



Full wwPDB X-ray Structure Validation Report

Mar 1, 2014 – 03:23 AM GMT

PDB ID : 2O1T
Title : Structure of Middle plus C-terminal domains (M+C) of GRP94
Authors : Dollins, D.E.; Warren, J.J.; Immormino, R.M.; Gewirth, D.T.
Deposited on : 2006-11-29
Resolution : 3.20 Å(reported)

This is a full wwPDB validation report for a publicly released PDB entry.
We welcome your comments at validation@mail.wwpdb.org
A user guide is available at <http://wwpdb.org/ValidationPDFNotes.html>

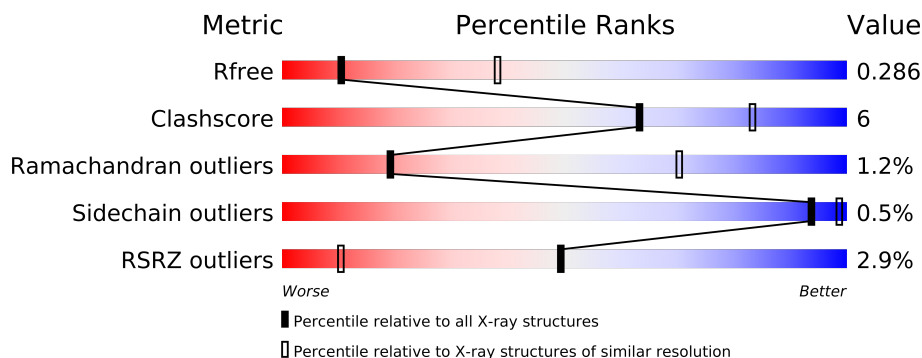
The following versions of software and data (see [references](#)) were used in the production of this report:

MolProbity : 4.02b-467
Mogul : 1.15 2013
Xtriage (Phenix) : dev-1323
EDS : stable22639
Percentile statistics : 21963
Refmac : 5.8.0049
CCP4 : 6.3.0 (Settle)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et. al. (1996)
Validation Pipeline (wwPDB-VP) : stable22683

1 Overall quality at a glance

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}	66092	1824 (3.30-3.10)
Clashscore	79885	1078 (3.26-3.14)
Ramachandran outliers	78287	1059 (3.26-3.14)
Sidechain outliers	78261	1058 (3.26-3.14)
RSRZ outliers	66119	1825 (3.30-3.10)

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 on the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density.

Mol	Chain	Length	Quality of chain
1	A	450	
1	B	450	
1	C	450	
1	D	450	
1	E	450	
1	F	450	
1	G	450	
1	H	450	
1	I	450	
1	J	450	

2 Entry composition

There is only 1 type of molecule in this entry. The entry contains 33009 atoms, of which 0 are hydrogen and 0 are deuterium.

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	413	Total	C	N	O	S	0	0	0
			3301	2101	549	638	13			
1	B	413	Total	C	N	O	S	0	0	0
			3301	2101	549	638	13			
1	C	413	Total	C	N	O	S	0	0	0
			3301	2101	549	638	13			
1	D	413	Total	C	N	O	S	0	0	0
			3301	2101	549	638	13			
1	E	413	Total	C	N	O	S	0	0	0
			3301	2101	549	638	13			
1	F	413	Total	C	N	O	S	0	0	0
			3301	2101	549	638	13			
1	G	413	Total	C	N	O	S	0	0	0
			3300	2101	548	638	13			
1	H	413	Total	C	N	O	S	0	0	0
			3301	2101	549	638	13			
1	I	413	Total	C	N	O	S	0	0	0
			3301	2101	549	638	13			
1	J	413	Total	C	N	O	S	0	0	0
			3301	2101	549	638	13			

There are 200 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	316	MET	-	EXPRESSION TAG	UNP P41148
A	317	GLY	-	EXPRESSION TAG	UNP P41148
A	318	SER	-	EXPRESSION TAG	UNP P41148
A	319	SER	-	EXPRESSION TAG	UNP P41148
A	320	HIS	-	EXPRESSION TAG	UNP P41148
A	321	HIS	-	EXPRESSION TAG	UNP P41148
A	322	HIS	-	EXPRESSION TAG	UNP P41148
A	323	HIS	-	EXPRESSION TAG	UNP P41148
A	324	HIS	-	EXPRESSION TAG	UNP P41148

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Chain	Residue	Modelled	Actual	Comment	Reference
A	325	HIS	-	EXPRESSION TAG	UNP P41148
A	326	SER	-	EXPRESSION TAG	UNP P41148
A	327	SER	-	EXPRESSION TAG	UNP P41148
A	328	GLY	-	EXPRESSION TAG	UNP P41148
A	329	LEU	-	EXPRESSION TAG	UNP P41148
A	330	VAL	-	EXPRESSION TAG	UNP P41148
A	331	PRO	-	EXPRESSION TAG	UNP P41148
A	332	ARG	-	EXPRESSION TAG	UNP P41148
A	333	GLY	-	EXPRESSION TAG	UNP P41148
A	334	SER	-	EXPRESSION TAG	UNP P41148
A	335	HIS	-	EXPRESSION TAG	UNP P41148
B	316	MET	-	EXPRESSION TAG	UNP P41148
B	317	GLY	-	EXPRESSION TAG	UNP P41148
B	318	SER	-	EXPRESSION TAG	UNP P41148
B	319	SER	-	EXPRESSION TAG	UNP P41148
B	320	HIS	-	EXPRESSION TAG	UNP P41148
B	321	HIS	-	EXPRESSION TAG	UNP P41148
B	322	HIS	-	EXPRESSION TAG	UNP P41148
B	323	HIS	-	EXPRESSION TAG	UNP P41148
B	324	HIS	-	EXPRESSION TAG	UNP P41148
B	325	HIS	-	EXPRESSION TAG	UNP P41148
B	326	SER	-	EXPRESSION TAG	UNP P41148
B	327	SER	-	EXPRESSION TAG	UNP P41148
B	328	GLY	-	EXPRESSION TAG	UNP P41148
B	329	LEU	-	EXPRESSION TAG	UNP P41148
B	330	VAL	-	EXPRESSION TAG	UNP P41148
B	331	PRO	-	EXPRESSION TAG	UNP P41148
B	332	ARG	-	EXPRESSION TAG	UNP P41148
B	333	GLY	-	EXPRESSION TAG	UNP P41148
B	334	SER	-	EXPRESSION TAG	UNP P41148
B	335	HIS	-	EXPRESSION TAG	UNP P41148
C	316	MET	-	EXPRESSION TAG	UNP P41148
C	317	GLY	-	EXPRESSION TAG	UNP P41148
C	318	SER	-	EXPRESSION TAG	UNP P41148
C	319	SER	-	EXPRESSION TAG	UNP P41148
C	320	HIS	-	EXPRESSION TAG	UNP P41148
C	321	HIS	-	EXPRESSION TAG	UNP P41148
C	322	HIS	-	EXPRESSION TAG	UNP P41148
C	323	HIS	-	EXPRESSION TAG	UNP P41148
C	324	HIS	-	EXPRESSION TAG	UNP P41148
C	325	HIS	-	EXPRESSION TAG	UNP P41148
C	326	SER	-	EXPRESSION TAG	UNP P41148

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Chain	Residue	Modelled	Actual	Comment	Reference
C	327	SER	-	EXPRESSION TAG	UNP P41148
C	328	GLY	-	EXPRESSION TAG	UNP P41148
C	329	LEU	-	EXPRESSION TAG	UNP P41148
C	330	VAL	-	EXPRESSION TAG	UNP P41148
C	331	PRO	-	EXPRESSION TAG	UNP P41148
C	332	ARG	-	EXPRESSION TAG	UNP P41148
C	333	GLY	-	EXPRESSION TAG	UNP P41148
C	334	SER	-	EXPRESSION TAG	UNP P41148
C	335	HIS	-	EXPRESSION TAG	UNP P41148
D	316	MET	-	EXPRESSION TAG	UNP P41148
D	317	GLY	-	EXPRESSION TAG	UNP P41148
D	318	SER	-	EXPRESSION TAG	UNP P41148
D	319	SER	-	EXPRESSION TAG	UNP P41148
D	320	HIS	-	EXPRESSION TAG	UNP P41148
D	321	HIS	-	EXPRESSION TAG	UNP P41148
D	322	HIS	-	EXPRESSION TAG	UNP P41148
D	323	HIS	-	EXPRESSION TAG	UNP P41148
D	324	HIS	-	EXPRESSION TAG	UNP P41148
D	325	HIS	-	EXPRESSION TAG	UNP P41148
D	326	SER	-	EXPRESSION TAG	UNP P41148
D	327	SER	-	EXPRESSION TAG	UNP P41148
D	328	GLY	-	EXPRESSION TAG	UNP P41148
D	329	LEU	-	EXPRESSION TAG	UNP P41148
D	330	VAL	-	EXPRESSION TAG	UNP P41148
D	331	PRO	-	EXPRESSION TAG	UNP P41148
D	332	ARG	-	EXPRESSION TAG	UNP P41148
D	333	GLY	-	EXPRESSION TAG	UNP P41148
D	334	SER	-	EXPRESSION TAG	UNP P41148
D	335	HIS	-	EXPRESSION TAG	UNP P41148
E	316	MET	-	EXPRESSION TAG	UNP P41148
E	317	GLY	-	EXPRESSION TAG	UNP P41148
E	318	SER	-	EXPRESSION TAG	UNP P41148
E	319	SER	-	EXPRESSION TAG	UNP P41148
E	320	HIS	-	EXPRESSION TAG	UNP P41148
E	321	HIS	-	EXPRESSION TAG	UNP P41148
E	322	HIS	-	EXPRESSION TAG	UNP P41148
E	323	HIS	-	EXPRESSION TAG	UNP P41148
E	324	HIS	-	EXPRESSION TAG	UNP P41148
E	325	HIS	-	EXPRESSION TAG	UNP P41148
E	326	SER	-	EXPRESSION TAG	UNP P41148
E	327	SER	-	EXPRESSION TAG	UNP P41148
E	328	GLY	-	EXPRESSION TAG	UNP P41148

