



# Full wwPDB/EMDatabank EM Map/Model Validation Report ⓘ

Feb 16, 2018 – 06:49 pm GMT

PDB ID : 5A1X  
EMDB ID: : EMD-2988  
Title : The structure of the COPI coat linkage III  
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 : 23.00 Å(reported)

This is a Full wwPDB/EMDatabank EM Map/Model Validation Report  
for a publicly released PDB/EMDB entry.

We welcome your comments at [validation@mail.wwpdb.org](mailto:validation@mail.wwpdb.org)

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

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MolProbity : 4.02b-467  
Percentile statistics : 20171227.v01 (using entries in the PDB archive December 27th 2017)  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et. al. (1996)  
Validation Pipeline (wwPDB-VP) : trunk30686

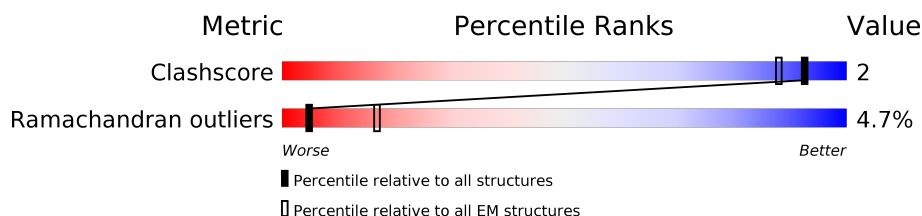
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*ELECTRON MICROSCOPY*

The reported resolution of this entry is 23.00 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	136279	1886
Ramachandran outliers	132675	1663

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  $\geq 3$ , 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%
1	I	181	87% 12%
1	J	181	88% 12%
2	C	1262	59% 5% 36%
2	K	1262	59% 5% 36%
3	D	905	80% 9% 11%
3	L	905	80% 9% 11%
4	E	874	59% 37%
4	M	874	88% 5% 6%
5	F	177	75% 21%

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Mol	Chain	Length	Quality of chain
5	N	177	<div><div></div><div>75%</div><div></div><div>•</div><div>21%</div></div>
6	G	968	<div><div></div><div>73%</div><div></div><div>10%</div><div>•</div><div>16%</div></div>
6	O	968	<div><div></div><div>73%</div><div></div><div>10%</div><div>•</div><div>16%</div></div>
7	H	511	<div><div></div><div>69%</div><div></div><div>5%</div><div></div><div>26%</div></div>
7	P	511	<div><div></div><div>69%</div><div></div><div>5%</div><div></div><div>26%</div></div>
7	Q	511	<div><div></div><div>44%</div><div></div><div>•</div><div>52%</div></div>

## 2 Entry composition

There are 7 unique types of molecules in this entry. The entry contains 32592 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		
1	I	159	Total	C	N	O	0	0
			636	318	159	159		
1	J	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		
2	K	813	Total	C	N	O	0	0
			3251	1626	813	812		

There are 76 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

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

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Chain	Residue	Modelled	Actual	Comment	Reference
K	1242	LYS	-	expression tag	UNP Q8CIE6
K	1243	GLY	-	expression tag	UNP Q8CIE6
K	1244	GLY	-	expression tag	UNP Q8CIE6
K	1245	GLY	-	expression tag	UNP Q8CIE6
K	1246	SER	-	expression tag	UNP Q8CIE6
K	1247	GLY	-	expression tag	UNP Q8CIE6
K	1248	GLY	-	expression tag	UNP Q8CIE6
K	1249	GLY	-	expression tag	UNP Q8CIE6
K	1250	SER	-	expression tag	UNP Q8CIE6
K	1251	GLY	-	expression tag	UNP Q8CIE6
K	1252	GLY	-	expression tag	UNP Q8CIE6
K	1253	SER	-	expression tag	UNP Q8CIE6
K	1254	ALA	-	expression tag	UNP Q8CIE6
K	1255	TRP	-	expression tag	UNP Q8CIE6
K	1256	SER	-	expression tag	UNP Q8CIE6
K	1257	HIS	-	expression tag	UNP Q8CIE6
K	1258	PRO	-	expression tag	UNP Q8CIE6
K	1259	GLN	-	expression tag	UNP Q8CIE6
K	1260	PHE	-	expression tag	UNP Q8CIE6
K	1261	GLU	-	expression tag	UNP Q8CIE6
K	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		
3	L	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	550	Total	C	N	O	0	0
			2199	1100	550	549		
4	M	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		
5	N	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		
6	O	813	Total	C	N	O	0	0
			3250	1626	813	811		

There are 30 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
O	-14	MET	-	expression tag	UNP Q9JIF7
O	-13	HIS	-	expression tag	UNP Q9JIF7
O	-12	HIS	-	expression tag	UNP Q9JIF7
O	-11	HIS	-	expression tag	UNP Q9JIF7
O	-10	HIS	-	expression tag	UNP Q9JIF7
O	-9	HIS	-	expression tag	UNP Q9JIF7
O	-8	HIS	-	expression tag	UNP Q9JIF7
O	-7	GLU	-	expression tag	UNP Q9JIF7
O	-6	ASN	-	expression tag	UNP Q9JIF7
O	-5	LEU	-	expression tag	UNP Q9JIF7
O	-4	TYR	-	expression tag	UNP Q9JIF7
O	-3	PHE	-	expression tag	UNP Q9JIF7

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Chain	Residue	Modelled	Actual	Comment	Reference
O	-2	GLN	-	expression tag	UNP Q9JIF7
O	-1	GLY	-	expression tag	UNP Q9JIF7
O	0	HIS	-	expression tag	UNP Q9JIF7

- Molecule 7 is a protein called COATOMER SUBUNIT DELTA.


