S	0	0	0
			1020	649	184	181	6			
2	E	116	Total	C	N	O	S	0	0	0
			912	581	159	166	6			

There are 6 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
D	759	GLY	-	expression tag	UNP Q9Y2U8

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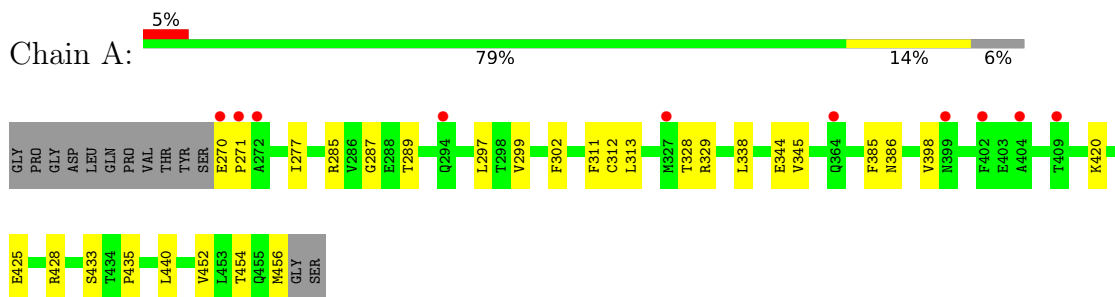
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Chain	Residue	Modelled	Actual	Comment	Reference
D	760	PRO	-	expression tag	UNP Q9Y2U8
D	761	GLY	-	expression tag	UNP Q9Y2U8
E	759	GLY	-	expression tag	UNP Q9Y2U8
E	760	PRO	-	expression tag	UNP Q9Y2U8
E	761	GLY	-	expression tag	UNP Q9Y2U8

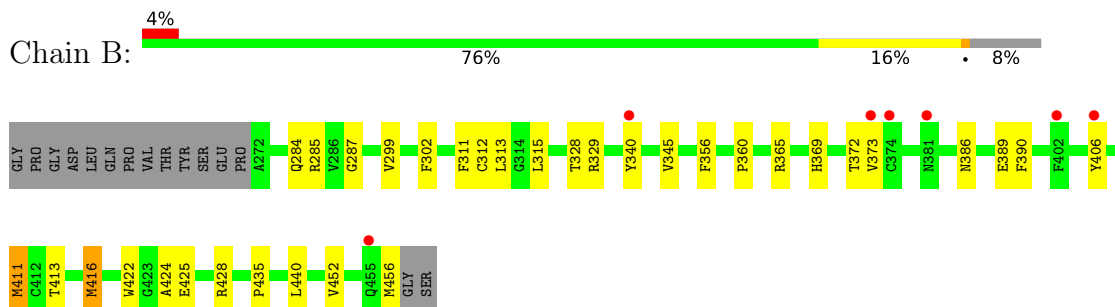
3 Residue-property plots [i](#)

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.

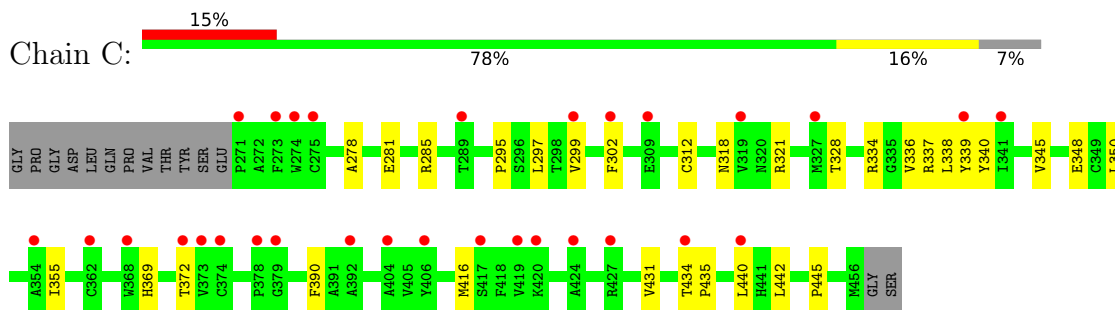
- Molecule 1: Mothers against decapentaplegic homolog 2