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Chain	Residue	Modelled	Actual	Comment	Reference
E	329	LEU	-	EXPRESSION TAG	UNP P41148
E	330	VAL	-	EXPRESSION TAG	UNP P41148
E	331	PRO	-	EXPRESSION TAG	UNP P41148
E	332	ARG	-	EXPRESSION TAG	UNP P41148
E	333	GLY	-	EXPRESSION TAG	UNP P41148
E	334	SER	-	EXPRESSION TAG	UNP P41148
E	335	HIS	-	EXPRESSION TAG	UNP P41148
F	316	MET	-	EXPRESSION TAG	UNP P41148
F	317	GLY	-	EXPRESSION TAG	UNP P41148
F	318	SER	-	EXPRESSION TAG	UNP P41148
F	319	SER	-	EXPRESSION TAG	UNP P41148
F	320	HIS	-	EXPRESSION TAG	UNP P41148
F	321	HIS	-	EXPRESSION TAG	UNP P41148
F	322	HIS	-	EXPRESSION TAG	UNP P41148
F	323	HIS	-	EXPRESSION TAG	UNP P41148
F	324	HIS	-	EXPRESSION TAG	UNP P41148
F	325	HIS	-	EXPRESSION TAG	UNP P41148
F	326	SER	-	EXPRESSION TAG	UNP P41148
F	327	SER	-	EXPRESSION TAG	UNP P41148
F	328	GLY	-	EXPRESSION TAG	UNP P41148
F	329	LEU	-	EXPRESSION TAG	UNP P41148
F	330	VAL	-	EXPRESSION TAG	UNP P41148
F	331	PRO	-	EXPRESSION TAG	UNP P41148
F	332	ARG	-	EXPRESSION TAG	UNP P41148
F	333	GLY	-	EXPRESSION TAG	UNP P41148
F	334	SER	-	EXPRESSION TAG	UNP P41148
F	335	HIS	-	EXPRESSION TAG	UNP P41148
G	316	MET	-	EXPRESSION TAG	UNP P41148
G	317	GLY	-	EXPRESSION TAG	UNP P41148
G	318	SER	-	EXPRESSION TAG	UNP P41148
G	319	SER	-	EXPRESSION TAG	UNP P41148
G	320	HIS	-	EXPRESSION TAG	UNP P41148
G	321	HIS	-	EXPRESSION TAG	UNP P41148
G	322	HIS	-	EXPRESSION TAG	UNP P41148
G	323	HIS	-	EXPRESSION TAG	UNP P41148
G	324	HIS	-	EXPRESSION TAG	UNP P41148
G	325	HIS	-	EXPRESSION TAG	UNP P41148
G	326	SER	-	EXPRESSION TAG	UNP P41148
G	327	SER	-	EXPRESSION TAG	UNP P41148
G	328	GLY	-	EXPRESSION TAG	UNP P41148
G	329	LEU	-	EXPRESSION TAG	UNP P41148
G	330	VAL	-	EXPRESSION TAG	UNP P41148

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Chain	Residue	Modelled	Actual	Comment	Reference
G	331	PRO	-	EXPRESSION TAG	UNP P41148
G	332	ARG	-	EXPRESSION TAG	UNP P41148
G	333	GLY	-	EXPRESSION TAG	UNP P41148
G	334	SER	-	EXPRESSION TAG	UNP P41148
G	335	HIS	-	EXPRESSION TAG	UNP P41148
H	316	MET	-	EXPRESSION TAG	UNP P41148
H	317	GLY	-	EXPRESSION TAG	UNP P41148
H	318	SER	-	EXPRESSION TAG	UNP P41148
H	319	SER	-	EXPRESSION TAG	UNP P41148
H	320	HIS	-	EXPRESSION TAG	UNP P41148
H	321	HIS	-	EXPRESSION TAG	UNP P41148
H	322	HIS	-	EXPRESSION TAG	UNP P41148
H	323	HIS	-	EXPRESSION TAG	UNP P41148
H	324	HIS	-	EXPRESSION TAG	UNP P41148
H	325	HIS	-	EXPRESSION TAG	UNP P41148
H	326	SER	-	EXPRESSION TAG	UNP P41148
H	327	SER	-	EXPRESSION TAG	UNP P41148
H	328	GLY	-	EXPRESSION TAG	UNP P41148
H	329	LEU	-	EXPRESSION TAG	UNP P41148
H	330	VAL	-	EXPRESSION TAG	UNP P41148
H	331	PRO	-	EXPRESSION TAG	UNP P41148
H	332	ARG	-	EXPRESSION TAG	UNP P41148
H	333	GLY	-	EXPRESSION TAG	UNP P41148
H	334	SER	-	EXPRESSION TAG	UNP P41148
H	335	HIS	-	EXPRESSION TAG	UNP P41148
I	316	MET	-	EXPRESSION TAG	UNP P41148
I	317	GLY	-	EXPRESSION TAG	UNP P41148
I	318	SER	-	EXPRESSION TAG	UNP P41148
I	319	SER	-	EXPRESSION TAG	UNP P41148
I	320	HIS	-	EXPRESSION TAG	UNP P41148
I	321	HIS	-	EXPRESSION TAG	UNP P41148
I	322	HIS	-	EXPRESSION TAG	UNP P41148
I	323	HIS	-	EXPRESSION TAG	UNP P41148
I	324	HIS	-	EXPRESSION TAG	UNP P41148
I	325	HIS	-	EXPRESSION TAG	UNP P41148
I	326	SER	-	EXPRESSION TAG	UNP P41148
I	327	SER	-	EXPRESSION TAG	UNP P41148
I	328	GLY	-	EXPRESSION TAG	UNP P41148
I	329	LEU	-	EXPRESSION TAG	UNP P41148
I	330	VAL	-	EXPRESSION TAG	UNP P41148
I	331	PRO	-	EXPRESSION TAG	UNP P41148
I	332	ARG	-	EXPRESSION TAG	UNP P41148

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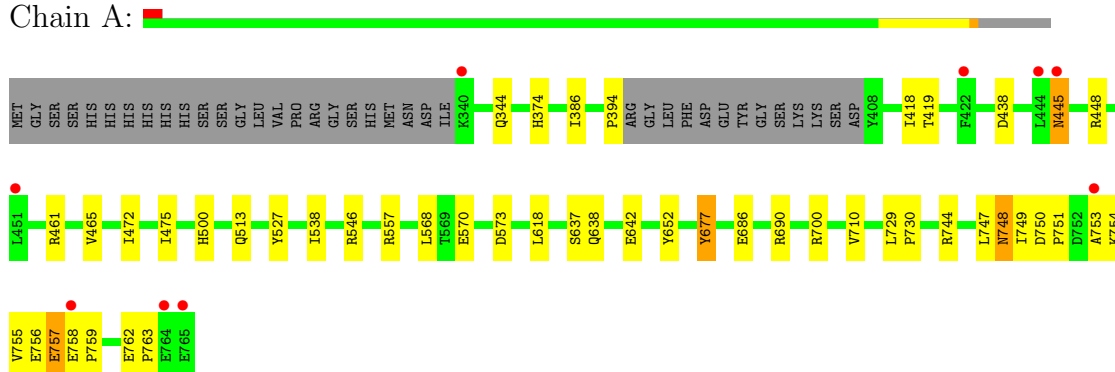
Chain	Residue	Modelled	Actual	Comment	Reference
I	333	GLY	-	EXPRESSION TAG	UNP P41148
I	334	SER	-	EXPRESSION TAG	UNP P41148
I	335	HIS	-	EXPRESSION TAG	UNP P41148
J	316	MET	-	EXPRESSION TAG	UNP P41148
J	317	GLY	-	EXPRESSION TAG	UNP P41148
J	318	SER	-	EXPRESSION TAG	UNP P41148
J	319	SER	-	EXPRESSION TAG	UNP P41148
J	320	HIS	-	EXPRESSION TAG	UNP P41148
J	321	HIS	-	EXPRESSION TAG	UNP P41148
J	322	HIS	-	EXPRESSION TAG	UNP P41148
J	323	HIS	-	EXPRESSION TAG	UNP P41148
J	324	HIS	-	EXPRESSION TAG	UNP P41148
J	325	HIS	-	EXPRESSION TAG	UNP P41148
J	326	SER	-	EXPRESSION TAG	UNP P41148
J	327	SER	-	EXPRESSION TAG	UNP P41148
J	328	GLY	-	EXPRESSION TAG	UNP P41148
J	329	LEU	-	EXPRESSION TAG	UNP P41148
J	330	VAL	-	EXPRESSION TAG	UNP P41148
J	331	PRO	-	EXPRESSION TAG	UNP P41148
J	332	ARG	-	EXPRESSION TAG	UNP P41148
J	333	GLY	-	EXPRESSION TAG	UNP P41148
J	334	SER	-	EXPRESSION TAG	UNP P41148
J	335	HIS	-	EXPRESSION TAG	UNP P41148

3 Residue-property plots

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors 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.