Mol	Chain	Residues	Atoms				AltConf	Trace
7	H	380	Total	C	N	O	0	0
			1520	760	380	380		
7	P	380	Total	C	N	O	0	0
			1520	760	380	380		
7	Q	245	Total	C	N	O	0	0
			981	490	245	246		

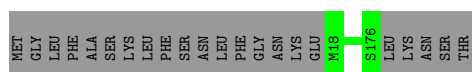


### 3 Residue-property plots [i](#)


These plots are drawn for all protein, RNA and DNA 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. 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. 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.

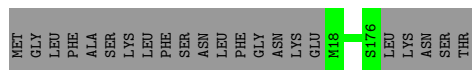
- Molecule 1: ADP-RIBOSYLATION FACTOR 1

Chain A: 




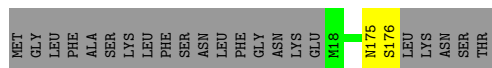
- Molecule 1: ADP-RIBOSYLATION FACTOR 1

Chain B: 




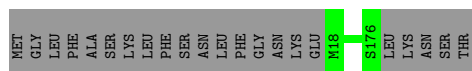
- Molecule 1: ADP-RIBOSYLATION FACTOR 1

Chain I: 



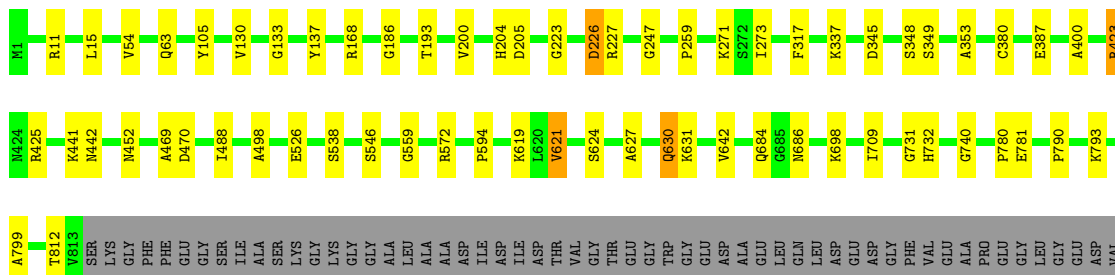
- Molecule 1: ADP-RIBOSYLATION FACTOR 1

Chain J: 



- Molecule 2: COATOMER SUBUNIT ALPHA

Chain C: 



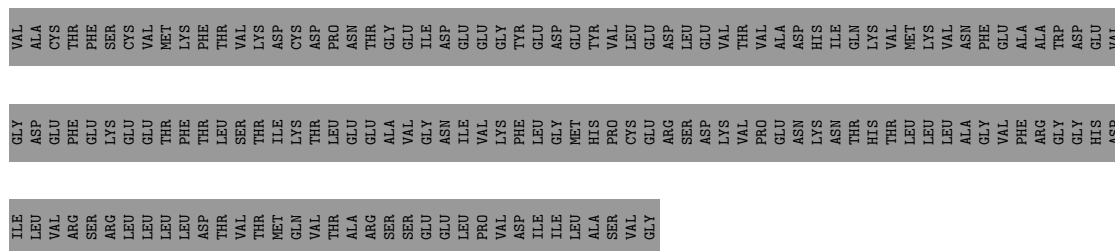
[illegible]

