wwPDB X-ray Structure Validation Summary Report (i)

Aug 20, 2023 – 12:44 PM EDT

PDB ID	:	2O1W
Title	:	Structure of N-terminal plus middle domains (N+M) of GRP94
Authors	:	Dollins, D.E.; Warren, J.J.; Immormino, R.M.; Gewirth, D.T.
Deposited on	:	2006-11-29
Resolution	:	3.40 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:

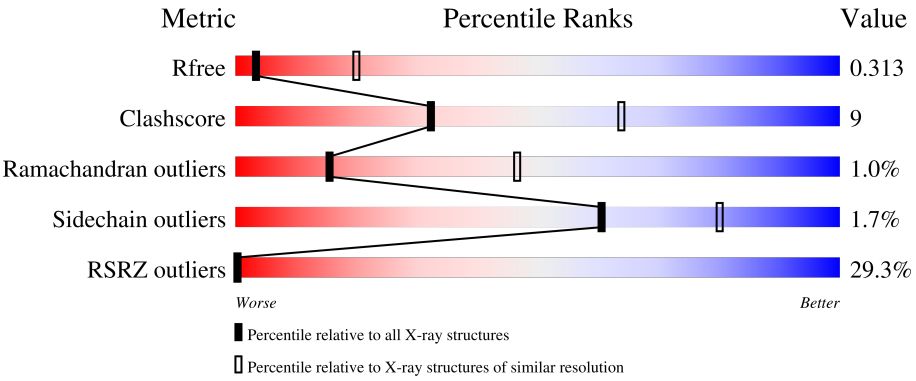
MolProbity	:	4.02b-467
Xtriage (Phenix)	:	1.13
EDS	:	2.35
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.35

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 3.40 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}	130704	1026 (3.48-3.32)
Clashscore	141614	1055 (3.48-3.32)
Ramachandran outliers	138981	1038 (3.48-3.32)
Sidechain outliers	138945	1038 (3.48-3.32)
RSRZ outliers	127900	2173 (3.50-3.30)

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	506	22% 66% 15% · 18%
1	B	506	17% 68% 23% · 7%
1	C	506	20% 65% 17% 18%
1	D	506	26% 67% 15% 18%
1	E	506	38% 69% 14% 18%

2 Entry composition (i)

There is only 1 type of molecule in this entry. The entry contains 17042 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 Endoplasmin.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	416	Total	C	N	O	S	0	1	0
			3333	2133	552	638	10			
1	B	469	Total	C	N	O	S	0	0	0
			3710	2373	615	709	13			
1	C	416	Total	C	N	O	S	0	0	0
			3333	2133	552	638	10			
1	D	416	Total	C	N	O	S	0	0	0
			3333	2133	552	638	10			
1	E	416	Total	C	N	O	S	0	0	0
			3333	2133	552	638	10			

There are 100 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	52	MET	-	expression tag	UNP P41148
A	53	GLY	-	expression tag	UNP P41148
A	54	SER	-	expression tag	UNP P41148
A	55	SER	-	expression tag	UNP P41148
A	56	HIS	-	expression tag	UNP P41148
A	57	HIS	-	expression tag	UNP P41148
A	58	HIS	-	expression tag	UNP P41148
A	59	HIS	-	expression tag	UNP P41148
A	60	HIS	-	expression tag	UNP P41148
A	61	HIS	-	expression tag	UNP P41148
A	62	SER	-	expression tag	UNP P41148
A	63	SER	-	expression tag	UNP P41148
A	64	GLY	-	expression tag	UNP P41148
A	65	LEU	-	expression tag	UNP P41148
A	66	VAL	-	expression tag	UNP P41148
A	67	PRO	-	expression tag	UNP P41148
A	68	ARG	-	expression tag	UNP P41148
A	69	GLY	-	expression tag	UNP P41148
A	70	SER	-	expression tag	UNP P41148