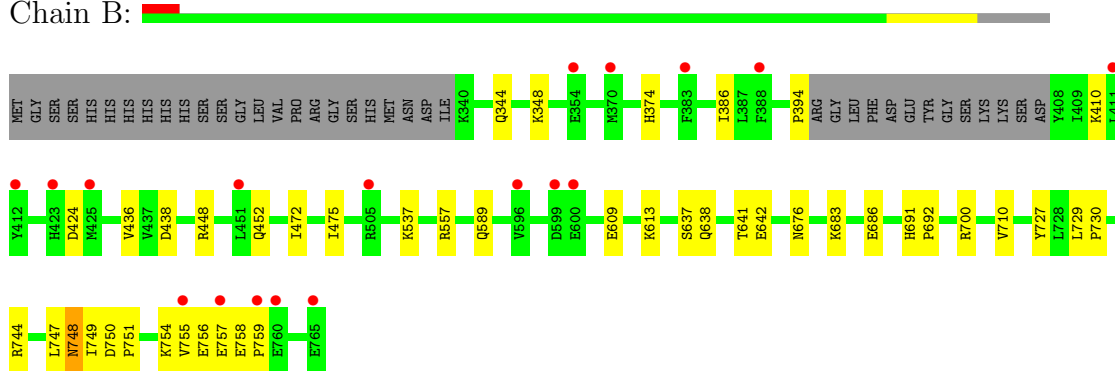
• Molecule 1: Endoplasmic

Chain A:



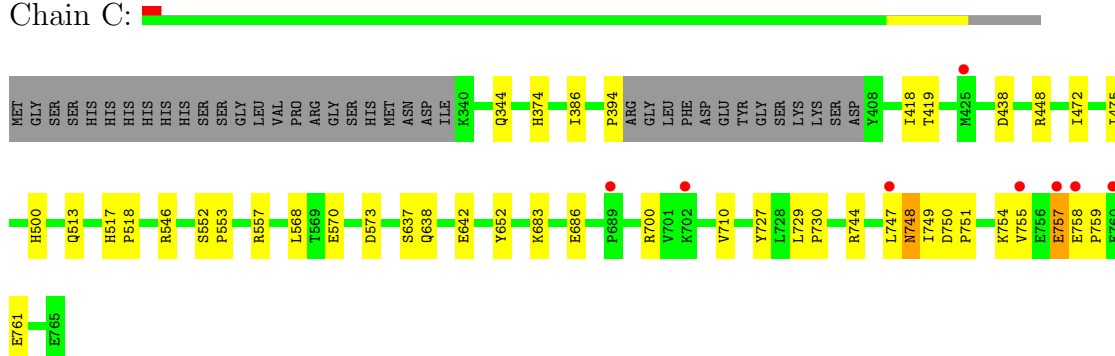
• Molecule 1: Endoplasmic

Chain B:



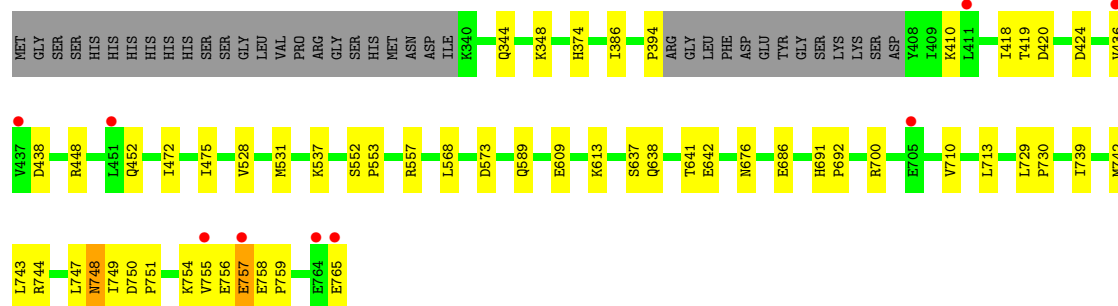
• Molecule 1: Endoplasmic

Chain C:



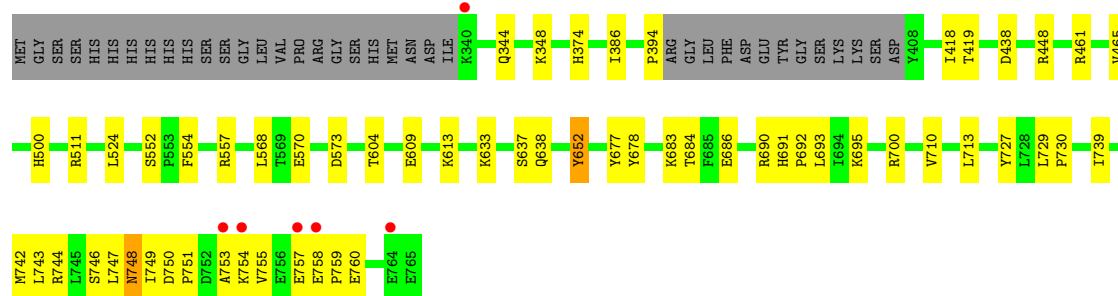
- Molecule 1: Endoplasmic

Chain D:



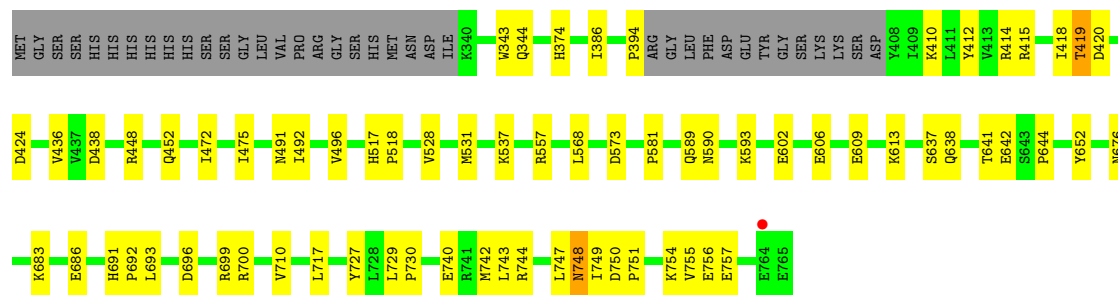
- Molecule 1: Endoplasmic

Chain E:



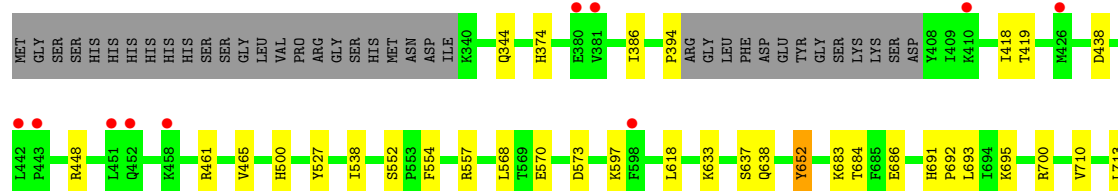
- Molecule 1: Endoplasmic

Chain F:



- Molecule 1: Endoplasmic

Chain G:





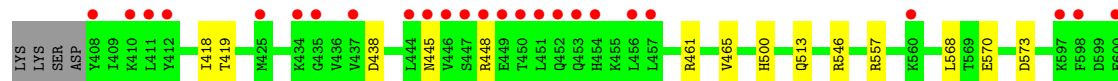
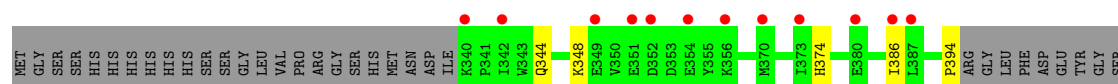
• Molecule 1: Endoplasmic

Chain H:



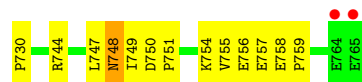
• Molecule 1: Endoplasmic

Chain I:



• Molecule 1: Endoplasmic

Chain J:



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	131.30Å 129.54Å 184.78Å 90.00° 99.91° 90.00°	Depositor
Resolution (Å)	20.00 – 3.20 45.52 – 3.20	Depositor EDS
% Data completeness (in resolution range)	99.7 (20.00-3.20) 99.7 (45.52-3.20)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.07	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.86 (at 3.19Å)	Xtriage
Refinement program	REFMAC 5.2.0019	Depositor
R, R_{free}	0.284 , 0.294 0.277 , 0.286	Depositor DCC
R_{free} test set	5021 reflections (5.26%)	DCC
Wilson B-factor (Å ²)	109.7	Xtriage
Anisotropy	0.216	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.25 , 165.8	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning	$\langle L \rangle = 0.43$, $\langle L^2 \rangle = 0.25$	Xtriage
Outliers	2 of 100402 reflections (0.002%)	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	33009	wwPDB-VP
Average B, all atoms (Å ²)	150.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 12.16% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

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	0.54	1/3368 (0.0%)	0.68	2/4543 (0.0%)
1	B	0.37	0/3368	0.61	1/4543 (0.0%)
1	C	0.42	0/3368	0.64	1/4543 (0.0%)
1	D	0.43	0/3368	0.64	1/4543 (0.0%)
1	E	0.53	0/3368	0.68	1/4543 (0.0%)
1	F	0.51	0/3368	0.66	1/4543 (0.0%)
1	G	0.43	0/3366	0.65	2/4540 (0.0%)
1	H	0.36	0/3368	0.61	1/4543 (0.0%)
1	I	0.35	0/3368	0.62	1/4543 (0.0%)
1	J	0.48	0/3368	0.65	1/4543 (0.0%)
All	All	0.45	1/33678 (0.0%)	0.64	12/45427 (0.0%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	677	TYR	CA-CB	-6.37	1.40	1.53

All (12) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	F	394	PRO	N-CA-CB	7.79	112.64	103.30
1	B	394	PRO	N-CA-CB	7.39	112.16	103.30
1	E	394	PRO	N-CA-CB	7.35	112.12	103.30
1	A	394	PRO	N-CA-CB	7.34	112.11	103.30
1	J	394	PRO	N-CA-CB	7.33	112.10	103.30
1	G	394	PRO	N-CA-CB	7.29	112.05	103.30
1	C	394	PRO	N-CA-CB	7.24	111.99	103.30
1	H	394	PRO	N-CA-CB	7.23	111.98	103.30
1	D	394	PRO	N-CA-CB	7.11	111.83	103.30
1	I	394	PRO	N-CA-CB	7.01	111.72	103.30
1	G	618	LEU	CA-CB-CG	5.24	127.36	115.30
1	A	618	LEU	CA-CB-CG	5.03	126.87	115.30

There are no chirality outliers.

There are no planarity outliers.

5.2 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 hydrogens added by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, and the number in parentheses is this value normalized per 1000 atoms of the molecule in the chain. The Symm-Clashes column gives symmetry related clashes, in the same way as for the Clashes column.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	3301	0	3196	44	4
1	B	3301	0	3196	25	0
1	C	3301	0	3196	40	0
1	D	3301	0	3196	51	1
1	E	3301	0	3196	69	1
1	F	3301	0	3196	59	5
1	G	3300	0	3194	47	1
1	H	3301	0	3196	36	0
1	I	3301	0	3196	29	2
1	J	3301	0	3196	62	0
All	All	33009	0	31958	360	7

Clashscore is defined as the number of clashes calculated for the entry per 1000 atoms (including hydrogens) of the entry. The overall clashscore for this entry is 6.

All (360) close contacts within the same asymmetric unit are listed below.

Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:C:757:GLU:OE2	1:J:677:TYR:HA	1.21	1.31
1:E:500:HIS:CE1	1:J:704:ASP:HB2	1.80	1.16
1:D:759:PRO:HD3	1:E:692:PRO:HD3	1.38	1.05
1:A:754:LYS:HD3	1:E:678:TYR:OH	1.61	1.00
1:C:757:GLU:OE2	1:J:677:TYR:CA	2.11	0.98
1:A:750:ASP:CG	1:E:652:TYR:HB2	1.84	0.97
1:F:652:TYR:CE2	1:J:756:GLU:CD	2.40	0.95
1:E:500:HIS:NE2	1:J:703:GLU:HB3	1.83	0.93
1:D:743:LEU:HD22	1:E:713:LEU:HG	1.52	0.91
1:C:757:GLU:CD	1:J:677:TYR:HA	1.91	0.90
1:E:500:HIS:HE1	1:J:704:ASP:HB2	1.39	0.87
1:C:754:LYS:HD3	1:J:678:TYR:CD2	2.10	0.85
1:H:692:PRO:HB3	1:I:754:LYS:HE3	1.63	0.81

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:F:743:LEU:HD22	1:G:713:LEU:HG	1.66	0.78
1:D:637:SER:HB2	1:D:686:GLU:HB3	1.66	0.78
1:F:637:SER:HB2	1:F:686:GLU:HB3	1.64	0.77
1:C:754:LYS:HD3	1:J:678:TYR:HD2	1.49	0.76
1:A:637:SER:HB2	1:A:686:GLU:HB3	1.68	0.75
1:I:637:SER:HB2	1:I:686:GLU:HB3	1.68	0.75
1:E:637:SER:HB2	1:E:686:GLU:HB3	1.68	0.75
1:H:637:SER:HB2	1:H:686:GLU:HB3	1.69	0.75
1:J:637:SER:HB2	1:J:686:GLU:HB3	1.69	0.74
1:B:637:SER:HB2	1:B:686:GLU:HB3	1.69	0.74
1:A:753:ALA:O	1:E:678:TYR:CE2	2.40	0.74
1:C:637:SER:HB2	1:C:686:GLU:HB3	1.69	0.73
1:D:758:GLU:HG3	1:E:695:LYS:HD3	1.73	0.71
1:A:642:GLU:HA	1:J:759:PRO:HB3	1.73	0.70
1:A:750:ASP:O	1:A:754:LYS:HB2	1.92	0.70
1:G:637:SER:HB2	1:G:686:GLU:HB3	1.74	0.69
1:C:750:ASP:O	1:C:754:LYS:HB2	1.92	0.69
1:E:750:ASP:O	1:E:754:LYS:HB2	1.93	0.68
1:D:750:ASP:HB3	1:D:754:LYS:HG2	1.75	0.68
1:A:750:ASP:CB	1:E:652:TYR:HB2	2.24	0.68
1:A:750:ASP:OD1	1:E:652:TYR:HB2	1.93	0.68
1:E:500:HIS:CD2	1:J:703:GLU:HB3	2.29	0.67
1:D:744:ARG:HG2	1:E:693:LEU:HD13	1.77	0.66
1:D:759:PRO:HD3	1:E:692:PRO:CD	2.22	0.65
1:F:740:GLU:OE2	1:G:691:HIS:NE2	2.28	0.65
1:D:742:MET:CE	1:E:742:MET:HE3	2.26	0.65
1:D:729:LEU:HD12	1:D:730:PRO:HD2	1.79	0.65
1:I:750:ASP:O	1:I:754:LYS:HB2	1.95	0.65
1:F:744:ARG:HD3	1:G:693:LEU:HB2	1.80	0.64
1:D:744:ARG:HD3	1:E:693:LEU:HB2	1.79	0.64
1:F:729:LEU:HD12	1:F:730:PRO:HD2	1.79	0.64
1:F:652:TYR:CE2	1:J:756:GLU:OE2	2.50	0.63
1:D:713:LEU:HG	1:E:743:LEU:HD22	1.81	0.63
1:F:717:LEU:HD13	1:G:743:LEU:HD13	1.81	0.63
1:A:753:ALA:O	1:E:678:TYR:CD2	2.52	0.62
1:C:748:ASN:O	1:J:652:TYR:CE1	2.52	0.62
1:J:729:LEU:HD12	1:J:730:PRO:HD2	1.79	0.62
1:B:729:LEU:HD12	1:B:730:PRO:HD2	1.83	0.61
1:C:757:GLU:CG	1:J:677:TYR:HA	2.30	0.61
1:A:690:ARG:O	1:J:758:GLU:HB3	2.00	0.61
1:H:750:ASP:HB3	1:H:754:LYS:HG2	1.83	0.61
1:G:750:ASP:O	1:G:754:LYS:HB2	2.00	0.61

