



wwPDB EM Map/Model Validation Report ⓘ

Apr 10, 2016 – 02:10 PM BST

PDB ID : 5A1U
EMDB ID: : EMD-2985
Title : The structure of the COPI coat triad
Authors : Dodonova, S.O.; Diestelkoetter-Bachert, P.; von Appen, A.; Hagen, W.J.H.; Beck, R.; Beck, M.; Wieland, F.; Briggs, J.A.G.
Deposited on : 2015-05-06
Resolution : 13.00 Å(reported)

This is a wwPDB EM Map/Model Validation Report for a publicly released PDB/EMDB entry.
For rigid body fitted models, validation errors reported here could stem from errors in the original structure(s) used in the fitting.
We welcome your comments at validation@mail.wwpdb.org
A user guide is available at
<http://wwpdb.org/validation/2016/EMValidationReportHelp>

MolProbity : 4.02b-467
Mogul : unknown
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et. al. (1996)
Validation Pipeline (wwPDB-VP) : trunk27241

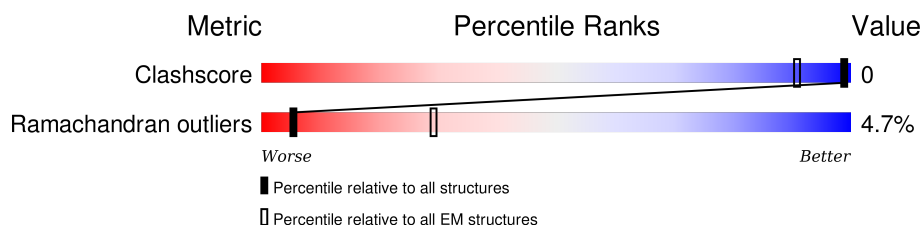
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 13.00 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)	EM structures (#Entries)
Clashscore	114402	924
Ramachandran outliers	111179	726

The table below summarises the geometric issues observed across the polymeric chains. The red, orange, yellow and green segments on the bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria. 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 $\leq 5\%$

Mol	Chain	Length	Quality of chain
1	A	181	88% 12%
1	B	181	88% 12%
2	C	1262	59% 5% 36%
3	D	905	80% 9% 11%
4	E	874	88% 5% • 6%
5	F	177	75% • 21%
6	G	968	73% 10% • 16%
7	H	511	25% • 74%

2 Entry composition

There are 7 unique types of molecules in this entry. The entry contains 15372 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, 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 ADP-RIBOSYLATION FACTOR 1.

Mol	Chain	Residues	Atoms				AltConf	Trace
1	A	159	Total	C	N	O	0	0
			636	318	159	159		
1	B	159	Total	C	N	O	0	0
			636	318	159	159		

- Molecule 2 is a protein called COATOMER SUBUNIT ALPHA.

Mol	Chain	Residues	Atoms				AltConf	Trace
2	C	813	Total	C	N	O	0	0
			3251	1626	813	812		

There are 38 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
C	1225	LEU	-	EXPRESSION TAG	UNP Q8CIE6
C	1226	GLU	-	EXPRESSION TAG	UNP Q8CIE6
C	1227	VAL	-	EXPRESSION TAG	UNP Q8CIE6
C	1228	LEU	-	EXPRESSION TAG	UNP Q8CIE6
C	1229	PHE	-	EXPRESSION TAG	UNP Q8CIE6
C	1230	GLN	-	EXPRESSION TAG	UNP Q8CIE6
C	1231	GLY	-	EXPRESSION TAG	UNP Q8CIE6
C	1232	PRO	-	EXPRESSION TAG	UNP Q8CIE6
C	1233	SER	-	EXPRESSION TAG	UNP Q8CIE6
C	1234	ALA	-	EXPRESSION TAG	UNP Q8CIE6
C	1235	TRP	-	EXPRESSION TAG	UNP Q8CIE6
C	1236	SER	-	EXPRESSION TAG	UNP Q8CIE6
C	1237	HIS	-	EXPRESSION TAG	UNP Q8CIE6
C	1238	PRO	-	EXPRESSION TAG	UNP Q8CIE6
C	1239	GLN	-	EXPRESSION TAG	UNP Q8CIE6
C	1240	PHE	-	EXPRESSION TAG	UNP Q8CIE6
C	1241	GLU	-	EXPRESSION TAG	UNP Q8CIE6
C	1242	LYS	-	EXPRESSION TAG	UNP Q8CIE6
C	1243	GLY	-	EXPRESSION TAG	UNP Q8CIE6