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Chain	Residue	Modelled	Actual	Comment	Reference
A	71	HIS	-	expression tag	UNP P41148
A	72	MET	-	expression tag	UNP P41148
A	287	GLY	-	see remark 999	UNP P41148
A	288	GLY	-	see remark 999	UNP P41148
A	289	GLY	-	see remark 999	UNP P41148
A	290	GLY	-	see remark 999	UNP P41148
B	52	MET	-	expression tag	UNP P41148
B	53	GLY	-	expression tag	UNP P41148
B	54	SER	-	expression tag	UNP P41148
B	55	SER	-	expression tag	UNP P41148
B	56	HIS	-	expression tag	UNP P41148
B	57	HIS	-	expression tag	UNP P41148
B	58	HIS	-	expression tag	UNP P41148
B	59	HIS	-	expression tag	UNP P41148
B	60	HIS	-	expression tag	UNP P41148
B	61	HIS	-	expression tag	UNP P41148
B	62	SER	-	expression tag	UNP P41148
B	63	SER	-	expression tag	UNP P41148
B	64	GLY	-	expression tag	UNP P41148
B	65	LEU	-	expression tag	UNP P41148
B	66	VAL	-	expression tag	UNP P41148
B	67	PRO	-	expression tag	UNP P41148
B	68	ARG	-	expression tag	UNP P41148
B	69	GLY	-	expression tag	UNP P41148
B	70	SER	-	expression tag	UNP P41148
B	71	HIS	-	expression tag	UNP P41148
B	72	MET	-	expression tag	UNP P41148
B	287	GLY	-	see remark 999	UNP P41148
B	288	GLY	-	see remark 999	UNP P41148
B	289	GLY	-	see remark 999	UNP P41148
B	290	GLY	-	see remark 999	UNP P41148
C	52	MET	-	expression tag	UNP P41148
C	53	GLY	-	expression tag	UNP P41148
C	54	SER	-	expression tag	UNP P41148
C	55	SER	-	expression tag	UNP P41148
C	56	HIS	-	expression tag	UNP P41148
C	57	HIS	-	expression tag	UNP P41148
C	58	HIS	-	expression tag	UNP P41148
C	59	HIS	-	expression tag	UNP P41148
C	60	HIS	-	expression tag	UNP P41148
C	61	HIS	-	expression tag	UNP P41148
C	62	SER	-	expression tag	UNP P41148