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:750:ASP:HB3	1:A:754:LYS:HG2	1.82	0.61
1:F:374:HIS:HD2	1:F:386:ILE:HG12	1.65	0.61
1:H:729:LEU:HD12	1:H:730:PRO:HD2	1.83	0.61
1:C:750:ASP:HB3	1:C:754:LYS:HG2	1.83	0.60
1:D:744:ARG:NH2	1:D:755:VAL:HB	2.16	0.60
1:A:700:ARG:HD2	1:A:710:VAL:HG22	1.84	0.60
1:C:754:LYS:HD3	1:J:678:TYR:CE2	2.37	0.59
1:H:569:THR:O	1:I:667:TYR:OH	2.18	0.59
1:F:652:TYR:HE2	1:J:756:GLU:OE2	1.84	0.59
1:A:729:LEU:HD12	1:A:730:PRO:HD2	1.85	0.59
1:F:743:LEU:CD2	1:G:713:LEU:HG	2.32	0.59
1:A:642:GLU:HG2	1:J:759:PRO:HB2	1.85	0.58
1:H:374:HIS:HD2	1:H:386:ILE:HG12	1.68	0.58
1:B:374:HIS:HD2	1:B:386:ILE:HG12	1.67	0.58
1:E:500:HIS:CD2	1:E:500:HIS:H	2.20	0.58
1:F:691:HIS:HE1	1:G:744:ARG:HD3	1.67	0.58
1:C:700:ARG:HD2	1:C:710:VAL:HG22	1.84	0.58
1:D:692:PRO:HD3	1:E:758:GLU:HB2	1.86	0.58
1:F:742:MET:CE	1:G:742:MET:HE3	2.34	0.58
1:I:700:ARG:HD2	1:I:710:VAL:HG22	1.86	0.58
1:A:642:GLU:HG2	1:J:759:PRO:CB	2.33	0.57
1:G:683:LYS:HE3	1:G:727:TYR:CE1	2.38	0.57
1:A:418:ILE:HG22	1:A:419:THR:HG22	1.86	0.57
1:H:557:ARG:HD3	1:H:638:GLN:O	2.04	0.57
1:B:744:ARG:NH2	1:B:755:VAL:HB	2.20	0.57
1:I:729:LEU:HD12	1:I:730:PRO:HD2	1.85	0.57
1:D:374:HIS:HD2	1:D:386:ILE:HG12	1.70	0.57
1:F:557:ARG:HD3	1:F:638:GLN:O	2.05	0.56
1:G:700:ARG:HD2	1:G:710:VAL:HG22	1.88	0.56
1:G:729:LEU:HD12	1:G:730:PRO:HD2	1.88	0.56
1:C:344:GLN:NE2	1:C:438:ASP:OD2	2.37	0.56
1:I:750:ASP:HB3	1:I:754:LYS:HG2	1.87	0.56
1:J:744:ARG:NH2	1:J:755:VAL:HB	2.21	0.56
1:E:750:ASP:HB3	1:E:754:LYS:HG2	1.88	0.56
1:D:750:ASP:HB3	1:D:754:LYS:CG	2.36	0.56
1:D:557:ARG:HD3	1:D:638:GLN:O	2.05	0.56
1:C:757:GLU:OE2	1:J:676:ASN:O	2.25	0.55
1:J:374:HIS:HD2	1:J:386:ILE:HG12	1.69	0.55
1:B:557:ARG:HD3	1:B:638:GLN:O	2.06	0.55
1:F:743:LEU:HD13	1:G:717:LEU:HD13	1.88	0.55
1:I:344:GLN:NE2	1:I:438:ASP:OD2	2.38	0.55
1:G:750:ASP:HB3	1:G:754:LYS:HG2	1.89	0.55

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:F:742:MET:HE3	1:G:742:MET:CE	2.37	0.55
1:E:729:LEU:HD12	1:E:730:PRO:HD2	1.88	0.55
1:E:700:ARG:HD2	1:E:710:VAL:HG22	1.89	0.55
1:F:652:TYR:CD2	1:J:756:GLU:OE1	2.60	0.54
1:A:754:LYS:HD3	1:E:678:TYR:HH	1.68	0.54
1:F:652:TYR:CZ	1:J:756:GLU:HG2	2.43	0.54
1:H:744:ARG:NH2	1:H:755:VAL:HB	2.23	0.54
1:B:750:ASP:HB3	1:B:754:LYS:HG2	1.90	0.54
1:J:557:ARG:HD3	1:J:638:GLN:O	2.08	0.53
1:F:744:ARG:HG2	1:G:693:LEU:HD13	1.91	0.53
1:H:693:LEU:HD13	1:I:744:ARG:HG2	1.91	0.53
1:F:750:ASP:HB3	1:F:754:LYS:HG2	1.88	0.53
1:D:759:PRO:HA	1:E:690:ARG:O	2.08	0.53
1:F:742:MET:HE3	1:G:742:MET:HE1	1.91	0.53
1:A:344:GLN:NE2	1:A:438:ASP:OD2	2.38	0.53
1:D:742:MET:HE2	1:E:742:MET:CE	2.39	0.53
1:A:754:LYS:HD3	1:E:678:TYR:CZ	2.43	0.53
1:D:750:ASP:O	1:D:754:LYS:HB2	2.10	0.52
1:C:729:LEU:HD12	1:C:730:PRO:HD2	1.92	0.52
1:G:344:GLN:NE2	1:G:438:ASP:OD2	2.41	0.52
1:J:344:GLN:NE2	1:J:438:ASP:OD2	2.39	0.52
1:G:744:ARG:NH2	1:G:755:VAL:HB	2.24	0.52
1:H:467:LYS:HD3	1:J:529:GLU:OE2	2.10	0.52
1:A:570:GLU:HB2	1:A:573:ASP:CG	2.30	0.52
1:C:761:GLU:OE2	1:J:676:ASN:O	2.28	0.52
1:A:374:HIS:HD2	1:A:386:ILE:HG12	1.73	0.52
1:E:744:ARG:NH2	1:E:755:VAL:HB	2.25	0.52
1:E:570:GLU:HB2	1:E:573:ASP:CG	2.30	0.52
1:D:742:MET:HE3	1:E:742:MET:HE3	1.92	0.52
1:E:344:GLN:NE2	1:E:438:ASP:OD2	2.40	0.52
1:E:683:LYS:HE3	1:E:727:TYR:CE1	2.45	0.52
1:J:750:ASP:HB3	1:J:754:LYS:HG2	1.93	0.51
1:I:374:HIS:HD2	1:I:386:ILE:HG12	1.75	0.51
1:D:528:VAL:HA	1:D:531:MET:SD	2.50	0.51
1:C:500:HIS:CD2	1:C:500:HIS:H	2.29	0.51
1:D:759:PRO:HG3	1:E:692:PRO:HD2	1.92	0.51
1:A:750:ASP:HB2	1:E:652:TYR:HB2	1.92	0.51
1:F:374:HIS:CD2	1:F:386:ILE:HG12	2.46	0.50
1:F:744:ARG:NH2	1:F:755:VAL:HB	2.25	0.50
1:F:742:MET:HE1	1:G:742:MET:HE3	1.92	0.50
1:I:570:GLU:HB2	1:I:573:ASP:CG	2.31	0.50
1:F:424:ASP:CG	1:F:452:GLN:HE21	2.15	0.50

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:I:744:ARG:NH2	1:I:755:VAL:HB	2.27	0.50
1:A:500:HIS:H	1:A:500:HIS:CD2	2.28	0.50
1:G:374:HIS:HD2	1:G:386:ILE:HG12	1.77	0.50
1:D:742:MET:HE2	1:E:742:MET:HE3	1.92	0.50
1:H:374:HIS:CD2	1:H:386:ILE:HG12	2.47	0.50
1:I:557:ARG:HD3	1:I:638:GLN:O	2.11	0.50
1:F:414:ARG:O	1:F:415:ARG:HB2	2.12	0.50
1:C:557:ARG:HD3	1:C:638:GLN:O	2.11	0.49
1:H:380:GLU:CD	1:J:533:GLU:HB2	2.33	0.49
1:F:700:ARG:HD2	1:F:710:VAL:HG22	1.94	0.49
1:E:374:HIS:HD2	1:E:386:ILE:HG12	1.77	0.49
1:C:744:ARG:NH2	1:C:755:VAL:HB	2.26	0.49
1:H:692:PRO:HB3	1:I:754:LYS:CE	2.40	0.49
1:G:570:GLU:HB2	1:G:573:ASP:CG	2.32	0.49
1:H:750:ASP:O	1:H:754:LYS:HB2	2.12	0.49
1:F:472:ILE:O	1:F:475:ILE:HG12	2.13	0.49
1:F:652:TYR:CD2	1:J:756:GLU:CD	2.86	0.49
1:F:742:MET:CE	1:G:742:MET:CE	2.90	0.49
1:C:418:ILE:HG22	1:C:419:THR:HG22	1.95	0.49
1:H:344:GLN:NE2	1:H:438:ASP:OD2	2.43	0.49
1:F:683:LYS:HE3	1:F:727:TYR:CE1	2.48	0.48
1:A:750:ASP:HB2	1:E:652:TYR:CB	2.44	0.48
1:C:374:HIS:HD2	1:C:386:ILE:HG12	1.78	0.48
1:C:757:GLU:HG2	1:J:677:TYR:CA	2.44	0.48
1:F:691:HIS:CE1	1:G:744:ARG:HD3	2.47	0.48
1:B:344:GLN:NE2	1:B:438:ASP:OD2	2.41	0.48
1:H:743:LEU:HD22	1:I:713:LEU:HG	1.94	0.48
1:E:418:ILE:HG22	1:E:419:THR:HG22	1.94	0.48
1:J:754:LYS:C	1:J:756:GLU:H	2.16	0.48
1:F:652:TYR:CE2	1:J:756:GLU:CG	2.97	0.48
1:G:557:ARG:HD3	1:G:638:GLN:O	2.13	0.48
1:D:742:MET:CE	1:E:742:MET:CE	2.91	0.48
1:D:472:ILE:O	1:D:475:ILE:HG12	2.14	0.48
1:F:537:LYS:HE2	1:F:589:GLN:HB2	1.96	0.48
1:F:700:ARG:HD2	1:F:710:VAL:CG2	2.44	0.48
1:I:418:ILE:HG22	1:I:419:THR:HG22	1.95	0.48
1:D:739:ILE:HD12	1:E:739:ILE:HD12	1.96	0.48
1:F:750:ASP:O	1:F:754:LYS:HB2	2.14	0.47
1:H:750:ASP:HB3	1:H:754:LYS:CG	2.44	0.47
1:G:418:ILE:HG22	1:G:419:THR:HG22	1.96	0.47
1:E:552:SER:OG	1:E:554:PHE:HD1	1.97	0.47
1:D:759:PRO:CD	1:E:692:PRO:HD3	2.27	0.47

