wwPDB X-ray Structure Validation Summary Report (i)

Oct 29, 2024 – 06:38 AM EDT

PDB ID	:	3O4X
Title	:	Crystal structure of complex between amino and carboxy terminal fragments of mDia1
Authors	:	Eck, M.J.; Nezami, A.; Toms, A.V.
Deposited on	:	2010-07-27
Resolution	:	3.20 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 (i) 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 (i)) were used in the production of this report:

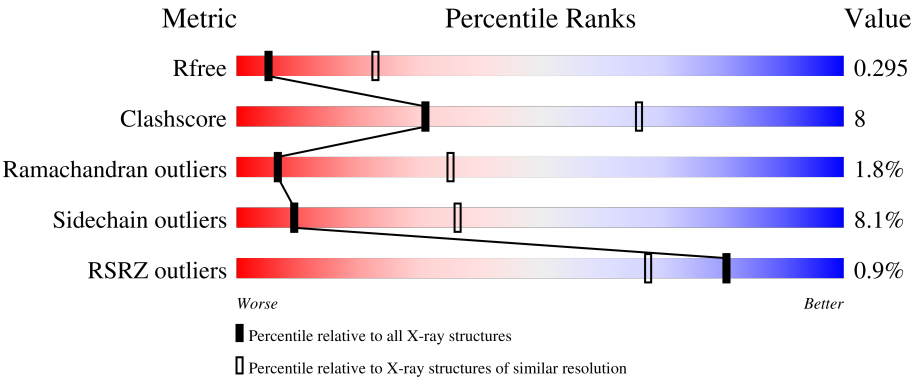
MolProbity	:	4.02b-467
Xtriage (Phenix)	:	1.20.1
EDS	:	3.0
Percentile statistics	:	20231227.v01 (using entries in the PDB archive December 27th 2023)
CCP4	:	9.0.003 (Gargrove)
Density-Fitness	:	1.0.11
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.39

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:
X-RAY DIFFRACTION

The reported resolution of this entry is 3.20 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}	164625	1370 (3.20-3.20)
Clashscore	180529	1497 (3.20-3.20)
Ramachandran outliers	177936	1479 (3.20-3.20)
Sidechain outliers	177891	1478 (3.20-3.20)
RSRZ outliers	164620	1371 (3.20-3.20)

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 <=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	330	70% 24%
1	B	330	71% 22%
1	C	330	71% 21% 6%
1	D	330	74% 20%
2	E	467	69% 19% 5% 7%

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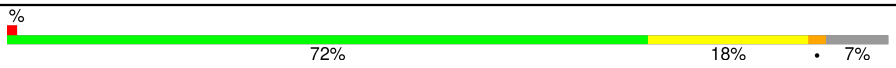
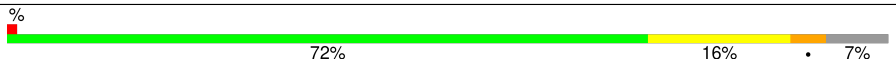
Mol	Chain	Length	Quality of chain
2	F	467	
2	G	467	
2	H	467	

2 Entry composition (i)

There are 3 unique types of molecules in this entry. The entry contains 24335 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 Protein diaphanous homolog 1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	317	Total	C	N	O	S	0	0	0
			2552	1605	440	485	22			
1	B	318	Total	C	N	O	S	0	0	0
			2559	1609	441	487	22			
1	C	311	Total	C	N	O	S	0	0	0
			2508	1579	432	475	22			
1	D	319	Total	C	N	O	S	0	0	0
			2568	1614	442	490	22			

There are 8 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	129	GLY	-	expression tag	UNP O08808
A	130	SER	-	expression tag	UNP O08808
B	129	GLY	-	expression tag	UNP O08808
B	130	SER	-	expression tag	UNP O08808
C	129	GLY	-	expression tag	UNP O08808
C	130	SER	-	expression tag	UNP O08808
D	129	GLY	-	expression tag	UNP O08808
D	130	SER	-	expression tag	UNP O08808