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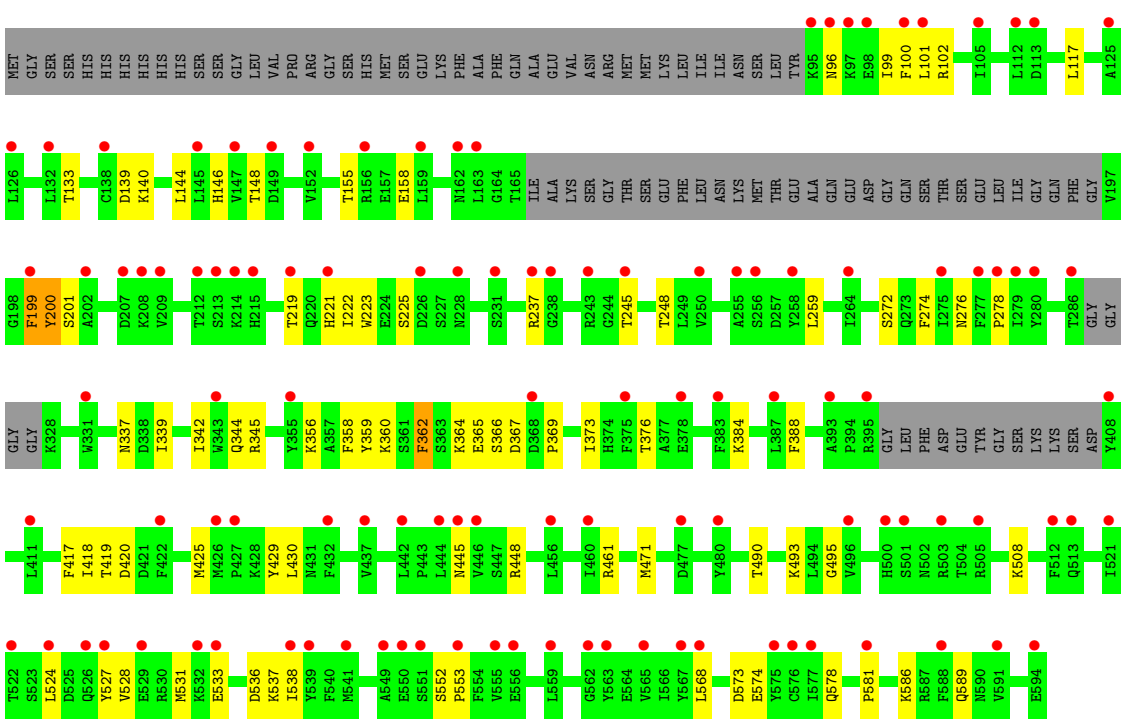
Chain	Residue	Modelled	Actual	Comment	Reference
C	63	SER	-	expression tag	UNP P41148
C	64	GLY	-	expression tag	UNP P41148
C	65	LEU	-	expression tag	UNP P41148
C	66	VAL	-	expression tag	UNP P41148
C	67	PRO	-	expression tag	UNP P41148
C	68	ARG	-	expression tag	UNP P41148
C	69	GLY	-	expression tag	UNP P41148
C	70	SER	-	expression tag	UNP P41148
C	71	HIS	-	expression tag	UNP P41148
C	72	MET	-	expression tag	UNP P41148
C	287	GLY	-	see remark 999	UNP P41148
C	288	GLY	-	see remark 999	UNP P41148
C	289	GLY	-	see remark 999	UNP P41148
C	290	GLY	-	see remark 999	UNP P41148
D	52	MET	-	expression tag	UNP P41148
D	53	GLY	-	expression tag	UNP P41148
D	54	SER	-	expression tag	UNP P41148
D	55	SER	-	expression tag	UNP P41148
D	56	HIS	-	expression tag	UNP P41148
D	57	HIS	-	expression tag	UNP P41148
D	58	HIS	-	expression tag	UNP P41148
D	59	HIS	-	expression tag	UNP P41148
D	60	HIS	-	expression tag	UNP P41148
D	61	HIS	-	expression tag	UNP P41148
D	62	SER	-	expression tag	UNP P41148
D	63	SER	-	expression tag	UNP P41148
D	64	GLY	-	expression tag	UNP P41148
D	65	LEU	-	expression tag	UNP P41148
D	66	VAL	-	expression tag	UNP P41148
D	67	PRO	-	expression tag	UNP P41148
D	68	ARG	-	expression tag	UNP P41148
D	69	GLY	-	expression tag	UNP P41148
D	70	SER	-	expression tag	UNP P41148
D	71	HIS	-	expression tag	UNP P41148
D	72	MET	-	expression tag	UNP P41148
D	287	GLY	-	see remark 999	UNP P41148
D	288	GLY	-	see remark 999	UNP P41148
D	289	GLY	-	see remark 999	UNP P41148
D	290	GLY	-	see remark 999	UNP P41148

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.