- Molecule 2: COATOMER SUBUNIT ALPHA

Chain K:  59% 5% 36%

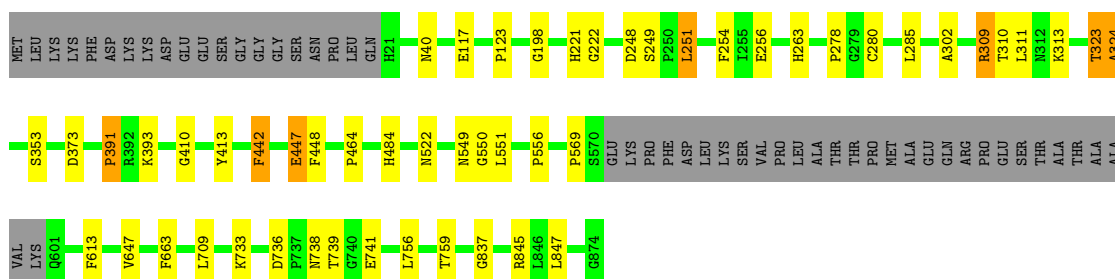
GLN	ALA	ASN	ALA	ALA	HIS	LEU	A799	R424	R168
GLY	ALA	LEU	GLY	GLN	ILE	GLY	R11	R425	R186
PRO	SER	PHE	LEU	GLN	LEU	GLY	T812	R441	R187
SER	TYR	PHE	LEU	ASN	ALA	GLN	R813	R442	R188
ALA	ARG	LYS	ILE	THR	SER	GLU	SER	R443	R189
PRO	PRO	LEU	THR	GLY	PHE	GLU	LYS	R444	R190
SER	ILE	LYS	ILE	VAL	GLY	GLY	GLY	R445	R191
HIS	TYR	ASN	CYS	VAL	PHE	GLY	PHE	R446	R192
PRO	ARG	PHE	ARG	ALA	THR	GLY	PHE	R447	R193
GLN	GLY	LYS	GLU	VAL	ALA	GLY	GLU	R448	R194
PHE	LYS	THR	TYR	GLY	MET	ASP	GLY	R449	R195
GLU	PRO	ALA	ILE	LEU	ARG	ASP	SER	R450	R196
GLY	VAL	ALA	VAL	LYS	LEU	VAL	ILE	R451	R197
LYS	GLY	THR	GLY	LEU	LEU	VAL	LYS	R452	R198
GLY	GLY	THR	GLY	GLN	GLY	GLU	LYS	R453	R199
GLY	GLY	LEU	ILE	GLN	GLY	LEU	GLY	R454	R200
GLY	GLY	LEU	GLY	VAL	VAL	PRO	GLY	R455	R201
GLY	GLY	LEU	ARG	VAL	GLY	PRO	GLY	R456	R202
GLY	GLY	GLU	MET	GLY	ILE	GLY	ALA	R457	R203
GLY	GLY	LEU	GLY	ILE	GLY	LEU	LYS	R458	R204
GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	R459	R205
GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	R460	R206
GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	R461	R207
GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	R462	R208
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GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	R471	R217
GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	R472	R218
GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	R473	R219
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GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	R475	R221
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GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	R482	R228
GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	R483	R229
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GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	R494	R240
GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	R495	R241
GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	R496	R242
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GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	R506	R252
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GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	R519	R265
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GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	R521	R267
GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	R522	R268
GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	R523	R269
GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	R524	R270
GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	R525	R271
GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	R526	R272
GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	R527	R273
GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	R528	R274
GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	R529	R275
GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	R530	R276
GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	R531	R277
GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	R532	R278
GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	R533	R279
GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	R534	R280
GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	R535	R281
GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	R536	R282
GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	R537	R283
GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	R538	R284
GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	R539	R285
GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	R540	R286
GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	R541	R287
GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	R542	R288
GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	R543	R289
GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	R544	R290
GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	R545	R291
GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	R546	R292
GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	R547	R293
GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	R548	R294
GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	R549	R295
GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	R550	R296
GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	R551	R297
GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	R552	R298
GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	R553	R299
GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	R554	R300
GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	R555	R301
GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	R556	R302
GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	R557	R303
GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	R558	R304
GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	R559	R305
GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	R560	R306
GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	R561	R307
GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	R562	R308
GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	R563	R309
GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	R564	R310
GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	R565	R311
GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	R566	R312
GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	R567	R313
GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	R568	R314
GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	R569	R315
GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	R570	R316
GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	R571	R317
GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	R572	R318
GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	R573	R319
GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	R574	R320
GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	R575	R321
GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	R576	R322
GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	R577	R323
GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	R578	R324
GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	R579	R325
GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	R580	R326
GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	R581	R327
GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	R582	R328
GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	R583	R329
GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	R584	R330
GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	R585	R331
GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	R586	R332
GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	R587	R333
GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	R588	R334
GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	R589	R335
GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	R590	R336
GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	R591	R337
GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	R592	R338
GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	R593	R339
GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	R594	R340
GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	R595	R341
GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	R596	R342
GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	R597	R343
GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	R598	R344
GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	R599	R345
GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	R600	R346
GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	R601	R347
GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	R602	