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:C:700:ARG:HD2	1:C:710:VAL:CG2	2.43	0.47
1:I:700:ARG:HD2	1:I:710:VAL:CG2	2.44	0.47
1:A:700:ARG:HD2	1:A:710:VAL:CG2	2.44	0.47
1:C:747:LEU:O	1:C:748:ASN:CB	2.62	0.47
1:A:744:ARG:NH2	1:A:755:VAL:HB	2.30	0.47
1:I:500:HIS:H	1:I:500:HIS:CD2	2.32	0.47
1:E:461:ARG:O	1:E:465:VAL:HG23	2.15	0.47
1:F:644:PRO:HD3	1:G:740:GLU:OE2	2.14	0.47
1:E:700:ARG:HD2	1:E:710:VAL:CG2	2.45	0.47
1:B:750:ASP:O	1:B:754:LYS:HB2	2.15	0.47
1:D:344:GLN:NE2	1:D:438:ASP:OD2	2.41	0.47
1:J:472:ILE:O	1:J:475:ILE:HG12	2.15	0.47
1:E:557:ARG:HD3	1:E:638:GLN:O	2.15	0.47
1:A:461:ARG:O	1:A:465:VAL:HG23	2.15	0.47
1:I:461:ARG:O	1:I:465:VAL:HG23	2.15	0.47
1:B:759:PRO:HB3	1:C:642:GLU:HA	1.97	0.46
1:B:374:HIS:CD2	1:B:386:ILE:HG12	2.48	0.46
1:F:693:LEU:HD13	1:G:744:ARG:HG2	1.97	0.46
1:H:424:ASP:CG	1:H:452:GLN:HE21	2.19	0.46
1:C:570:GLU:HB2	1:C:573:ASP:CG	2.35	0.46
1:E:500:HIS:CD2	1:J:703:GLU:OE1	2.68	0.46
1:G:700:ARG:HD2	1:G:710:VAL:CG2	2.46	0.46
1:J:641:THR:HG22	1:J:642:GLU:HG3	1.97	0.46
1:B:683:LYS:HE3	1:B:727:TYR:CE1	2.51	0.46
1:B:700:ARG:HD2	1:B:710:VAL:HG22	1.97	0.46
1:H:692:PRO:HD3	1:I:758:GLU:HB2	1.97	0.46
1:B:609:GLU:O	1:B:613:LYS:HD3	2.15	0.46
1:G:461:ARG:O	1:G:465:VAL:HG23	2.16	0.46
1:F:754:LYS:C	1:F:756:GLU:H	2.18	0.46
1:C:757:GLU:HG2	1:J:677:TYR:CB	2.46	0.46
1:H:700:ARG:HD2	1:H:710:VAL:HG22	1.98	0.45
1:H:472:ILE:O	1:H:475:ILE:HG12	2.16	0.45
1:J:348:LYS:HB2	1:J:348:LYS:HE3	1.73	0.45
1:C:568:LEU:HB3	1:C:573:ASP:HB3	1.98	0.45
1:F:344:GLN:NE2	1:F:438:ASP:OD2	2.43	0.45
1:C:748:ASN:O	1:J:652:TYR:CD1	2.70	0.45
1:A:557:ARG:HD3	1:A:638:GLN:O	2.17	0.45
1:C:758:GLU:N	1:C:759:PRO:CD	2.80	0.45
1:H:609:GLU:O	1:H:613:LYS:HD3	2.17	0.45
1:I:683:LYS:HE3	1:I:727:TYR:CE1	2.51	0.45
1:C:683:LYS:HE3	1:C:727:TYR:CE1	2.51	0.45
1:J:424:ASP:CG	1:J:452:GLN:HE21	2.20	0.45

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:F:609:GLU:O	1:F:613:LYS:HD3	2.17	0.45
1:F:410:LYS:HB2	1:F:436:VAL:HG12	1.99	0.45
1:E:747:LEU:O	1:E:748:ASN:CB	2.64	0.45
1:D:754:LYS:C	1:D:756:GLU:H	2.19	0.45
1:B:700:ARG:HD2	1:B:710:VAL:CG2	2.47	0.45
1:D:759:PRO:HG3	1:E:691:HIS:HA	1.98	0.45
1:C:754:LYS:CE	1:J:678:TYR:HE2	2.30	0.45
1:I:568:LEU:HB3	1:I:573:ASP:HB3	1.98	0.45
1:A:374:HIS:CD2	1:A:386:ILE:HG12	2.51	0.45
1:A:758:GLU:N	1:A:759:PRO:CD	2.80	0.45
1:E:695:LYS:HE2	1:E:695:LYS:HB3	1.79	0.44
1:H:537:LYS:HE2	1:H:589:GLN:HB2	1.99	0.44
1:F:528:VAL:HA	1:F:531:MET:SD	2.57	0.44
1:A:750:ASP:OD1	1:A:753:ALA:HB3	2.17	0.44
1:G:568:LEU:HB3	1:G:573:ASP:HB3	2.00	0.44
1:H:641:THR:HG22	1:H:642:GLU:HG3	1.99	0.44
1:D:568:LEU:HB3	1:D:573:ASP:HB3	1.99	0.44
1:D:374:HIS:CD2	1:D:386:ILE:HG12	2.50	0.44
1:F:568:LEU:HB3	1:F:573:ASP:HB3	2.00	0.44
1:G:758:GLU:N	1:G:759:PRO:CD	2.81	0.44
1:F:754:LYS:HB3	1:G:692:PRO:HB3	1.99	0.44
1:H:700:ARG:HD2	1:H:710:VAL:CG2	2.48	0.44
1:H:528:VAL:HA	1:H:531:MET:SD	2.57	0.44
1:B:754:LYS:C	1:B:756:GLU:H	2.21	0.44
1:F:641:THR:HG22	1:F:642:GLU:HG3	2.00	0.44
1:F:691:HIS:HA	1:F:692:PRO:HD2	1.78	0.44
1:J:374:HIS:CD2	1:J:386:ILE:HG12	2.50	0.44
1:D:348:LYS:HE3	1:D:348:LYS:HB2	1.71	0.44
1:F:750:ASP:HB3	1:F:754:LYS:CG	2.48	0.43
1:H:348:LYS:HE3	1:H:348:LYS:HB2	1.74	0.43
1:F:418:ILE:HG22	1:F:419:THR:HG22	2.00	0.43
1:D:759:PRO:CG	1:E:692:PRO:HD2	2.48	0.43
1:J:410:LYS:HB2	1:J:436:VAL:HG12	2.00	0.43
1:J:537:LYS:HE2	1:J:589:GLN:HB2	2.00	0.43
1:I:747:LEU:O	1:I:748:ASN:CB	2.66	0.43
1:B:641:THR:HG22	1:B:642:GLU:HG3	1.98	0.43
1:C:513:GLN:HB3	1:C:546:ARG:NH1	2.33	0.43
1:E:374:HIS:CD2	1:E:386:ILE:HG12	2.53	0.43
1:B:472:ILE:O	1:B:475:ILE:HG12	2.18	0.43
1:A:757:GLU:HB2	1:E:677:TYR:CB	2.49	0.43
1:B:691:HIS:HA	1:B:692:PRO:HD2	1.80	0.43
1:D:691:HIS:HA	1:D:692:PRO:HD2	1.79	0.43