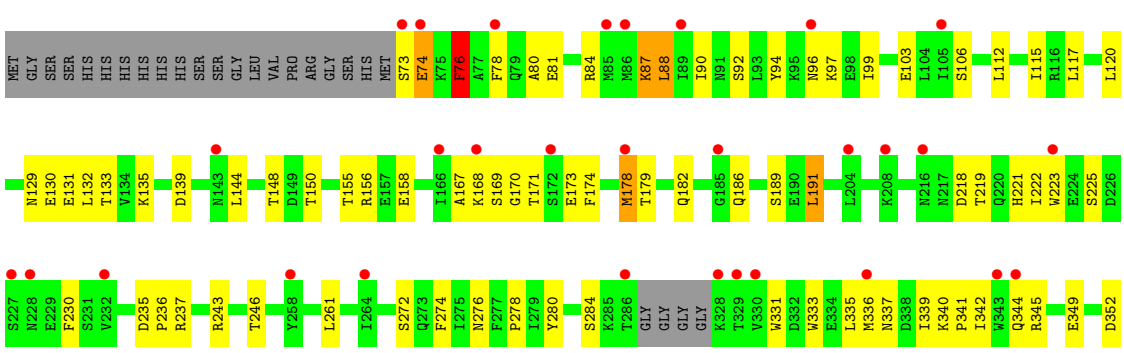
• Molecule 1: Endoplasmin

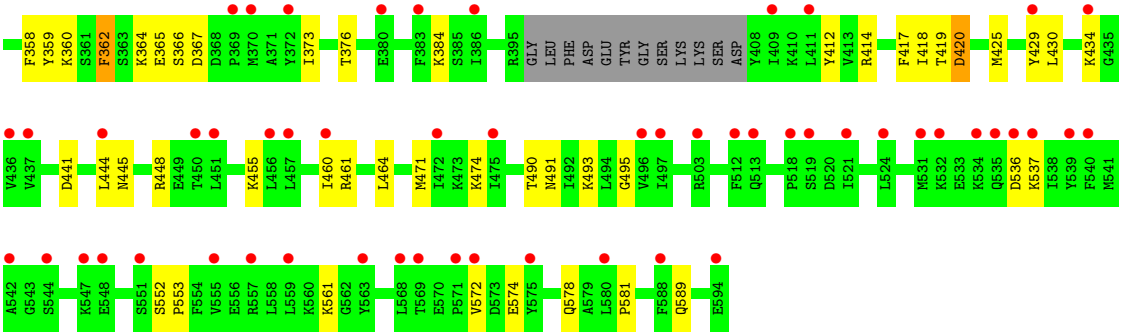
Chain A:



• Molecule 1: Endoplasmin

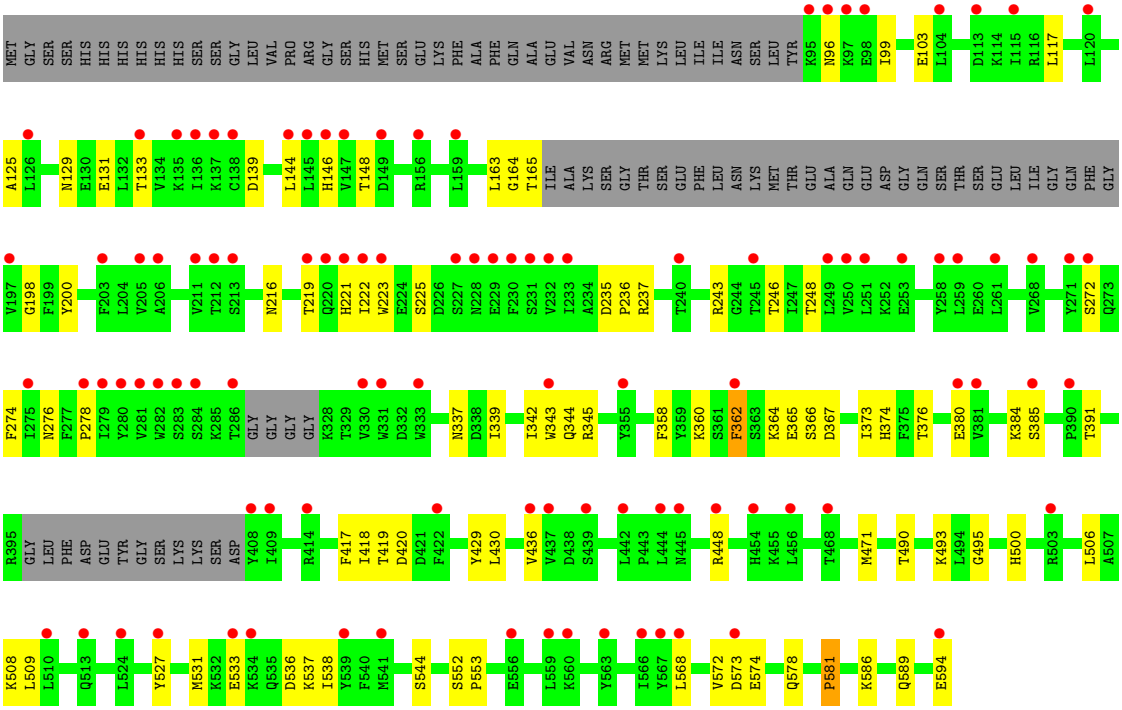
Chain B:





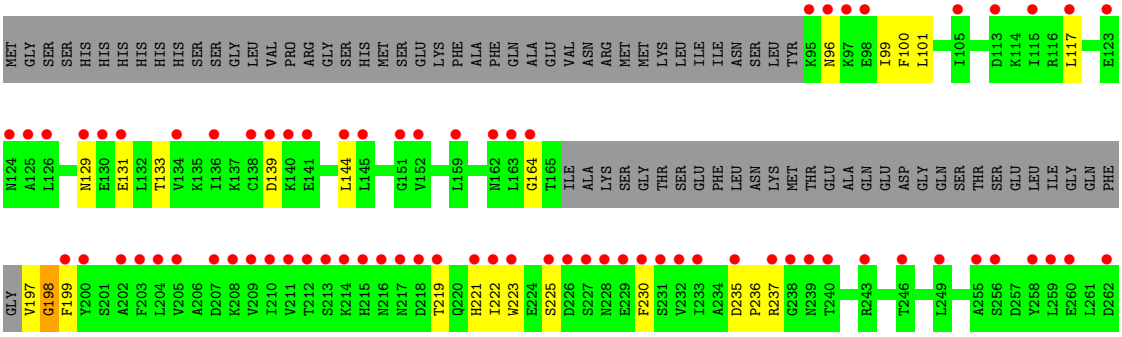
• Molecule 1: Endoplasmin

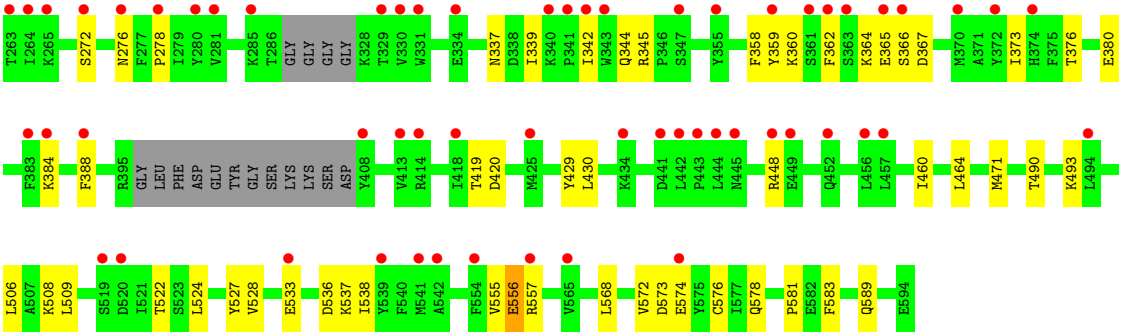
Chain C:

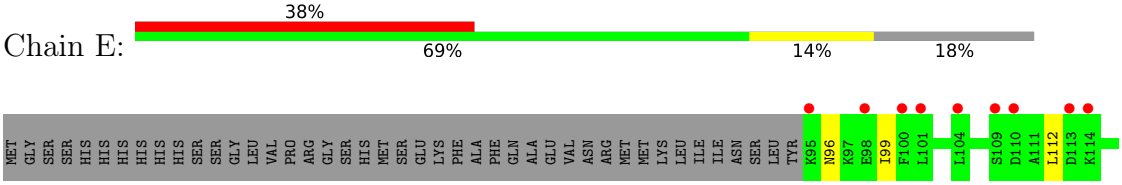


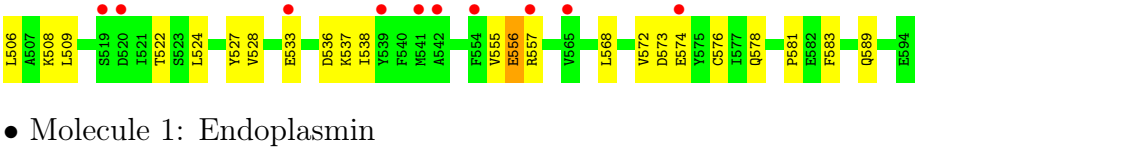
• Molecule 1: Endoplasmin

Chain D:



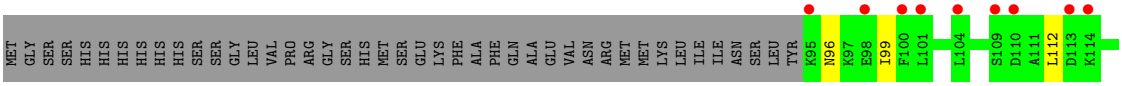


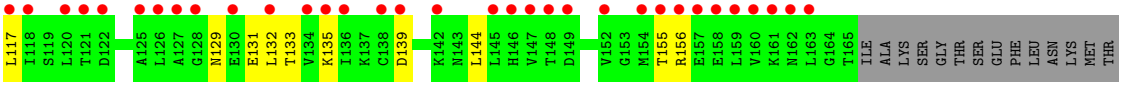


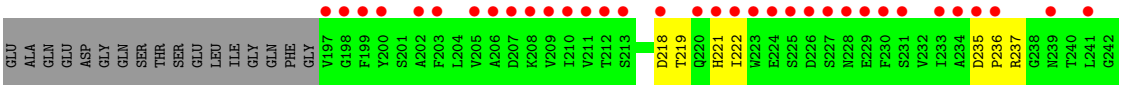


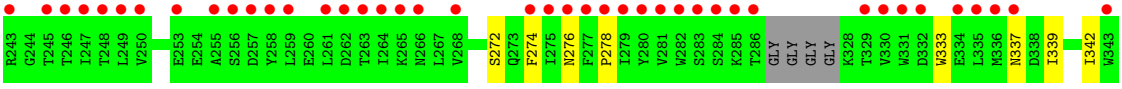
• Molecule 1: Endoplasmin

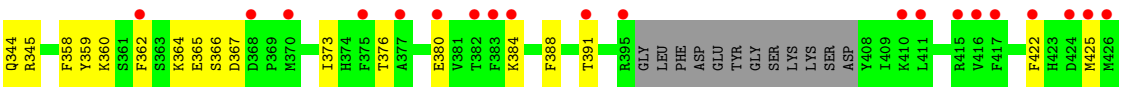
Chain E:

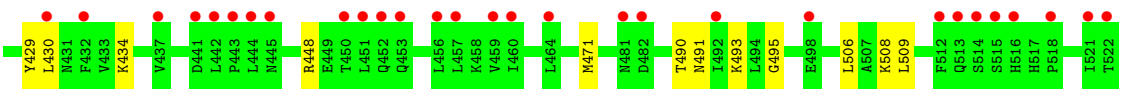


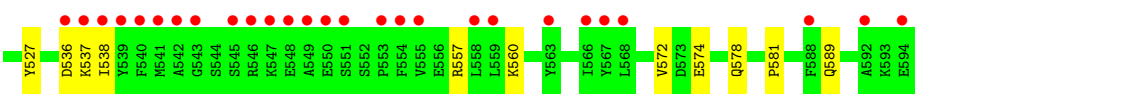












4 Data and refinement statistics (i)

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α, β, γ	210.33Å 137.50Å 133.15Å 90.00° 124.10° 90.00°	Depositor
Resolution (Å)	47.30 – 3.40 47.73 – 3.40	Depositor EDS
% Data completeness (in resolution range)	100.0 (47.30-3.40) 98.1 (47.73-3.40)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.07	Depositor
$< I/\sigma(I) >$ [1]	1.68 (at 3.40Å)	Xtriage
Refinement program	REFMAC 5.2.0019	Depositor
R, R_{free}	0.314 , 0.332 0.294 , 0.313	Depositor DCC
R_{free} test set	2122 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å^2)	148.6	Xtriage
Anisotropy	0.199	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.32 , 247.5	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	17042	wwPDB-VP
Average B, all atoms (Å^2)	195.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.99% 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	0.49	0/3400	0.56	0/4599
1	B	0.83	9/3783 (0.2%)	0.71	3/5117 (0.1%)
1	C	0.57	3/3400 (0.1%)	0.56	0/4599
1	D	0.53	1/3400 (0.0%)	0.58	1/4599 (0.0%)
1	E	0.37	0/3400	0.52	0/4599
All	All	0.58	13/17383 (0.1%)	0.59	4/23513 (0.0%)