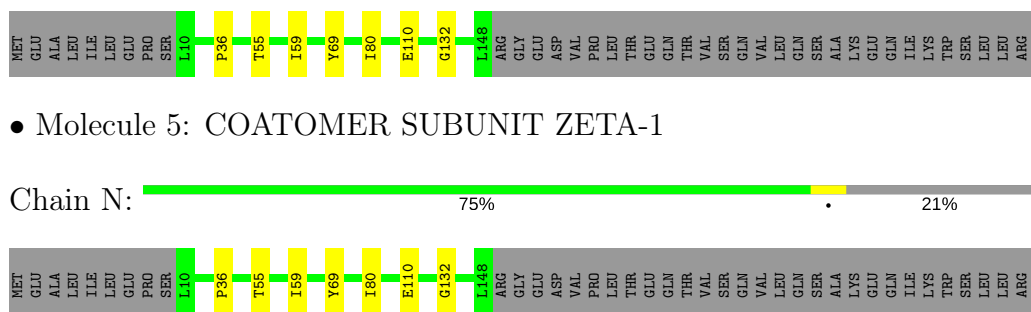
- Molecule 4: COATOMER SUBUNIT GAMMA-1

Chain M:  88% 5% • 6%



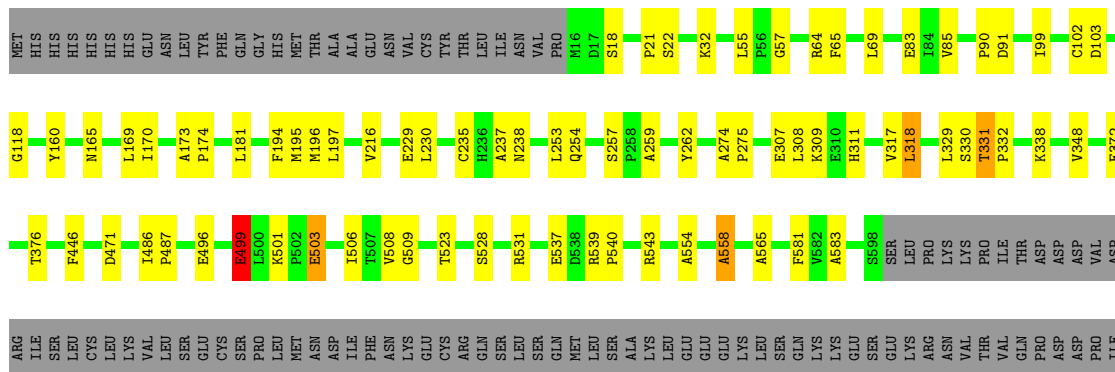
• Molecule 5: COATOMER SUBUNIT ZETA-1

Chain F:  75% 1% 21%



• Molecule 6: COATOMER SUBUNIT BETA

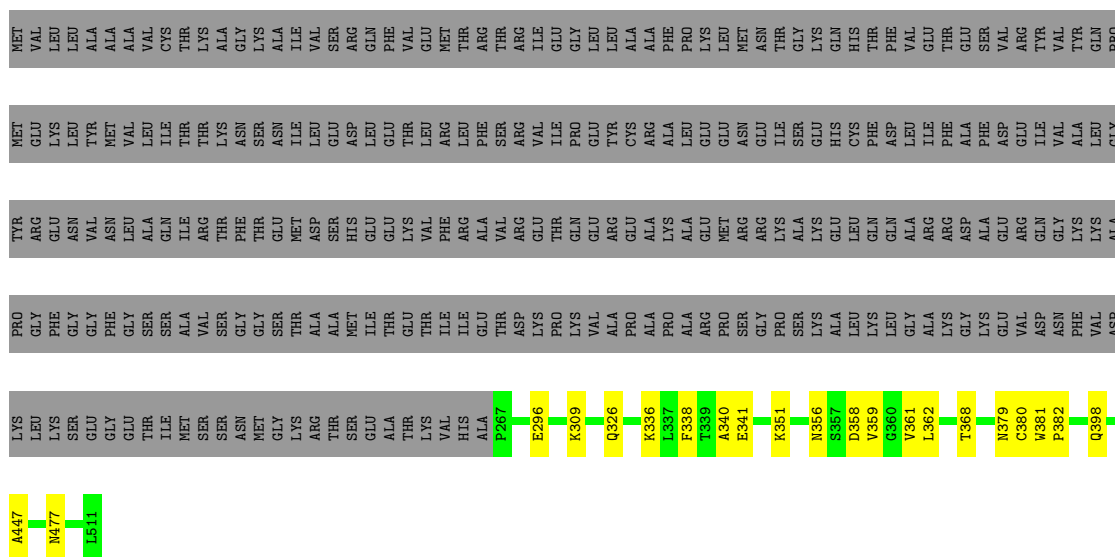
Chain G:  73% 10% • 16%







Opinion	Percentage
Doing a good job	44%
Doing a bad job	52%



## 4 Experimental information

Property	Value	Source
Reconstruction method	TOMOGRAPHY	Depositor
Imposed symmetry	POINT, C2	Depositor
Number of tilted images used	421	Depositor
Resolution determination method	Not provided	Depositor
CTF correction method	PHASE FLIPPING OF INDIVIDUAL TILTS	Depositor
Microscope	FEI TITAN KRIOS	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	0.68	0/792
1	B	0.43	0/635	0.69	0/792
1	I	0.43	0/635	0.69	0/792
1	J	0.43	0/635	0.69	0/792
2	C	1.55	8/3250 (0.2%)	1.71	14/4061 (0.3%)
2	K	1.55	8/3250 (0.2%)	1.71	14/4061 (0.3%)
3	D	1.60	16/3210 (0.5%)	1.72	24/4011 (0.6%)
3	L	1.60	16/3210 (0.5%)	1.72	24/4011 (0.6%)
4	E	1.52	2/2198 (0.1%)	1.58	9/2746 (0.3%)
4	M	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%)
5	N	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%)
6	O	1.50	7/3248 (0.2%)	1.71	23/4057 (0.6%)
7	H	1.21	0/1518	1.35	8/1893 (0.4%)
7	P	1.20	0/1518	1.34	8/1893 (0.4%)
7	Q	1.04	0/980	1.05	1/1222 (0.1%)
All	All	1.44	70/32570 (0.2%)	1.59	173/40674 (0.4%)

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
2	K	0	4
3	D	0	2
3	L	0	2
4	E	0	4
4	M	0	4
5	F	0	1
5	N	0	1

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Mol	Chain	#Chirality outliers	#Planarity outliers
6	G	0	14
6	O	0	14
All	All	0	50