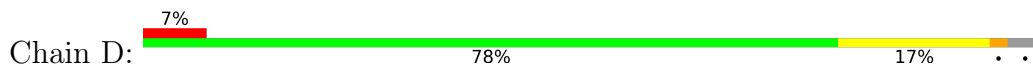
- Molecule 1: Mothers against decapentaplegic homolog 2

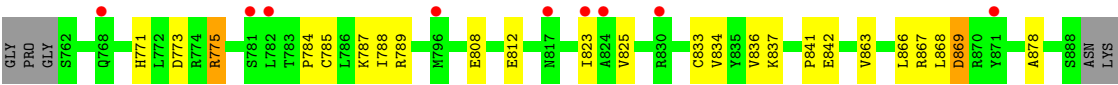


- Molecule 1: Mothers against decapentaplegic homolog 2

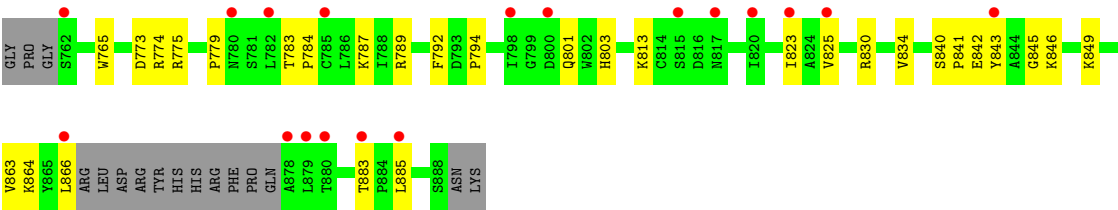


- Molecule 2: Inner nuclear membrane protein Man1





● Molecule 2: Inner nuclear membrane protein Man1



4 Data and refinement statistics

Property	Value	Source
Space group	P 65	Depositor
Cell constants a, b, c, α , β , γ	176.81Å 176.81Å 73.85Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	42.47 – 2.79 42.47 – 2.79	Depositor EDS
% Data completeness (in resolution range)	91.3 (42.47-2.79) 97.0 (42.47-2.79)	Depositor EDS
R_{merge}	0.15	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.11 (at 2.81Å)	Xtriage
Refinement program	PHENIX 1.12rc2_2821: ???	Depositor
R, R_{free}	0.242 , 0.269 0.244 , 0.269	Depositor DCC
R_{free} test set	1526 reflections (4.63%)	wwPDB-VP
Wilson B-factor (Å ²)	65.8	Xtriage
Anisotropy	0.439	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 60.8	EDS
L-test for twinning ²	$\langle L \rangle = 0.51$, $\langle L^2 \rangle = 0.34$	Xtriage
Estimated twinning fraction	0.017 for h,-h-k,-l	Xtriage
F_o, F_c correlation	0.91	EDS
Total number of atoms	6383	wwPDB-VP
Average B, all atoms (Å ²)	78.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.96% 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	0.12	0/1531	0.32	0/2081
1	B	0.11	0/1514	0.34	0/2057
1	C	0.10	0/1522	0.33	0/2068
2	D	0.10	0/1048	0.34	0/1419
2	E	0.11	0/934	0.33	0/1264
All	All	0.11	0/6549	0.33	0/8889

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

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	1492	0	1443	21	0
1	B	1476	0	1430	21	0
1	C	1483	0	1438	19	0
2	D	1020	0	1009	17	0
2	E	912	0	907	22	0
All	All	6383	0	6227	94	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 7.