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:H:380:GLU:OE1	1:J:533:GLU:HB2	2.19	0.43
1:D:424:ASP:CG	1:D:452:GLN:HE21	2.22	0.43
1:B:537:LYS:HE2	1:B:589:GLN:HB2	2.01	0.43
1:H:754:LYS:C	1:H:756:GLU:H	2.21	0.43
1:I:374:HIS:CD2	1:I:386:ILE:HG12	2.53	0.43
1:C:517:HIS:HA	1:C:518:PRO:HD2	1.78	0.43
1:J:609:GLU:O	1:J:613:LYS:HD3	2.19	0.43
1:B:348:LYS:HB2	1:B:348:LYS:HE3	1.76	0.43
1:D:729:LEU:HA	1:D:730:PRO:HD2	1.85	0.43
1:B:410:LYS:HB2	1:B:436:VAL:HG12	1.99	0.43
1:H:602:GLU:O	1:H:606:GLU:HG3	2.19	0.43
1:J:500:HIS:CD2	1:J:500:HIS:H	2.37	0.42
1:D:758:GLU:N	1:D:759:PRO:CD	2.82	0.42
1:F:492:ILE:O	1:F:496:VAL:HG23	2.19	0.42
1:C:472:ILE:O	1:C:475:ILE:HG12	2.20	0.42
1:D:755:VAL:HA	1:E:692:PRO:HG3	2.00	0.42
1:F:693:LEU:HB2	1:G:744:ARG:HD3	1.99	0.42
1:H:463:LYS:NZ	1:J:529:GLU:O	2.53	0.42
1:D:418:ILE:HG22	1:D:419:THR:HG22	2.01	0.42
1:D:410:LYS:HB2	1:D:436:VAL:HG12	2.01	0.42
1:G:500:HIS:H	1:G:500:HIS:CD2	2.36	0.42
1:A:729:LEU:HA	1:A:730:PRO:HD2	1.81	0.42
1:A:568:LEU:HB3	1:A:573:ASP:HB3	2.00	0.42
1:E:568:LEU:HB3	1:E:573:ASP:HB3	2.01	0.42
1:G:374:HIS:CD2	1:G:386:ILE:HG12	2.55	0.42
1:C:729:LEU:HA	1:C:730:PRO:HD2	1.80	0.42
1:J:683:LYS:HE3	1:J:727:TYR:CE1	2.54	0.42
1:B:750:ASP:HB3	1:B:754:LYS:CG	2.50	0.42
1:H:410:LYS:HB2	1:H:436:VAL:HG12	2.02	0.42
1:G:633:LYS:HG3	1:G:684:THR:HG23	2.01	0.42
1:C:552:SER:HA	1:C:553:PRO:HD3	1.94	0.42
1:A:750:ASP:HB3	1:A:754:LYS:CG	2.49	0.42
1:J:747:LEU:O	1:J:748:ASN:CB	2.68	0.42
1:A:527:TYR:CE2	1:A:538:ILE:HG23	2.54	0.42
1:A:642:GLU:HG2	1:J:759:PRO:HB3	1.99	0.42
1:D:742:MET:SD	1:E:743:LEU:HD23	2.60	0.42
1:C:374:HIS:CD2	1:C:386:ILE:HG12	2.55	0.42
1:E:758:GLU:N	1:E:759:PRO:CD	2.83	0.42
1:J:418:ILE:HG22	1:J:419:THR:HG22	2.01	0.42
1:I:348:LYS:HE3	1:I:348:LYS:HB2	1.90	0.42
1:F:517:HIS:HA	1:F:518:PRO:HD2	1.87	0.42
1:F:747:LEU:O	1:F:748:ASN:CB	2.67	0.42

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:747:LEU:O	1:A:748:ASN:CB	2.68	0.42
1:C:754:LYS:HZ3	1:J:678:TYR:HE2	1.62	0.41
1:F:692:PRO:HG3	1:G:754:LYS:HB3	2.02	0.41
1:E:633:LYS:HG3	1:E:684:THR:HG23	2.02	0.41
1:B:424:ASP:CG	1:B:452:GLN:HE21	2.23	0.41
1:F:590:ASN:HD22	1:F:593:LYS:HE3	1.85	0.41
1:C:757:GLU:CG	1:J:677:TYR:CA	2.98	0.41
1:G:747:LEU:O	1:G:748:ASN:CB	2.67	0.41
1:I:758:GLU:N	1:I:759:PRO:CD	2.83	0.41
1:A:513:GLN:HB3	1:A:546:ARG:NH1	2.35	0.41
1:G:695:LYS:HE2	1:G:695:LYS:HB3	1.88	0.41
1:D:641:THR:HG22	1:D:642:GLU:HG3	2.02	0.41
1:A:754:LYS:C	1:A:756:GLU:N	2.74	0.41
1:J:750:ASP:O	1:J:754:LYS:HB2	2.20	0.41
1:J:758:GLU:N	1:J:759:PRO:CD	2.82	0.41
1:J:700:ARG:HD2	1:J:710:VAL:HG22	2.02	0.41
1:G:527:TYR:CE2	1:G:538:ILE:HG23	2.55	0.41
1:D:759:PRO:CA	1:E:690:ARG:O	2.68	0.41
1:B:758:GLU:N	1:B:759:PRO:CD	2.84	0.41
1:A:472:ILE:O	1:A:475:ILE:HG12	2.20	0.41
1:A:762:GLU:N	1:A:763:PRO:CD	2.84	0.41
1:A:570:GLU:HB2	1:A:573:ASP:OD2	2.21	0.41
1:F:642:GLU:HA	1:G:759:PRO:HB3	2.03	0.41
1:D:700:ARG:HD2	1:D:710:VAL:CG2	2.50	0.41
1:D:765:GLU:O	1:E:604:THR:HG23	2.21	0.41
1:F:744:ARG:CD	1:G:693:LEU:HB2	2.50	0.41
1:G:552:SER:OG	1:G:554:PHE:HD1	2.04	0.41
1:H:747:LEU:O	1:H:748:ASN:CB	2.68	0.41
1:D:537:LYS:HE2	1:D:589:GLN:HB2	2.01	0.41
1:B:747:LEU:O	1:B:748:ASN:CB	2.68	0.41
1:G:597:LYS:HE3	1:G:597:LYS:HB2	1.94	0.41
1:E:524:LEU:HD23	1:E:524:LEU:HA	1.87	0.41
1:E:511:ARG:HA	1:E:511:ARG:HD3	1.97	0.41
1:J:568:LEU:HB3	1:J:573:ASP:HB3	2.03	0.41
1:I:762:GLU:N	1:I:763:PRO:CD	2.84	0.41
1:H:683:LYS:HE3	1:H:727:TYR:CE1	2.55	0.41
1:G:762:GLU:N	1:G:763:PRO:CD	2.84	0.41
1:E:348:LYS:HB2	1:E:348:LYS:HE3	1.91	0.41
1:A:750:ASP:CB	1:E:652:TYR:CB	2.95	0.41
1:I:695:LYS:HE2	1:I:695:LYS:HB3	1.87	0.40
1:F:691:HIS:NE2	1:G:740:GLU:OE2	2.54	0.40
1:E:729:LEU:HA	1:E:730:PRO:HD2	1.79	0.40

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:E:609:GLU:O	1:E:613:LYS:HD3	2.22	0.40
1:F:602:GLU:O	1:F:606:GLU:HG3	2.21	0.40
1:H:570:GLU:HB2	1:H:573:ASP:CG	2.41	0.40
1:H:627:LEU:HB3	1:H:630:LYS:HB2	2.03	0.40
1:D:552:SER:HA	1:D:553:PRO:HD3	1.96	0.40
1:E:500:HIS:N	1:E:500:HIS:CD2	2.85	0.40
1:E:500:HIS:ND1	1:J:704:ASP:HB2	2.28	0.40
1:D:700:ARG:HD2	1:D:710:VAL:HG22	2.02	0.40
1:I:513:GLN:HB3	1:I:546:ARG:NH1	2.36	0.40
1:D:609:GLU:O	1:D:613:LYS:HD3	2.21	0.40
1:D:747:LEU:O	1:D:748:ASN:CB	2.70	0.40

All (7) 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	Distance(Å)	Clash(Å)
1:E:753:ALA:O	1:G:652:TYR:OH[1_455]	1.62	0.58
1:A:677:TYR:CB	1:D:757:GLU:OE1[2_655]	1.73	0.47
1:F:699:ARG:NH2	1:I:445:ASN:O[1_655]	1.74	0.46
1:A:445:ASN:ND2	1:F:412:TYR:CD1[1_565]	1.91	0.29
1:F:696:ASP:OD2	1:I:445:ASN:ND2[1_655]	2.03	0.17
1:A:445:ASN:O	1:F:415:ARG:O[1_565]	2.07	0.13
1:A:445:ASN:OD1	1:F:343:TRP:CZ2[1_565]	2.17	0.03

5.3 Torsion angles

5.3.1 Protein backbone ⓘ

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	409/450 (91%)	361 (88%)	44 (11%)	4 (1%)	22	74
1	B	409/450 (91%)	364 (89%)	40 (10%)	5 (1%)	19	70
1	C	409/450 (91%)	365 (89%)	40 (10%)	4 (1%)	22	74
1	D	409/450 (91%)	368 (90%)	35 (9%)	6 (2%)	15	64
1	E	409/450 (91%)	357 (87%)	47 (12%)	5 (1%)	19	70