- Molecule 2 is a protein called Protein diaphanous homolog 1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	E	433	Total	C	N	O	S	0	0	0
			3525	2230	602	672	21			
2	H	433	Total	C	N	O	S	0	0	0
			3525	2230	602	672	21			
2	G	433	Total	C	N	O	S	0	0	0
			3525	2230	602	672	21			
2	F	433	Total	C	N	O	S	0	0	0
			3525	2230	602	672	21			

There are 8 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
E	734	GLY	-	expression tag	UNP O08808
E	735	SER	-	expression tag	UNP O08808
H	734	GLY	-	expression tag	UNP O08808
H	735	SER	-	expression tag	UNP O08808
G	734	GLY	-	expression tag	UNP O08808
G	735	SER	-	expression tag	UNP O08808
F	734	GLY	-	expression tag	UNP O08808
F	735	SER	-	expression tag	UNP O08808

- Molecule 3 is water.

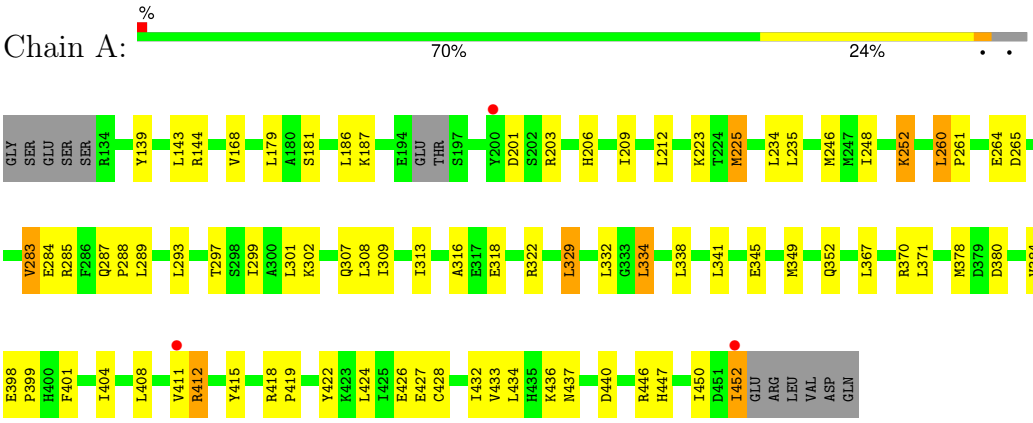
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	8	Total O 8 8	0	0
3	B	9	Total O 9 9	0	0
3	C	6	Total O 6 6	0	0
3	D	8	Total O 8 8	0	0
3	E	5	Total O 5 5	0	0
3	H	4	Total O 4 4	0	0
3	G	6	Total O 6 6	0	0
3	F	2	Total O 2 2	0	0

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.

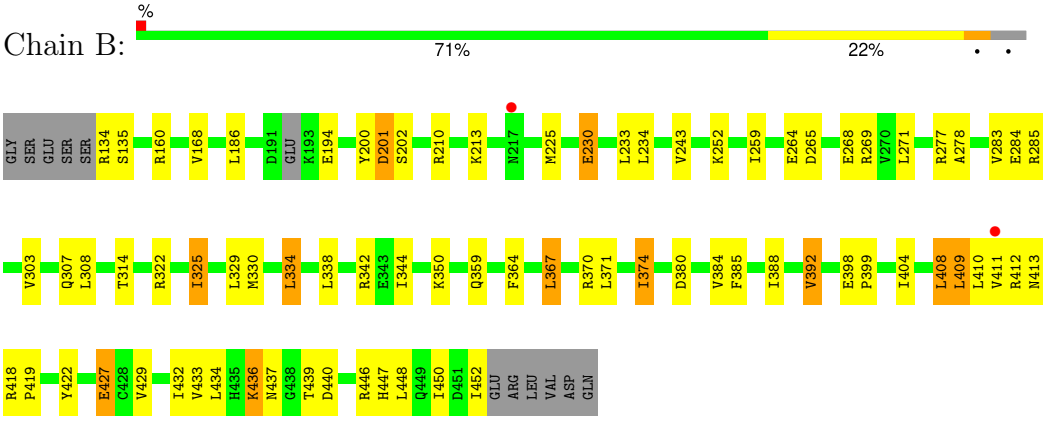
• Molecule 1: Protein diaphanous homolog 1