All (94) 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:E:784:PRO:HD3	2:E:841:PRO:HG3	1.68	0.74
1:A:338:LEU:HD13	1:A:440:LEU:HD21	1.72	0.71
2:D:823:ILE:HG22	2:D:836:VAL:HG22	1.75	0.68
1:A:425:GLU:HG2	2:D:771:HIS:HB3	1.77	0.66
2:D:869:ASP:OD1	2:D:869:ASP:N	2.26	0.65
2:E:789:ARG:HH12	2:E:864:LYS:HB2	1.62	0.64
2:E:840:SER:HB3	2:E:843:TYR:HD1	1.62	0.64
2:D:787:LYS:NZ	2:D:833:CYS:SG	2.72	0.63
1:B:369:HIS:HB3	1:B:372:THR:HG23	1.81	0.62
2:E:774:ARG:HH11	2:E:774:ARG:HA	1.63	0.62
1:C:338:LEU:HD13	1:C:440:LEU:HD21	1.83	0.60
2:D:775:ARG:HH11	2:D:775:ARG:HB2	1.66	0.60
1:A:285:ARG:NH2	1:A:289:THR:OG1	2.39	0.55
1:C:278:ALA:HB1	1:C:285:ARG:NH1	2.22	0.55
2:E:825:VAL:HG12	2:E:834:VAL:HG13	1.89	0.54
1:C:336:VAL:HG12	1:C:355:ILE:HG21	1.89	0.54
1:A:328:THR:HG21	1:A:435:PRO:HG2	1.90	0.54
1:B:328:THR:HG21	1:B:435:PRO:HG2	1.89	0.54
1:B:373:VAL:HG11	1:B:422:TRP:O	2.08	0.54
1:C:281:GLU:OE1	1:C:318:ASN:ND2	2.37	0.53
2:D:775:ARG:HD3	2:D:775:ARG:H	1.75	0.52
1:B:425:GLU:CD	2:E:775:ARG:HH22	2.17	0.51
1:B:365:ARG:NH1	1:B:389:GLU:OE1	2.44	0.51
2:E:773:ASP:OD1	2:E:775:ARG:HG2	2.10	0.51
2:E:845:GLY:O	2:E:849:LYS:HG3	2.11	0.51
1:A:285:ARG:NH1	1:A:287:GLY:O	2.41	0.50
1:A:452:VAL:O	1:A:456:MET:HG3	2.11	0.50
1:C:328:THR:HG21	1:C:435:PRO:HG2	1.94	0.50
1:C:431:VAL:O	1:C:434:THR:HG22	2.11	0.50
2:E:774:ARG:NH2	2:E:779:PRO:HG3	2.27	0.50
2:E:842:GLU:N	2:E:842:GLU:OE1	2.44	0.49
1:C:369:HIS:HB3	1:C:372:THR:HG23	1.94	0.49
2:D:867:ARG:NH1	2:D:869:ASP:OD2	2.46	0.49
2:E:803:HIS:HB2	2:E:825:VAL:HG21	1.94	0.48
2:D:808:GLU:O	2:D:812:GLU:HG3	2.13	0.48
1:B:285:ARG:NH2	1:B:287:GLY:O	2.46	0.48
2:D:825:VAL:HG12	2:D:834:VAL:HG13	1.94	0.48
1:B:428:ARG:NH1	1:B:435:PRO:HD3	2.28	0.48
1:C:442:LEU:HB3	1:C:445:PRO:HD2	1.96	0.47
2:E:823:ILE:HD12	2:E:885:LEU:HD12	1.95	0.47
2:D:837:LYS:HD2	2:D:878:ALA:HB1	1.97	0.47
2:D:785:CYS:HB2	2:D:866:LEU:O	2.15	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:295:PRO:HB2	1:C:339:TYR:HE1	1.80	0.47
2:E:840:SER:HB3	2:E:843:TYR:CD1	2.47	0.47
2:E:846:LYS:HA	2:E:846:LYS:HD2	1.80	0.47
1:A:313:LEU:O	1:A:329:ARG:NH2	2.43	0.46
1:C:299:VAL:HB	1:C:336:VAL:HG22	1.97	0.46
1:B:369:HIS:HB2	2:E:775:ARG:HB2	1.96	0.46
1:C:281:GLU:OE2	1:C:321:ARG:NH1	2.47	0.46
1:B:299:VAL:HG22	1:B:311:PHE:HB3	1.98	0.46
1:B:360:PRO:HB2	1:B:411:MET:HE2	1.97	0.46
2:E:774:ARG:CZ	2:E:779:PRO:HG3	2.45	0.46
1:A:420:LYS:HD2	1:A:428:ARG:NH1	2.30	0.46