All (70) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	K	621	VAL	C-N	6.92	1.45	1.33
2	C	621	VAL	C-N	6.90	1.45	1.33
3	L	330	MET	N-CA	-6.79	1.32	1.46
3	D	330	MET	N-CA	-6.79	1.32	1.46
4	M	198	GLY	CA-C	-6.44	1.41	1.51
4	E	198	GLY	CA-C	-6.43	1.41	1.51
3	L	378	TYR	N-CA	-6.38	1.33	1.46
3	D	378	TYR	N-CA	-6.38	1.33	1.46
3	D	537	THR	N-CA	-6.34	1.33	1.46
3	L	537	THR	N-CA	-6.30	1.33	1.46
6	G	118	GLY	CA-C	-6.28	1.41	1.51
6	O	118	GLY	CA-C	-6.28	1.41	1.51
3	L	723	GLY	CA-C	-6.27	1.41	1.51
3	D	723	GLY	CA-C	-6.26	1.41	1.51
3	D	799	PRO	C-N	6.18	1.44	1.33
3	L	799	PRO	C-N	6.16	1.44	1.33
3	D	464	GLN	N-CA	-6.11	1.34	1.46
3	L	464	GLN	N-CA	-6.08	1.34	1.46
3	D	186	LYS	C-N	5.99	1.43	1.33
3	L	186	LYS	C-N	5.96	1.43	1.33
2	K	631	LYS	N-CA	-5.93	1.34	1.46
4	E	123	PRO	N-CA	-5.92	1.37	1.47
2	C	631	LYS	N-CA	-5.91	1.34	1.46
4	M	123	PRO	N-CA	-5.91	1.37	1.47
3	L	331	GLY	CA-C	-5.91	1.42	1.51
3	D	331	GLY	CA-C	-5.85	1.42	1.51
3	L	227	GLY	CA-C	-5.78	1.42	1.51
3	D	227	GLY	CA-C	-5.77	1.42	1.51
2	K	204	HIS	N-CA	-5.76	1.34	1.46
2	C	204	HIS	N-CA	-5.76	1.34	1.46
3	D	373	GLY	N-CA	-5.71	1.37	1.46
3	L	373	GLY	N-CA	-5.70	1.37	1.46
4	M	837	GLY	N-CA	-5.69	1.37	1.46
6	O	509	GLY	CA-C	-5.62	1.42	1.51
6	G	509	GLY	CA-C	-5.60	1.42	1.51

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	K	259	PRO	CA-C	-5.46	1.42	1.52
2	C	259	PRO	CA-C	-5.45	1.42	1.52
6	G	539	ARG	C-N	5.45	1.44	1.34
2	K	186	GLY	N-CA	-5.45	1.37	1.46
6	O	539	ARG	C-N	5.44	1.44	1.34
2	C	186	GLY	N-CA	-5.44	1.37	1.46
5	F	132	GLY	N-CA	-5.34	1.38	1.46
4	M	613	PHE	N-CA	-5.32	1.35	1.46
5	N	132	GLY	N-CA	-5.31	1.38	1.46
6	O	57	GLY	N-CA	5.29	1.53	1.46
6	G	57	GLY	N-CA	5.28	1.53	1.46
2	K	740	GLY	CA-C	-5.23	1.43	1.51
2	C	740	GLY	CA-C	-5.22	1.43	1.51
3	L	466	LYS	N-CA	-5.22	1.35	1.46
3	D	466	LYS	N-CA	-5.19	1.35	1.46
6	O	160	TYR	N-CA	-5.19	1.35	1.46
6	G	160	TYR	N-CA	-5.18	1.35	1.46
2	K	353	ALA	N-CA	-5.17	1.36	1.46
3	D	504	GLY	N-CA	5.17	1.53	1.46
3	D	310	ALA	N-CA	-5.16	1.36	1.46
2	K	130	VAL	C-N	5.16	1.46	1.34
3	L	504	GLY	N-CA	5.16	1.53	1.46
2	C	130	VAL	C-N	5.16	1.46	1.34
2	C	353	ALA	N-CA	-5.16	1.36	1.46
3	L	310	ALA	N-CA	-5.15	1.36	1.46
3	D	509	GLY	N-CA	-5.14	1.38	1.46
3	L	509	GLY	N-CA	-5.14	1.38	1.46
3	D	586	SER	N-CA	-5.11	1.36	1.46
3	L	586	SER	N-CA	-5.11	1.36	1.46
6	G	565	ALA	N-CA	-5.05	1.36	1.46
6	G	857	GLN	N-CA	-5.04	1.36	1.46
3	L	371	GLY	CA-C	-5.04	1.43	1.51
3	D	371	GLY	CA-C	-5.04	1.43	1.51
6	O	565	ALA	N-CA	-5.04	1.36	1.46
6	O	857	GLN	N-CA	-5.03	1.36	1.46

All (173) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
6	O	496	GLU	N-CA-C	7.84	132.17	111.00
6	G	496	GLU	N-CA-C	7.81	132.09	111.00
4	E	302	ALA	C-N-CA	7.07	139.37	121.70