Chain A:



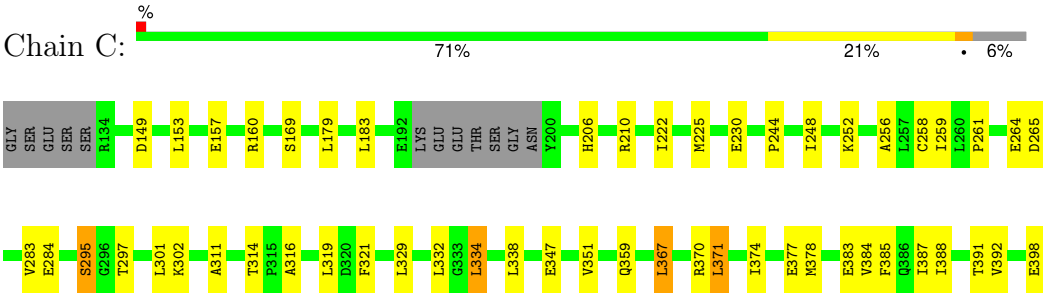
• Molecule 1: Protein diaphanous homolog 1

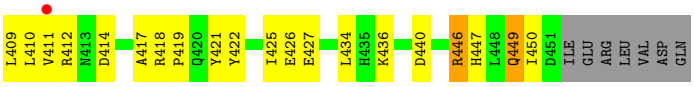
Chain B:



• Molecule 1: Protein diaphanous homolog 1

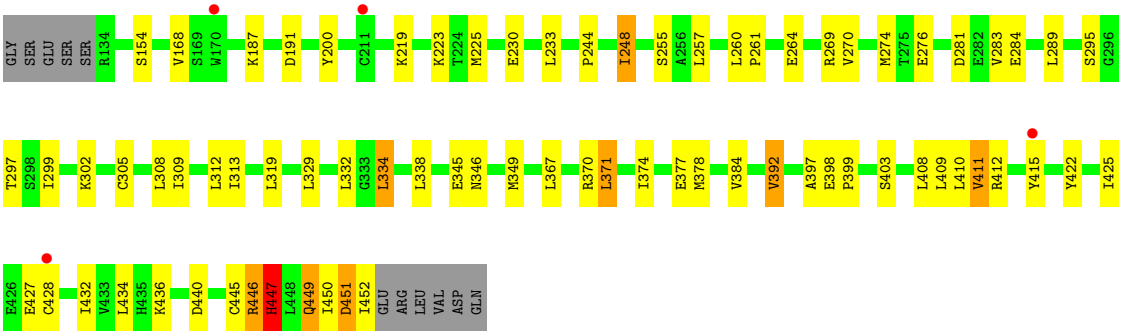
Chain C:





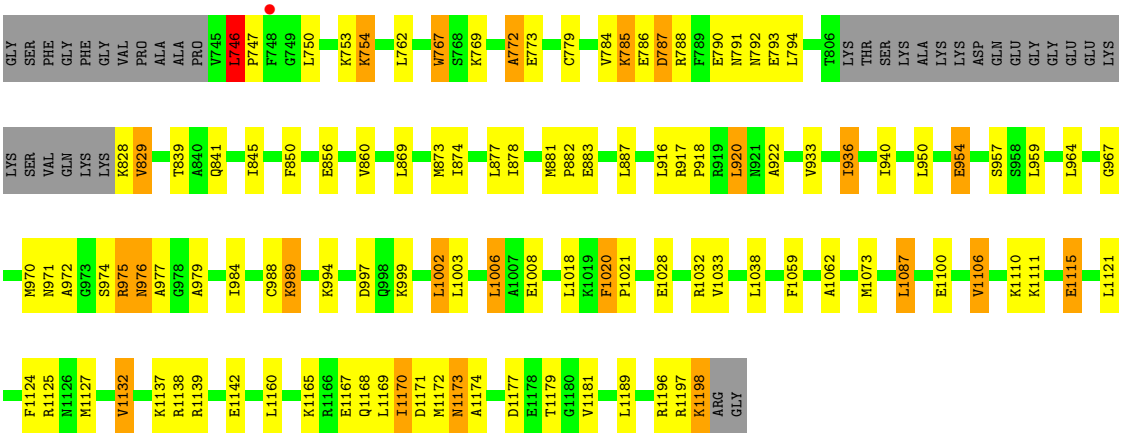
• Molecule 1: Protein diaphanous homolog 1