1:C:339:TYR:HD1	1:C:340:TYR:H	1.64	0.46
1:A:270:GLU:HB2	1:A:271:PRO:HD3	1.98	0.45
1:C:337:ARG:HB2	1:C:348:GLU:HB3	1.99	0.45
2:D:788:ILE:HG12	2:D:863:VAL:HG22	1.99	0.45
1:C:302:PHE:O	1:C:312:CYS:HB3	2.16	0.45
1:A:425:GLU:OE2	2:D:775:ARG:NH2	2.38	0.45
1:C:337:ARG:HG2	1:C:350:LEU:HD11	1.97	0.45
1:B:340:TYR:HD1	1:B:345:VAL:HG22	1.82	0.45
1:B:313:LEU:O	1:B:329:ARG:NH2	2.46	0.44
2:E:783:THR:HG21	2:E:866:LEU:O	2.16	0.44
1:A:299:VAL:HG22	1:A:311:PHE:HB3	1.99	0.44
2:D:775:ARG:HB2	2:D:775:ARG:NH1	2.30	0.44
1:A:297:LEU:N	1:A:338:LEU:O	2.51	0.44
1:A:398:VAL:HG23	1:A:456:MET:SD	2.58	0.43
1:A:302:PHE:O	1:A:312:CYS:HB3	2.18	0.43
1:A:344:GLU:OE2	1:A:386:ASN:ND2	2.50	0.43
2:E:765:TRP:CD2	2:E:813:LYS:HD3	2.54	0.43
1:B:424:ALA:HB3	2:E:775:ARG:NH2	2.34	0.43
1:B:413:THR:HA	1:B:440:LEU:O	2.19	0.42
1:A:456:MET:HE3	1:A:456:MET:HB3	1.88	0.42
1:B:406:TYR:HD1	1:B:406:TYR:O	2.03	0.42
1:B:411:MET:HE3	1:B:411:MET:HB2	1.86	0.42
1:A:454:THR:HG22	1:C:302:PHE:CD2	2.55	0.42
1:B:452:VAL:O	1:B:456:MET:HG2	2.20	0.42
2:E:792:PHE:HE2	2:E:794:PRO:HG3	1.84	0.42
1:B:386:ASN:OD1	1:B:389:GLU:HG3	2.20	0.42
1:A:428:ARG:HD3	1:A:433:SER:O	2.20	0.41
1:C:340:TYR:HD1	1:C:345:VAL:HG22	1.84	0.41
1:A:277:ILE:HG12	1:A:440:LEU:HG	2.03	0.41
2:E:787:LYS:O	2:E:863:VAL:HA	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:302:PHE:O	1:B:312:CYS:HB3	2.20	0.41
2:E:830:ARG:HD3	2:E:830:ARG:O	2.21	0.41
1:A:345:VAL:CG1	1:A:385:PHE:HB3	2.51	0.41
1:A:420:LYS:HD2	1:A:428:ARG:HH12	1.85	0.41
1:B:390:PHE:HD1	1:B:411:MET:HG2	1.85	0.41
1:C:297:LEU:HD22	1:C:338:LEU:HD12	2.03	0.41
1:B:356:PHE:O	1:B:416:MET:HA	2.21	0.40
1:C:390:PHE:CE2	1:C:445:PRO:HB3	2.57	0.40
2:D:842:GLU:OE1	2:D:842:GLU:N	2.54	0.40
2:D:773:ASP:OD1	2:D:775:ARG:NH1	2.54	0.40
2:D:784:PRO:HD3	2:D:841:PRO:HG3	2.03	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	185/200 (92%)	180 (97%)	5 (3%)	0	100	100
1	B	183/200 (92%)	178 (97%)	5 (3%)	0	100	100
1	C	184/200 (92%)	180 (98%)	4 (2%)	0	100	100
2	D	125/132 (95%)	119 (95%)	6 (5%)	0	100	100
2	E	112/132 (85%)	108 (96%)	4 (4%)	0	100	100
All	All	789/864 (91%)	765 (97%)	24 (3%)	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	162/172 (94%)	162 (100%)	0	100	100
1	B	160/172 (93%)	156 (98%)	4 (2%)	42	76
1	C	161/172 (94%)	159 (99%)	2 (1%)	63	87
2	D	112/115 (97%)	108 (96%)	4 (4%)	31	66
2	E	101/115 (88%)	99 (98%)	2 (2%)	48	80
All	All	696/746 (93%)	684 (98%)	12 (2%)	53	83