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	M	302	ALA	C-N-CA	7.04	139.30	121.70
2	K	54	VAL	N-CA-C	-6.93	92.30	111.00
2	C	54	VAL	N-CA-C	-6.90	92.36	111.00
6	G	486	ILE	O-C-N	-6.79	108.19	121.10
6	O	486	ILE	O-C-N	-6.78	108.21	121.10
6	O	869	THR	N-CA-C	-6.72	92.85	111.00
6	G	869	THR	N-CA-C	-6.72	92.86	111.00
4	M	756	LEU	N-CA-C	-6.71	92.89	111.00
3	D	490	TYR	N-CA-C	-6.64	93.08	111.00
3	L	490	TYR	N-CA-C	-6.63	93.10	111.00
6	G	486	ILE	CA-C-N	6.60	135.58	117.10
6	O	486	ILE	CA-C-N	6.58	135.52	117.10
3	D	286	VAL	N-CA-C	-6.52	93.39	111.00
3	L	286	VAL	N-CA-C	-6.51	93.42	111.00
6	G	792	LEU	N-CA-C	-6.43	93.63	111.00
7	H	90	ILE	CA-C-N	6.42	135.08	117.10
7	P	90	ILE	CA-C-N	6.42	135.08	117.10
6	O	792	LEU	N-CA-C	-6.42	93.68	111.00
3	D	461	ILE	N-CA-C	-6.41	93.70	111.00
3	L	461	ILE	N-CA-C	-6.41	93.70	111.00
4	E	254	PHE	N-CA-C	-6.40	93.71	111.00
4	M	254	PHE	N-CA-C	-6.40	93.72	111.00
4	E	324	ALA	N-CA-C	6.32	128.07	111.00
4	M	324	ALA	N-CA-C	6.30	128.01	111.00
5	F	69	TYR	O-C-N	6.30	132.78	122.70
5	N	69	TYR	O-C-N	6.29	132.76	122.70
3	D	642	GLU	O-C-N	6.29	132.76	122.70
3	L	204	SER	N-CA-C	-6.27	94.08	111.00
3	L	642	GLU	O-C-N	6.26	132.71	122.70
3	D	204	SER	N-CA-C	-6.25	94.12	111.00
2	K	400	ALA	N-CA-C	-6.25	94.14	111.00
2	C	400	ALA	N-CA-C	-6.23	94.18	111.00
7	P	66	MET	N-CA-C	-6.23	94.19	111.00
7	H	66	MET	N-CA-C	-6.22	94.21	111.00
3	D	78	ASP	C-N-CA	6.22	137.25	121.70
3	D	196	GLY	CA-C-O	6.19	131.75	120.60
3	L	78	ASP	C-N-CA	6.18	137.16	121.70
3	L	613	ILE	N-CA-C	-6.18	94.31	111.00
3	D	573	LEU	N-CA-C	-6.18	94.32	111.00
3	D	613	ILE	N-CA-C	-6.17	94.33	111.00
3	L	573	LEU	N-CA-C	-6.17	94.33	111.00
3	L	196	GLY	CA-C-O	6.17	131.71	120.60

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	L	469	PHE	N-CA-C	-6.12	94.49	111.00
3	D	469	PHE	N-CA-C	-6.11	94.50	111.00
7	H	56	TYR	N-CA-C	-6.01	94.77	111.00
7	P	56	TYR	N-CA-C	-6.00	94.79	111.00
6	G	376	THR	N-CA-C	-5.91	95.05	111.00
6	O	376	THR	N-CA-C	-5.90	95.07	111.00
4	M	738	ASN	N-CA-C	-5.88	95.13	111.00
2	C	223	GLY	N-CA-C	-5.88	98.41	113.10
2	K	223	GLY	N-CA-C	-5.87	98.42	113.10
4	M	709	LEU	N-CA-C	-5.82	95.28	111.00
2	C	732	HIS	C-N-CA	5.69	135.92	121.70
2	C	105	TYR	N-CA-C	-5.69	95.65	111.00
2	K	105	TYR	N-CA-C	-5.69	95.65	111.00
5	F	80	ILE	N-CA-C	-5.68	95.65	111.00
2	K	732	HIS	C-N-CA	5.68	135.91	121.70
5	N	80	ILE	N-CA-C	-5.68	95.66	111.00
4	M	759	THR	N-CA-C	-5.67	95.68	111.00
4	M	550	GLY	C-N-CA	5.67	135.87	121.70
6	O	499	GLU	N-CA-C	5.66	126.27	111.00
4	E	550	GLY	C-N-CA	5.65	135.83	121.70
3	L	75	GLY	N-CA-C	-5.65	98.97	113.10
6	G	499	GLU	N-CA-C	5.65	126.25	111.00
3	D	75	GLY	N-CA-C	-5.64	99.00	113.10
4	M	222	GLY	N-CA-C	-5.64	99.00	113.10
4	E	222	GLY	N-CA-C	-5.63	99.03	113.10
3	L	182	GLU	N-CA-C	-5.62	95.83	111.00
3	D	182	GLU	N-CA-C	-5.62	95.84	111.00
4	E	391	PRO	N-CA-C	5.60	126.67	112.10
2	C	15	LEU	N-CA-C	-5.60	95.89	111.00
2	K	15	LEU	N-CA-C	-5.60	95.89	111.00
6	G	818	ILE	N-CA-C	-5.59	95.89	111.00
4	M	391	PRO	N-CA-C	5.58	126.62	112.10
6	O	818	ILE	N-CA-C	-5.58	95.93	111.00
6	G	503	GLU	N-CA-C	-5.57	95.97	111.00
6	O	503	GLU	N-CA-C	-5.56	95.98	111.00
6	O	196	MET	N-CA-C	-5.55	96.01	111.00
6	G	196	MET	N-CA-C	-5.54	96.04	111.00
3	D	429	GLY	N-CA-C	-5.51	99.32	113.10
6	G	195	MET	N-CA-C	-5.51	96.12	111.00
6	G	170	ILE	CA-C-N	5.51	132.52	117.10
6	O	170	ILE	CA-C-N	5.50	132.50	117.10
7	P	477	ASN	C-N-CA	-5.50	107.95	121.70