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Chain	Residue	Modelled	Actual	Comment	Reference
C	1244	GLY	-	EXPRESSION TAG	UNP Q8CIE6
C	1245	GLY	-	EXPRESSION TAG	UNP Q8CIE6
C	1246	SER	-	EXPRESSION TAG	UNP Q8CIE6
C	1247	GLY	-	EXPRESSION TAG	UNP Q8CIE6
C	1248	GLY	-	EXPRESSION TAG	UNP Q8CIE6
C	1249	GLY	-	EXPRESSION TAG	UNP Q8CIE6
C	1250	SER	-	EXPRESSION TAG	UNP Q8CIE6
C	1251	GLY	-	EXPRESSION TAG	UNP Q8CIE6
C	1252	GLY	-	EXPRESSION TAG	UNP Q8CIE6
C	1253	SER	-	EXPRESSION TAG	UNP Q8CIE6
C	1254	ALA	-	EXPRESSION TAG	UNP Q8CIE6
C	1255	TRP	-	EXPRESSION TAG	UNP Q8CIE6
C	1256	SER	-	EXPRESSION TAG	UNP Q8CIE6
C	1257	HIS	-	EXPRESSION TAG	UNP Q8CIE6
C	1258	PRO	-	EXPRESSION TAG	UNP Q8CIE6
C	1259	GLN	-	EXPRESSION TAG	UNP Q8CIE6
C	1260	PHE	-	EXPRESSION TAG	UNP Q8CIE6
C	1261	GLU	-	EXPRESSION TAG	UNP Q8CIE6
C	1262	LYS	-	EXPRESSION TAG	UNP Q8CIE6

- Molecule 3 is a protein called COATOMER SUBUNIT BETA'.

Mol	Chain	Residues	Atoms				AltConf	Trace
3	D	803	Total	C	N	O	0	0
			3211	1606	803	802		

- Molecule 4 is a protein called COATOMER SUBUNIT GAMMA-1.

Mol	Chain	Residues	Atoms				AltConf	Trace
4	E	824	Total	C	N	O	0	0
			3294	1648	824	822		

- Molecule 5 is a protein called COATOMER SUBUNIT ZETA-1.

Mol	Chain	Residues	Atoms				AltConf	Trace
5	F	139	Total	C	N	O	0	0
			555	278	139	138		

- Molecule 6 is a protein called COATOMER SUBUNIT BETA.

Mol	Chain	Residues	Atoms				AltConf	Trace
6	G	813	Total	C	N	O	0	0
			3250	1626	813	811		

There are 15 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
G	-14	MET	-	EXPRESSION TAG	UNP Q9JIF7
G	-13	HIS	-	EXPRESSION TAG	UNP Q9JIF7
G	-12	HIS	-	EXPRESSION TAG	UNP Q9JIF7
G	-11	HIS	-	EXPRESSION TAG	UNP Q9JIF7
G	-10	HIS	-	EXPRESSION TAG	UNP Q9JIF7
G	-9	HIS	-	EXPRESSION TAG	UNP Q9JIF7
G	-8	HIS	-	EXPRESSION TAG	UNP Q9JIF7
G	-7	GLU	-	EXPRESSION TAG	UNP Q9JIF7
G	-6	ASN	-	EXPRESSION TAG	UNP Q9JIF7
G	-5	LEU	-	EXPRESSION TAG	UNP Q9JIF7
G	-4	TYR	-	EXPRESSION TAG	UNP Q9JIF7
G	-3	PHE	-	EXPRESSION TAG	UNP Q9JIF7
G	-2	GLN	-	EXPRESSION TAG	UNP Q9JIF7
G	-1	GLY	-	EXPRESSION TAG	UNP Q9JIF7
G	0	HIS	-	EXPRESSION TAG	UNP Q9JIF7

- Molecule 7 is a protein called COATOMER SUBUNIT DELTA.

Mol	Chain	Residues	Atoms				AltConf	Trace
7	H	135	Total	C	N	O	0	0
			539	270	135	134		

• Molecule 1: ADP-RIBOSYLATION FACTOR 1

MET	GLY	LEU	PHE	ALA	SER	LYS	LEU	PHE	SER	ASN	LEU	PHE	GLY	ASN	LYS	GLU	M18	S176	LEU	LYS	ASN	SER	THR
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Chain B: 88% 12%

MET	GLY	LEU	PHE	ALA	SER	LYS	LEU	PHE	SER	ASN	LEU	PHE	GLY	ASN	LYS	GLU	M18	S176	LEU	LYS	ASN	SER	THR
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Chain C:  59% 5% 36%