All (12) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	284	GLN
1	B	315	LEU
1	B	411	MET
1	B	416	MET
1	C	334	ARG
1	C	416	MET
2	D	775	ARG
2	D	789	ARG
2	D	868	LEU
2	D	869	ASP
2	E	801	GLN
2	E	883	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (8) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	291	HIS
1	A	294	GLN
1	A	400	GLN
1	A	447	GLN
1	B	358	GLN
1	C	358	GLN
1	C	387	ASN
2	E	882	ASN

5.3.3 RNA [i](#)

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

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	187/200 (93%)	0.46	10 (5%) 32 24	36, 59, 104, 134	0
1	B	185/200 (92%)	0.50	7 (3%) 44 35	41, 60, 87, 103	0
1	C	186/200 (93%)	1.18	30 (16%) 4 4	53, 97, 125, 161	0
2	D	127/132 (96%)	0.83	9 (7%) 22 16	51, 75, 113, 137	0
2	E	116/132 (87%)	1.14	18 (15%) 5 4	50, 96, 132, 162	0
All	All	801/864 (92%)	0.79	74 (9%) 14 10	36, 73, 118, 162	0

All (74) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	341	ILE	5.1
2	E	879	LEU	4.6
2	E	782	LEU	4.5
2	E	762	SER	4.4
1	C	374	CYS	4.4
1	C	354	ALA	3.9
2	E	785	CYS	3.8
1	C	339	TYR	3.8
1	B	340	TYR	3.7
1	C	271	PRO	3.6
1	B	406	TYR	3.6
1	C	368	TRP	3.5
2	D	782	LEU	3.3
2	E	843	TYR	3.3
2	D	796	MET	3.3
2	D	817	ASN	3.3
1	C	327	MET	3.2
2	D	781	SER	3.2
1	C	319	VAL	3.1
1	A	402	PHE	3.1

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Mol	Chain	Res	Type	RSRZ
1	C	424	ALA	3.1
2	E	823	ILE	3.0
1	A	364	GLN	3.0
1	C	362	CYS	2.9
2	E	885	LEU	2.9
1	C	434	THR	2.8
1	C	406	TYR	2.8
1	C	302	PHE	2.8
1	B	381	ASN	2.7
1	B	374	CYS	2.7
2	E	817	ASN	2.7
2	E	825	VAL	2.7
1	C	420	LYS	2.7
1	C	419	VAL	2.6
1	C	299	VAL	2.6
1	B	455	GLN	2.6
2	D	823	ILE	2.5
1	C	392	ALA	2.5
1	A	270	GLU	2.5
1	C	273	PHE	2.5
1	A	327	MET	2.5
1	B	373	VAL	2.4
1	A	272	ALA	2.4
2	E	878	ALA	2.4
2	E	866	LEU	2.4
1	C	275	CYS	2.4
1	C	440	LEU	2.4
2	E	820	ILE	2.4
1	C	274	TRP	2.4
1	A	271	PRO	2.3
2	D	830	ARG	2.3
1	A	404	ALA	2.3
2	E	883	THR	2.3
1	B	402	PHE	2.3
1	A	409	THR	2.3
2	E	798	ILE	2.2
1	C	404	ALA	2.2
1	C	379	GLY	2.2
1	C	309	GLU	2.2
1	C	372	THR	2.2
1	C	427	ARG	2.2
2	E	800	ASP	2.2

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Mol	Chain	Res	Type	RSRZ
1	C	289	THR	2.1
2	E	815	SER	2.1
2	D	768	GLN	2.1
1	C	373	VAL	2.1
2	D	824	ALA	2.1
1	A	294	GLN	2.1
2	E	780	ASN	2.1
1	C	417	SER	2.1
2	E	880	THR	2.0
1	A	399	ASN	2.0
2	D	871	TYR	2.0
1	C	378	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.