Chain D:



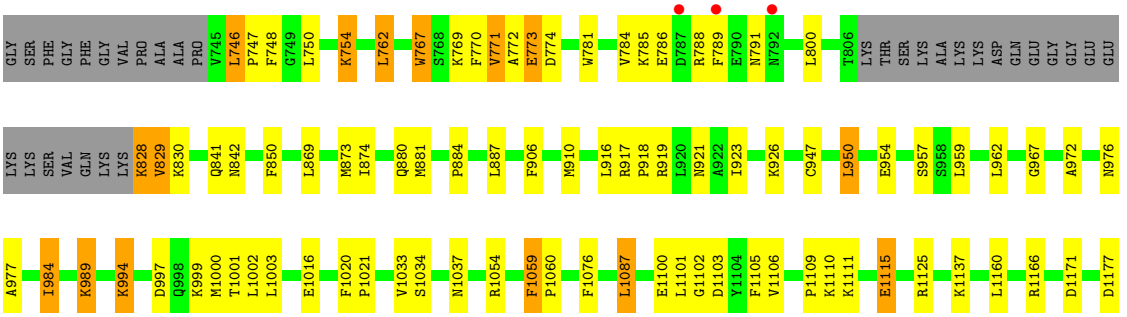
• Molecule 2: Protein diaphanous homolog 1

Chain E:



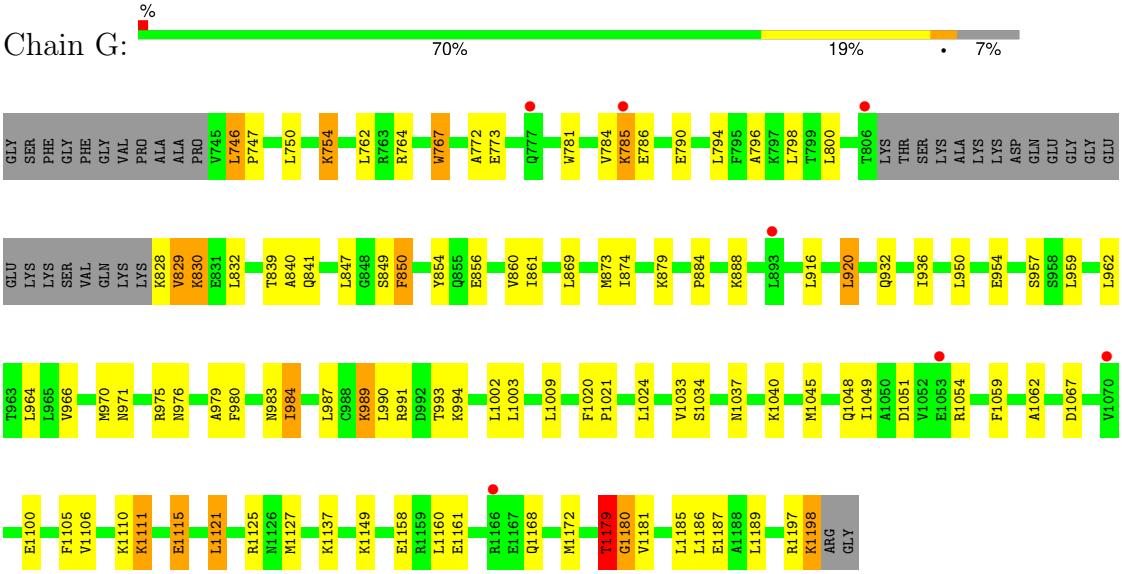
• Molecule 2: Protein diaphanous homolog 1

Chain H:



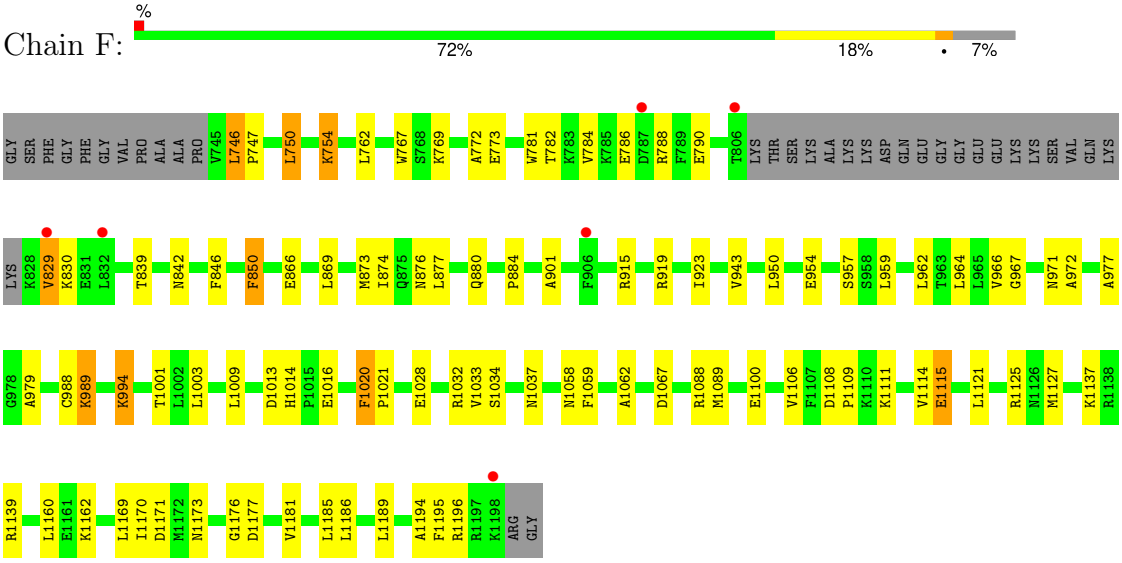
• Molecule 2: Protein diaphanous homolog 1

Chain G:



• Molecule 2: Protein diaphanous homolog 1

Chain F:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α, β, γ	95.76Å 206.83Å 131.06Å 90.00° 105.94° 90.00°	Depositor
Resolution (Å)	20.12 – 3.20 20.12 – 3.20	Depositor EDS
% Data completeness (in resolution range)	100.0 (20.12-3.20) 98.6 (20.12-3.20)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.11	Depositor
$< I/\sigma(I) >$ [1]	2.45 (at 3.22Å)	Xtriage
Refinement program	REFMAC 5.5.0109	Depositor
R, R_{free}	0.233 , 0.298 0.232 , 0.295	Depositor DCC
R_{free} test set	3981 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å^2)	66.5	Xtriage
Anisotropy	0.118	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.28 , 77.1	EDS
L-test for twinning[2]	$< \|L\| > = 0.44$, $< L^2 > = 0.27$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.91	EDS
Total number of atoms	24335	wwPDB-VP
Average B, all atoms (Å^2)	107.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.73% of the height of the origin peak. No significant pseudotranslation is detected.*

[1] Intensities estimated from amplitudes.

[2] Theoretical values of $< |L| >$, $< L^2 >$ 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	0.36	0/2588	0.58	0/3483
1	B	0.37	0/2595	0.56	0/3493
1	C	0.37	0/2544	0.55	1/3425 (0.0%)
1	D	0.36	0/2605	0.55	1/3508 (0.0%)
2	E	0.37	0/3580	0.55	0/4799
2	F	0.36	0/3580	0.53	0/4799
2	G	0.36	0/3580	0.53	0/4799
2	H	0.38	0/3580	0.53	0/4799
All	All	0.37	0/24652	0.55	2/33105 (0.0%)

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	C	371	LEU	CA-CB-CG	6.41	130.03	115.30
1	D	371	LEU	CA-CB-CG	5.18	127.21	115.30

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	2552	0	2563	59	0
1	B	2559	0	2570	73	0
1	C	2508	0	2519	57	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	D	2568	0	2577	47	0
2	E	3525	0	3552	65	0
2	F	3525	0	3552	57	0
2	G	3525	0	3552	67	0
2	H	3525	0	3552	52	0
3	A	8	0	0	0	0
3	B	9	0	0	1	0
3	C	6	0	0	0	0
3	D	8	0	0	0	0
3	E	5	0	0	0	0
3	F	2	0	0	0	0
3	G	6	0	0	1	0
3	H	4	0	0	0	0
All	All	24335	0	24437	396	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 8.