ASN	ALA	ALA	ALA	HIS	LEU	A799	M424	MI
ASN	GLN	GLN	GLY	ILE	GLY	R11	R425	
PHE	LEU	LEU	LEU	LEU	LYS	R812	K441	R11
PHE	LEU	LYS	ASN	GLY	GLN	R813	N442	L15
LEU	THR	ILE	GLY	SER	GLU	LYS	M452	V64
LYS	ILE	ILE	VAL	PHE	GLU	GLY	PHE	Q63
ASN	CYS	CYS	PRO	GLU	GLY	PHE	A469	
PHE	ARG	ALA	ALA	THR	GLY	ALA	D470	Q63
LYS	GLU	VAL	GLY	MET	GLY	TRP	GLU	Y105
THR	TYR	GLY	LEU	ARG	ASP	GLY	ILE	Y105
ALA	ILE	LEU	LYS	ARG	VAL	ILE	A498	Y130
ALA	VAL	ALA	LEU	LEU	VAL	ALA	A498	Y130
THR	GLY	GLY	LEU	HIS	GLU	SER	LYS	G133
PHE	LEU	ASN	ASN	HIS	GLU	SER	ASP	G133
ALA	CYS	ASP	ASP	ASP	ASP	LYS	E526	
ALA	MET	LEU	LEU	GLN	LEU	GLY	LYS	Y137
ARG	GLU	ILE	ILE	VAL	GLU	LYS	S538	Y137
ARG	ILE	GLN	GLN	GLY	LEU	GLY	GLY	R168
LEU	ILE	ARG	ARG	VAL	PRO	GLY	S546	R168
LEU	GLU	ARG	LEU	ILE	ALA	ALA	GLY	G186
LEU	ARG	LEU	GLN	GLN	GLU	LEU	GLY	G186
GLY	LYS	LYS	LEU	PHE	LEU	ALA	G559	
PRO	LEU	CYS	LEU	GLY	ASP	ALA	R572	T193
LYS	PRO	TYR	TYR	PRO	VAL	ASP	ALA	V200
LYS	LYS	GLN	GLN	TYR	VAL	ASP	P594	V200
PRO	GLU	LYS	LEU	LYS	SER	ASP	ILE	E204
GLU	GLU	LEU	LEU	LYS	SER	ASP	GLY	D205
VAL	THR	THR	THR	GLN	GLY	ILE	K619	
ALA	LEU	THR	THR	LEU	VAL	ASP	I670	
ASP	ASP	VAL	VAL	PHE	SER	THR	V631	G223
GLN	GLN	GLN	GLN	LEU	SER	VAL	GLY	G223
THR	GLN	LYS	LYS	GLN	SER	GLY	S624	D226
ARG	LYS	PHE	THR	THR	ALA	THR	GLY	R227
LYS	ARG	GLU	GLU	TYR	GLU	GLU	GLY	G247
ILE	ILE	GLY	ALA	ALA	ASP	GLY	GLY	G247
CYS	GLY	ALA	ALA	ARG	GLY	TRP	Q630	P259
LEU	GLU	VAL	VAL	GLY	PHE	GLY	K631	P259
SER	MET	GLU	GLU	ARG	PHE	GLU	GLY	
ALA	ALA	LYS	LYS	THR	VAL	ASP	V642	K271
GLU	ALA	PHE	ALA	THR	PRO	ALA	ALA	K271
LYS	TYR	ARG	TYR	TYR	PRO	GLY	Q684	S272
ASN	PHE	SER	GLN	TYR	THR	LEU	G685	S272
PRO	THR	ILE	ALA	GLN	LYS	GLN	G686	I273
THR	HIS	ILE	LEU	ALA	LYS	GLN	GLY	F317
SER	SER	LEU	LEU	LEU	GLY	LEU	GLY	F317
ASP	ASN	LEU	PRO	PRO	THR	ASP	K698	K337
ALA	ASN	SER	SER	CYS	SER	GLU	GLY	K337
CYS	VAL	VAL	VAL	LEU	PRO	ASP	I709	D345
GLN	GLN	PRO	PRO	PRO	THR	GLY	GLY	D345
PRO	PRO	LEU	LEU	SER	GLN	PHE	G731	S348
VAL	VAL	LEU	LEU	THR	ILE	VAL	H732	S348
HIS	HIS	VAL	VAL	TYR	TRP	GLU	GLY	S349
ASN	MET	VAL	VAL	TYR	CYS	ALA	G740	A353
ASP	ILE	ASP	ASP	SER	ASN	PRO	PRO	A353
MET	ILE	ASN	ASN	TYR	ASN	ASN	P780	C380
HIS	LEU	ASN	ASN	PRO	ASN	GLU	E781	C380
ASN	VAL	LYS	LYS	ASN	SER	GLY	GLY	E387
PRO	LEU	GLN	GLN	ARG	GLN	LEU	GLY	E387
PHE	ARG	GLU	GLU	ASN	LEU	GLY	P790	A400
ASP	THR	ILE	ILE	TRP	PRO	GLU	GLY	A400
ILE	LEU	ALA	ALA	LYS	VAL	ASP	K793	A400
LEU	LEU	GLU	GLU	ASN	THR	ASP	VAL	R422