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	M	733	LYS	N-CA-C	-5.50	96.16	111.00
6	O	195	MET	N-CA-C	-5.50	96.16	111.00
3	L	429	GLY	N-CA-C	-5.49	99.37	113.10
7	H	477	ASN	C-N-CA	-5.49	107.98	121.70
7	Q	477	ASN	C-N-CA	-5.47	108.02	121.70
5	F	110	GLU	N-CA-C	-5.47	96.24	111.00
4	M	847	LEU	N-CA-C	-5.47	96.24	111.00
2	C	630	GLN	N-CA-C	-5.46	96.25	111.00
2	K	630	GLN	N-CA-C	-5.46	96.25	111.00
5	N	110	GLU	N-CA-C	-5.46	96.26	111.00
3	L	115	LEU	N-CA-C	-5.44	96.31	111.00
3	D	115	LEU	N-CA-C	-5.44	96.31	111.00
6	O	558	ALA	N-CA-C	-5.42	96.37	111.00
2	C	273	ILE	N-CA-C	-5.40	96.41	111.00
6	G	558	ALA	N-CA-C	-5.40	96.42	111.00
2	K	273	ILE	N-CA-C	-5.40	96.42	111.00
3	D	642	GLU	CA-C-O	-5.40	108.77	120.10
2	C	226	ASP	N-CA-C	-5.39	96.46	111.00
2	K	226	ASP	N-CA-C	-5.39	96.46	111.00
4	M	736	ASP	CA-C-O	-5.38	108.79	120.10
4	M	845	ARG	N-CA-C	-5.38	96.46	111.00
4	M	285	LEU	O-C-N	-5.37	114.11	122.70
4	E	285	LEU	O-C-N	-5.36	114.12	122.70
3	L	642	GLU	CA-C-O	-5.36	108.84	120.10
6	G	318	LEU	N-CA-C	5.34	125.42	111.00
7	H	90	ILE	CA-C-O	-5.34	108.88	120.10
6	O	318	LEU	N-CA-C	5.34	125.42	111.00
7	P	90	ILE	CA-C-O	-5.32	108.92	120.10
4	M	647	VAL	N-CA-C	-5.32	96.65	111.00
7	P	49	VAL	N-CA-C	-5.30	96.69	111.00
7	H	49	VAL	N-CA-C	-5.30	96.70	111.00
3	L	441	VAL	N-CA-C	-5.29	96.72	111.00
3	D	441	VAL	N-CA-C	-5.28	96.74	111.00
6	O	64	ARG	N-CA-C	5.22	125.11	111.00
3	L	394	PHE	N-CA-C	-5.22	96.90	111.00
3	D	394	PHE	N-CA-C	-5.20	96.96	111.00
7	H	19	ARG	C-N-CA	5.20	134.69	121.70
7	P	19	ARG	C-N-CA	5.20	134.70	121.70
6	G	64	ARG	N-CA-C	5.20	125.03	111.00
2	C	423	ARG	C-N-CA	5.18	134.66	121.70
2	K	423	ARG	C-N-CA	5.18	134.65	121.70
7	H	48	PHE	N-CA-C	-5.17	97.04	111.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	D	21	VAL	N-CA-C	-5.17	97.05	111.00
2	C	200	VAL	O-C-N	5.16	130.96	122.70
3	D	268	ASN	N-CA-C	-5.16	97.07	111.00
4	M	663	PHE	N-CA-C	-5.16	97.08	111.00
7	P	48	PHE	N-CA-C	-5.16	97.08	111.00
3	L	21	VAL	N-CA-C	-5.15	97.09	111.00
3	L	268	ASN	N-CA-C	-5.15	97.10	111.00
6	G	775	LEU	N-CA-C	-5.14	97.13	111.00
6	O	169	LEU	N-CA-C	-5.13	97.15	111.00
6	G	868	VAL	N-CA-C	-5.12	97.17	111.00
2	K	200	VAL	O-C-N	5.12	130.90	122.70
6	O	775	LEU	N-CA-C	-5.12	97.17	111.00
6	G	229	GLU	C-N-CA	5.12	134.51	121.70
6	O	229	GLU	C-N-CA	5.12	134.50	121.70
6	O	868	VAL	N-CA-C	-5.12	97.18	111.00
6	G	169	LEU	N-CA-C	-5.11	97.19	111.00
3	D	104	CYS	C-N-CA	5.11	134.46	121.70
3	L	104	CYS	C-N-CA	5.10	134.46	121.70
2	K	168	ARG	N-CA-C	-5.09	97.26	111.00
3	L	543	LEU	O-C-N	-5.09	114.56	122.70
2	C	168	ARG	N-CA-C	-5.08	97.27	111.00
3	L	114	ILE	N-CA-C	-5.08	97.30	111.00
4	M	447	GLU	C-N-CA	5.07	134.36	121.70
4	E	447	GLU	C-N-CA	5.06	134.35	121.70
4	E	248	ASP	O-C-N	-5.06	114.61	122.70
6	G	165	ASN	C-N-CA	5.06	134.34	121.70
3	D	114	ILE	N-CA-C	-5.06	97.35	111.00
6	O	165	ASN	C-N-CA	5.05	134.33	121.70
6	O	797	PHE	N-CA-C	-5.05	97.36	111.00
2	C	684	GLN	C-N-CA	5.05	132.90	122.30
3	D	543	LEU	O-C-N	-5.04	114.63	122.70
4	M	248	ASP	O-C-N	-5.04	114.64	122.70
6	O	805	LYS	N-CA-C	-5.04	97.41	111.00
6	G	797	PHE	N-CA-C	-5.03	97.42	111.00
6	G	805	LYS	N-CA-C	-5.03	97.42	111.00
2	K	684	GLN	C-N-CA	5.03	132.86	122.30
3	D	218	ASN	O-C-N	5.03	130.74	122.70
3	D	20	SER	C-N-CA	5.02	134.25	121.70
3	L	20	SER	C-N-CA	5.02	134.24	121.70
2	K	709	ILE	C-N-CA	5.01	134.23	121.70
3	L	218	ASN	O-C-N	5.01	130.72	122.70
2	C	709	ILE	C-N-CA	5.01	134.22	121.70