The worst 5 of 13 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	87	LYS	CE-NZ	18.68	1.95	1.49
1	C	164	GLY	C-N	12.88	1.63	1.34
1	B	87	LYS	CD-CE	10.94	1.78	1.51
1	B	87	LYS	CG-CD	10.16	1.86	1.52
1	C	165	THR	CB-OG1	8.56	1.60	1.43

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	B	87	LYS	CD-CE-NZ	-10.41	87.76	111.70
1	B	76	PHE	CB-CG-CD2	-6.54	116.22	120.80
1	B	87	LYS	CG-CD-CE	-5.73	94.70	111.90
1	D	557	ARG	NE-CZ-NH2	-5.34	117.63	120.30

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	3333	0	3257	52	1
1	B	3710	0	3611	111	5
1	C	3333	0	3258	82	1
1	D	3333	0	3258	48	0
1	E	3333	0	3258	47	3
All	All	17042	0	16642	297	5

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 9.

The worst 5 of 297 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:B:87:LYS:CE	1:B:87:LYS:CD	1.78	1.61
1:B:87:LYS:CD	1:B:87:LYS:CG	1.87	1.49
1:B:455:LYS:CB	1:C:594:GLU:HB2	1.45	1.44
1:B:414:ARG:NH2	1:C:578:GLN:HG2	1.38	1.36
1:B:414:ARG:NH2	1:C:578:GLN:CG	1.89	1.34

All (5) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:349:GLU:O	1:E:560:LYS:NZ[4_555]	1.61	0.59
1:B:561:LYS:NZ	1:C:544:SER:OG[2_655]	2.04	0.16
1:A:445:ASN:OD1	1:B:284:SER:OG[4_545]	2.08	0.12
1:B:349:GLU:C	1:E:560:LYS:NZ[4_555]	2.12	0.08
1:B:352:ASP:N	1:E:557:ARG:NH2[4_555]	2.13	0.07

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	408/506 (81%)	381 (93%)	23 (6%)	4 (1%)	15	46
1	B	463/506 (92%)	409 (88%)	47 (10%)	7 (2%)	10	36
1	C	408/506 (81%)	379 (93%)	27 (7%)	2 (0%)	29	61
1	D	408/506 (81%)	379 (93%)	24 (6%)	5 (1%)	13	41
1	E	408/506 (81%)	379 (93%)	27 (7%)	2 (0%)	29	61
All	All	2095/2530 (83%)	1927 (92%)	148 (7%)	20 (1%)	15	46

5 of 20 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	199	PHE
1	B	168	LYS
1	B	365	GLU
1	A	200	TYR
1	A	365	GLU

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	365/456 (80%)	361 (99%)	4 (1%)	73	86
1	B	400/456 (88%)	386 (96%)	14 (4%)	36	65
1	C	365/456 (80%)	360 (99%)	5 (1%)	67	83
1	D	365/456 (80%)	361 (99%)	4 (1%)	73	86
1	E	365/456 (80%)	361 (99%)	4 (1%)	73	86
All	All	1860/2280 (82%)	1829 (98%)	31 (2%)	60	80

5 of 31 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	376	THR

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Mol	Chain	Res	Type
1	E	117	LEU
1	B	448	ARG
1	E	391	THR
1	D	376	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (2) such sidechains are listed below:

Mol	Chain	Res	Type
1	B	182	GLN
1	C	578	GLN

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 monosaccharides 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)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
1	C	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	C	164:GLY	C	165:THR	N	1.63

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	416/506 (82%)	1.40	112 (26%)	0	0	179, 194, 209, 226	0
1	B	469/506 (92%)	1.22	84 (17%)	1	1	179, 195, 223, 253	0
1	C	416/506 (82%)	1.21	103 (24%)	0	0	179, 194, 209, 226	0
1	D	416/506 (82%)	1.65	132 (31%)	0	0	179, 194, 209, 226	0
1	E	416/506 (82%)	2.99	194 (46%)	0	0	179, 194, 209, 226	0
All	All	2133/2530 (84%)	1.68	625 (29%)	0	0	179, 194, 211, 253	0

The worst 5 of 625 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	E	285	LYS	54.7
1	E	286	THR	26.6
1	E	198	GLY	21.1
1	E	247	ILE	16.7
1	E	281	VAL	16.4

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 (i)

There are no such residues in this entry.