ALA	ALA	GLN
SER	TYR	PRO
ARG	PRO	ILE
PRO	ILE	TYR
GLY	ARG	GLY
LYS	LYS	PRO
PRO	VAL	GLU
GLY	LYS	LYS
CYS	PRO	CYS
LEU	LEU	SER
SER	GLY	GLY
ALA	ALA	TRP
TYR	GLY	SER
GLY	GLY	GLN
ILE	ILE	CYS
CYS	ARG	VAL
VAL	THR	THR
THR	THR	VAL
THR	THR	THR
GLU	GLY	LYS
LYS	ASP	VAL
ILE	ILE	GLY
LEU	ARG	ILE
ILE	ILE	SER
PRO	PRO	LEU
GLN	GLN	PHE
PHE	ARG	LEU
GLU	GLU	VAL
PHE	VAL	PHE

• Molecule 3: COATOMER SUBUNIT BETA'

Chain D: 80% 9% 11%

THR	ARG	K615	G331	M1
	ASN	F630	K336	D6
THR	VAL	F630	K336	D6
ASP	MET	E642	S350	R17
ILE	GLU	V662	P355	S20
ASN	ALA	Q694	G371	V21
LEU	LYS	G723	D372	H44
ASP	GLY	L734	G373	P59
ASP	PHE	Q735	Y378	T74
LEU	GLN	D739	A391	G75
LEU	PRO	A740	F394	D78
ASP	ALA	L762	S410	L89
ASP	GLN	S787	P426	C104
ASP	GLU	L788	G429	I114
ASP	GLY	A789	V441	L115
ASP	LYS	D790	I461	D119
ASP	PRO	F791	Q464	G140
ASP	ALA	E795	P465	E182
ASP	SER	F799	K466	K186
ASP	PRO	E803	F469	G196
ASP	VAL	ALA	S484	P200
ASP	ILE	PHE	Y490	S204
ASP	MET	VAL	G504	M218
ASP	ALA	VAL	G509	G227
ASP	SER	GLU	A513	T260
ASP	GLU	THR	T537	N268
ASP	LEU	GLU	L543	E272
ASP	LEU	TRP	N571	R273
ASP	GLU	PRO	R572	M284
ASP	VAL	ALA	L573	N285
ASP	ASP	LYS	D577	V286
ASP	LEU	THR	S586	A310
ASP	LEU	VAL	R601	K318
ASP	GLU	THR	ASN	A329
ASP	GLU	ASN	I613	M330
ASP	THR	GLU	P614	

• Molecule 4: COATOMER SUBUNIT GAMMA-1

Chain E: 88% 5% 6%

VAL	Q601	F613	V647	F663	L709	K733	D736	P737	N738	T739	G740	E741	L756	T759	G837	R845	L846	L847	G874	S353	D373	P391	R392	K393	G410	Y413	F442	E447	F448	P464	H484	N522	N549	G550	L551	P556	P569	S570	GLU	LYS	PRO	PHE	ASP	LEU	LYS	SER	VAL	PRO	LEU	ALA	THR	THR	PRO	MET	ALA	GLU	GLN	ARG	PRO	GLU	SER	THR	ALA	THR	ALA	ALA
MET	LEU	LYS	PHE	ASP	LYS	LYS	ASP	GLU	GLU	SER	GLY	GLY	ASN	PRO	LEU	GLN	H21	M40	E117	P123	G198	H221	G222	D248	S249	P250	L251	F254	I255	E256	H263	P278	C280	L285	A302	R309	T310	L311	N312	K313	T323	A324																								

• Molecule 5: COATOMER SUBUNIT ZETA-1

Chain F: 75% 21%

MET	GLU	ALA	LEU	ILE	LEU	GLU	PRO	SER	L10	P36	T55	I59	Y69	I80	E110	G132	L148	ARG	GLY	GLU	ASP	VAL	PRO	THR	GLU	GLN	SER	VAL	GLN	GLN	SER	ALA	LYS	GLN	TRP	LEU	LEU	ARG
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• Molecule 6: COATOMER SUBUNIT BETA