The worst 5 of 396 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:988:CYS:HA	2:E:1127:MET:HE1	1.34	1.09
1:D:446:ARG:O	1:D:447:HIS:HB2	1.66	0.94
2:G:754:LYS:H	2:G:754:LYS:HE2	1.32	0.94
1:B:410:LEU:HD11	1:C:371:LEU:HB2	1.47	0.94
2:E:828:LYS:N	2:E:829:VAL:HA	1.81	0.92

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	313/330 (95%)	299 (96%)	13 (4%)	1 (0%)	37 69
1	B	314/330 (95%)	296 (94%)	15 (5%)	3 (1%)	13 47
1	C	307/330 (93%)	289 (94%)	14 (5%)	4 (1%)	10 41
1	D	317/330 (96%)	296 (93%)	16 (5%)	5 (2%)	8 37
2	E	429/467 (92%)	390 (91%)	26 (6%)	13 (3%)	3 23
2	F	429/467 (92%)	387 (90%)	33 (8%)	9 (2%)	5 31
2	G	429/467 (92%)	389 (91%)	31 (7%)	9 (2%)	5 31
2	H	429/467 (92%)	384 (90%)	37 (9%)	8 (2%)	6 34
All	All	2967/3188 (93%)	2730 (92%)	185 (6%)	52 (2%)	7 35

5 of 52 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	264	GLU
1	C	264	GLU
1	D	447	HIS
1	D	451	ASP
2	E	975	ARG

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	287/299 (96%)	264 (92%)	23 (8%)	10 37
1	B	288/299 (96%)	270 (94%)	18 (6%)	15 46
1	C	282/299 (94%)	264 (94%)	18 (6%)	14 46
1	D	289/299 (97%)	262 (91%)	27 (9%)	7 29
2	E	391/416 (94%)	351 (90%)	40 (10%)	6 26
2	F	391/416 (94%)	363 (93%)	28 (7%)	12 41
2	G	391/416 (94%)	358 (92%)	33 (8%)	9 34
2	H	391/416 (94%)	358 (92%)	33 (8%)	9 34

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
All	All	2710/2860 (95%)	2490 (92%)	220 (8%)	9 36

5 of 220 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	E	1111	LYS
2	H	1003	LEU
2	F	1170	ILE
2	F	850	PHE
2	E	1132	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 43 such sidechains are listed below:

Mol	Chain	Res	Type
2	G	876	ASN
2	F	841	GLN
2	G	880	GLN
2	G	1039	GLN
2	F	876	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, 95^{th} 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	317/330 (96%)	-0.50	3 (0%)	81	68	15, 75, 117, 149	2 (0%)
1	B	318/330 (96%)	-0.51	2 (0%)	85	76	22, 79, 131, 157	2 (0%)
1	C	311/330 (94%)	-0.49	2 (0%)	85	76	15, 80, 129, 213	2 (0%)
1	D	319/330 (96%)	-0.05	4 (1%)	74	60	16, 112, 166, 198	2 (0%)
2	E	433/467 (92%)	-0.28	1 (0%)	92	87	47, 94, 144, 177	0
2	F	433/467 (92%)	0.13	6 (1%)	73	58	61, 133, 211, 256	0
2	G	433/467 (92%)	0.15	7 (1%)	70	55	68, 127, 172, 209	0
2	H	433/467 (92%)	-0.08	3 (0%)	84	73	40, 110, 166, 200	0
All	All	2997/3188 (94%)	-0.17	28 (0%)	81	68	15, 102, 173, 256	8 (0%)

The worst 5 of 28 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	407	HIS	5.1
1	D	415	TYR	5.0
2	F	787	ASP	3.3
2	F	1198	LYS	3.1
1	A	452	ILE	3.1

6.2 Non-standard residues in protein, DNA, RNA chains

There are no non-standard protein/DNA/RNA residues in this entry.

6.3 Carbohydrates

There are no monosaccharides 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.