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	F	409/450 (91%)	365 (89%)	36 (9%)	8 (2%)	11	56
1	G	409/450 (91%)	363 (89%)	42 (10%)	4 (1%)	22	74
1	H	409/450 (91%)	367 (90%)	36 (9%)	6 (2%)	15	64
1	I	409/450 (91%)	363 (89%)	42 (10%)	4 (1%)	22	74
1	J	409/450 (91%)	364 (89%)	40 (10%)	5 (1%)	19	70
All	All	4090/4500 (91%)	3637 (89%)	402 (10%)	51 (1%)	19	70

All (51) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	749	ILE
1	C	749	ILE
1	D	757	GLU
1	E	749	ILE
1	I	749	ILE
1	A	748	ASN
1	B	748	ASN
1	B	749	ILE
1	B	757	GLU
1	C	748	ASN
1	D	748	ASN
1	D	749	ILE
1	E	748	ASN
1	E	757	GLU
1	F	748	ASN
1	F	749	ILE
1	F	757	GLU
1	G	748	ASN
1	G	749	ILE
1	G	757	GLU
1	H	748	ASN
1	H	749	ILE
1	H	757	GLU
1	I	748	ASN
1	I	757	GLU
1	J	748	ASN
1	J	749	ILE
1	J	757	GLU
1	A	751	PRO
1	A	757	GLU

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Mol	Chain	Res	Type
1	C	751	PRO
1	C	757	GLU
1	E	751	PRO
1	G	751	PRO
1	I	751	PRO
1	F	420	ASP
1	J	420	ASP
1	B	676	ASN
1	D	420	ASP
1	D	751	PRO
1	E	746	SER
1	F	419	THR
1	F	676	ASN
1	F	751	PRO
1	H	420	ASP
1	H	676	ASN
1	B	751	PRO
1	D	676	ASN
1	H	751	PRO
1	J	751	PRO
1	F	581	PRO

5.3.2 Protein sidechains ⓘ

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	352/410 (86%)	349 (99%)	3 (1%)	87	97
1	B	352/410 (86%)	351 (100%)	1 (0%)	96	99
1	C	352/410 (86%)	350 (99%)	2 (1%)	92	98
1	D	352/410 (86%)	351 (100%)	1 (0%)	96	99
1	E	352/410 (86%)	349 (99%)	3 (1%)	87	97
1	F	352/410 (86%)	350 (99%)	2 (1%)	92	98
1	G	352/410 (86%)	350 (99%)	2 (1%)	92	98
1	H	352/410 (86%)	351 (100%)	1 (0%)	96	99
1	I	352/410 (86%)	351 (100%)	1 (0%)	96	99

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	J	352/410 (86%)	350 (99%)	2 (1%)	92	98
All	All	3520/4100 (86%)	3502 (100%)	18 (0%)	94	98

All (18) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	445	ASN
1	A	448	ARG
1	A	652	TYR
1	B	448	ARG
1	C	448	ARG
1	C	652	TYR
1	D	448	ARG
1	E	448	ARG
1	E	652	TYR
1	E	760	GLU
1	F	448	ARG
1	F	491	ASN
1	G	448	ARG
1	G	652	TYR
1	H	448	ARG
1	I	448	ARG
1	J	448	ARG
1	J	678	TYR

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

Mol	Chain	Res	Type
1	B	452	GLN
1	D	452	GLN
1	E	500	HIS
1	F	452	GLN
1	H	452	GLN
1	J	452	GLN

5.3.3 RNA ⓘ

There are no RNA chains 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 ⓘ

There are no carbohydrates in this entry.

5.6 Ligand geometry ⓘ

There are no ligands in this entry.

5.7 Other polymers ⓘ

There are no such residues in this entry.

5.8 Polymer linkage issues

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	413/450 (91%)	0.04	9 (2%) 59 14	129, 151, 152, 165	0
1	B	413/450 (91%)	0.25	18 (4%) 33 7	129, 151, 152, 165	0
1	C	413/450 (91%)	0.09	8 (1%) 64 18	129, 151, 152, 165	0
1	D	413/450 (91%)	0.03	9 (2%) 59 14	129, 151, 152, 165	0
1	E	413/450 (91%)	0.02	6 (1%) 70 21	129, 151, 152, 165	0
1	F	413/450 (91%)	-0.07	1 (0%) 93 66	129, 151, 152, 165	0
1	G	413/450 (91%)	0.21	11 (2%) 52 11	129, 151, 152, 165	0
1	H	413/450 (91%)	0.18	10 (2%) 56 13	129, 151, 152, 165	0
1	I	413/450 (91%)	0.56	41 (9%) 8 2	129, 151, 152, 165	0
1	J	413/450 (91%)	0.03	7 (1%) 67 19	129, 151, 152, 165	0
All	All	4130/4500 (91%)	0.14	120 (2%) 49 10	129, 151, 153, 165	0

All (120) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	I	386	ILE	10.2
1	I	387	LEU	8.4
1	B	765	GLU	8.3
1	H	757	GLU	7.4
1	A	765	GLU	6.5
1	I	452	GLN	6.1
1	I	451	LEU	5.9
1	I	449	GLU	5.7
1	G	765	GLU	5.4
1	A	340	LYS	5.1
1	I	454	HIS	4.9
1	B	600	GLU	4.7
1	D	765	GLU	4.5

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Mol	Chain	Res	Type	RSRZ
1	I	450	THR	4.4
1	B	755	VAL	4.3
1	I	434	LYS	4.1
1	I	600	GLU	4.1
1	I	340	LYS	4.1
1	I	437	VAL	4.0
1	A	444	LEU	4.0
1	C	702	LYS	4.0
1	I	435	GLY	3.8
1	C	760	GLU	3.8
1	I	354	GLU	3.7
1	C	757	GLU	3.7
1	I	342	ILE	3.7
1	I	457	LEU	3.6
1	G	442	LEU	3.6
1	F	764	GLU	3.6
1	I	411	LEU	3.6
1	H	765	GLU	3.5
1	I	349	GLU	3.5
1	I	444	LEU	3.5
1	I	370	MET	3.4
1	I	412	TYR	3.4
1	A	451	LEU	3.4
1	J	765	GLU	3.4
1	J	764	GLU	3.3
1	B	451	LEU	3.2
1	A	764	GLU	3.2
1	G	380	GLU	3.2
1	H	760	GLU	3.1
1	H	761	GLU	3.0
1	I	410	LYS	3.0
1	I	380	GLU	3.0
1	I	425	MET	2.9
1	I	446	VAL	2.9
1	B	599	ASP	2.9
1	I	445	ASN	2.9
1	I	408	TYR	2.8
1	I	448	ARG	2.8
1	D	411	LEU	2.8
1	I	447	SER	2.8
1	B	354	GLU	2.8
1	I	754	LYS	2.8

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Mol	Chain	Res	Type	RSRZ
1	G	452	GLN	2.7
1	A	758	GLU	2.7
1	E	758	GLU	2.7
1	B	760	GLU	2.7
1	A	445	ASN	2.6
1	B	757	GLU	2.6
1	B	759	PRO	2.6
1	G	381	VAL	2.6
1	H	764	GLU	2.6
1	B	383	PHE	2.6
1	I	597	LYS	2.6
1	C	689	PRO	2.6
1	G	451	LEU	2.6
1	H	697	MET	2.5
1	I	598	PHE	2.5
1	C	755	VAL	2.5
1	G	426	MET	2.5
1	J	442	LEU	2.5
1	I	351	GLU	2.5
1	B	596	VAL	2.4
1	H	678	TYR	2.4
1	G	598	PHE	2.4
1	G	443	PRO	2.4
1	A	422	PHE	2.4
1	I	456	LEU	2.4
1	I	560	LYS	2.4
1	E	753	ALA	2.4
1	C	758	GLU	2.3
1	B	505	ARG	2.3
1	G	410	LYS	2.3
1	H	702	LYS	2.3
1	I	352	ASP	2.3
1	E	764	GLU	2.3
1	J	452	GLN	2.3
1	B	423	HIS	2.3
1	D	755	VAL	2.3
1	H	705	GLU	2.3
1	I	765	GLU	2.3
1	J	448	ARG	2.3
1	B	425	MET	2.3
1	I	453	GLN	2.3
1	J	443	PRO	2.3

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Mol	Chain	Res	Type	RSRZ
1	I	755	VAL	2.3
1	B	412	TYR	2.3
1	D	436	VAL	2.2
1	I	356	LYS	2.2
1	D	757	GLU	2.2
1	B	411	LEU	2.2
1	D	705	GLU	2.2
1	A	753	ALA	2.2
1	D	451	LEU	2.1
1	G	458	LYS	2.1
1	E	754	LYS	2.1
1	I	373	ILE	2.1
1	C	425	MET	2.1
1	J	451	LEU	2.1
1	H	754	LYS	2.1
1	B	370	MET	2.1
1	E	757	GLU	2.1
1	D	764	GLU	2.1
1	E	340	LYS	2.1
1	B	388	PHE	2.1
1	D	437	VAL	2.0
1	C	747	LEU	2.0
1	I	764	GLU	2.0

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 carbohydrates 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.