Chain G: 73% 10% 16%

MET	HIS	HIS	HIS	HIS	HIS	HIS	ASN	GLU	LEU	TYR	PHE	GLN	GLY	HIS	MET	THR	ALA	ALA	GLU	ASN	VAL	CYS	TYR	THR	LEU	ILE	ASN	VAL	M16	D17	S19	P21	S22	K32	L42	L55	P56	G57	R64	F65	L69	E83	I84	V85	P90	D91	I99	C102
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4 Experimental information

Property	Value	Source
Reconstruction method	TOMOGRAPHY	Depositor
Imposed symmetry	POINT, Not provided	Depositor
Number of images	Not provided	Depositor
Resolution determination method	Not provided	Depositor
CTF correction method	PHASE FLIPPING OF INDIVIDUAL TILTS	Depositor
Microscope	OTHER	Depositor
Voltage (kV)	200	Depositor
Electron dose ($e^-/\text{\AA}^2$)	45	Depositor
Minimum defocus (nm)	1500	Depositor
Maximum defocus (nm)	4000	Depositor
Magnification	42000	Depositor
Image detector	GATAN MULTISCAN	Depositor

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 > 2$	RMSZ	# $ Z > 2$
1	A	0.43	0/635	0.69	0/792
1	B	0.43	0/635	0.69	0/792
2	C	1.55	8/3250 (0.2%)	1.71	14/4061 (0.3%)
3	D	1.60	17/3210 (0.5%)	1.72	24/4011 (0.6%)
4	E	1.52	4/3292 (0.1%)	1.63	19/4112 (0.5%)
5	F	1.55	1/554 (0.2%)	1.74	3/691 (0.4%)
6	G	1.50	7/3248 (0.2%)	1.71	23/4057 (0.6%)
7	H	1.46	0/538	1.76	7/671 (1.0%)
All	All	1.48	37/15362 (0.2%)	1.64	90/19187 (0.5%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
2	C	0	4
3	D	0	2
4	E	0	4
5	F	0	1
6	G	0	14
All	All	0	25

The worst 5 of 37 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	C	621	VAL	C-N	6.93	1.45	1.33
3	D	330	MET	N-CA	-6.80	1.32	1.46
4	E	198	GLY	CA-C	-6.43	1.41	1.51
3	D	378	TYR	N-CA	-6.38	1.33	1.46
3	D	537	THR	N-CA	-6.33	1.33	1.46

The worst 5 of 90 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
6	G	496	GLU	N-CA-C	7.82	132.11	111.00
4	E	302	ALA	C-N-CA	7.05	139.33	121.70
2	C	54	VAL	N-CA-C	-6.91	92.35	111.00
6	G	486	ILE	O-C-N	-6.80	108.18	121.10
6	G	869	THR	N-CA-C	-6.72	92.85	111.00

There are no chirality outliers.

5 of 25 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
2	C	317	PHE	Mainchain
2	C	380	CYS	Mainchain
2	C	559	GLY	Mainchain
2	C	63	GLN	Peptide
3	D	44	HIS	Mainchain

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	636	0	181	0	0
1	B	636	0	181	0	0
2	C	3251	0	869	0	0
3	D	3211	0	880	0	0
4	E	3294	0	852	1	0
5	F	555	0	148	0	0
6	G	3250	0	833	0	0
7	H	539	0	142	0	0
All	All	15372	0	4086	1	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 0.

All (1) 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)
4:E:249:SER:C	4:E:251:LEU:H	2.23	0.42

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 PDB entries followed by that with respect to all EM entries.

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	157/181 (87%)	153 (98%)	4 (2%)	0	100	100
1	B	157/181 (87%)	153 (98%)	4 (2%)	0	100	100
2	C	811/1262 (64%)	671 (83%)	97 (12%)	43 (5%)	2	29
3	D	801/905 (88%)	700 (87%)	64 (8%)	37 (5%)	3	33
4	E	820/874 (94%)	749 (91%)	40 (5%)	31 (4%)	4	37
5	F	137/177 (77%)	128 (93%)	7 (5%)	2 (2%)	13	57
6	G	809/968 (84%)	658 (81%)	84 (10%)	67 (8%)	1	18
7	H	133/511 (26%)	116 (87%)	16 (12%)	1 (1%)	24	69
All	All	3825/5059 (76%)	3328 (87%)	316 (8%)	181 (5%)	5	32

5 of 181 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	C	11	ARG
2	C	227	ARG
2	C	526	GLU
2	C	572	ARG
2	C	686	ASN

5.3.2 Protein sidechains [i](#)

There are no protein residues with a non-rotameric sidechain to report in this entry.

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

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

5.5 Carbohydrates ⓘ

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.