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
6	O	42	LEU	O-C-N	-5.01	114.69	122.70
6	G	338	LYS	O-C-N	5.01	130.71	122.70

There are no chirality outliers.

All (50) 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	119	ASP	Mainchain
3	D	44	HIS	Mainchain
4	E	309	ARG	Peptide
4	E	323	THR	Peptide
4	E	442	PHE	Peptide
4	E	447	GLU	Peptide
5	F	59	ILE	Mainchain
6	G	235	CYS	Peptide
6	G	254	GLN	Peptide
6	G	274	ALA	Peptide
6	G	309	LYS	Peptide
6	G	311	HIS	Peptide
6	G	329	LEU	Peptide
6	G	331	THR	Peptide
6	G	348	VAL	Peptide
6	G	471	ASP	Peptide
6	G	499	GLU	Mainchain
6	G	581	PHE	Peptide
6	G	65	PHE	Mainchain
6	G	897	LYS	Peptide
6	G	91	ASP	Mainchain
2	K	317	PHE	Mainchain
2	K	380	CYS	Mainchain
2	K	559	GLY	Mainchain
2	K	63	GLN	Peptide
3	L	119	ASP	Mainchain
3	L	44	HIS	Mainchain
4	M	309	ARG	Peptide
4	M	323	THR	Peptide
4	M	442	PHE	Peptide
4	M	447	GLU	Peptide

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Mol	Chain	Res	Type	Group
5	N	59	ILE	Mainchain
6	O	235	CYS	Peptide
6	O	254	GLN	Peptide
6	O	274	ALA	Peptide
6	O	309	LYS	Peptide
6	O	311	HIS	Peptide
6	O	329	LEU	Peptide
6	O	331	THR	Peptide
6	O	348	VAL	Peptide
6	O	471	ASP	Peptide
6	O	499	GLU	Mainchain
6	O	581	PHE	Peptide
6	O	65	PHE	Mainchain
6	O	897	LYS	Peptide
6	O	91	ASP	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
1	I	636	0	181	1	0
1	J	636	0	181	0	0
2	C	3251	0	869	0	0
2	K	3251	0	869	0	0
3	D	3211	0	880	0	0
3	L	3211	0	880	0	0
4	E	2199	0	570	0	0
4	M	3294	0	852	1	0
5	F	555	0	148	0	0
5	N	555	0	148	0	0
6	G	3250	0	833	0	0
6	O	3250	0	833	0	0
7	H	1520	0	403	38	0
7	P	1520	0	403	37	0
7	Q	981	0	261	35	0
All	All	32592	0	8673	62	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 2.

All (62) 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)
7:P:338:PHE:O	7:Q:380:CYS:C	1.68	1.32
7:H:380:CYS:C	7:Q:338:PHE:O	1.68	1.30
7:H:338:PHE:O	7:P:380:CYS:C	1.68	1.29
7:P:338:PHE:O	7:Q:380:CYS:CA	1.90	1.19
7:H:380:CYS:CA	7:Q:338:PHE:O	1.90	1.19
7:H:338:PHE:O	7:P:380:CYS:CA	1.90	1.18
7:H:380:CYS:CA	7:Q:338:PHE:C	2.30	0.99
7:P:338:PHE:C	7:Q:380:CYS:CA	2.30	0.97
7:H:338:PHE:C	7:P:380:CYS:CA	2.30	0.95
7:H:338:PHE:CA	7:P:381:TRP:N	2.29	0.95
7:P:338:PHE:CA	7:Q:381:TRP:N	2.29	0.95
7:H:338:PHE:C	7:P:381:TRP:N	2.24	0.91
7:H:381:TRP:N	7:Q:338:PHE:CA	2.29	0.91
7:H:381:TRP:N	7:Q:338:PHE:C	2.24	0.91
7:P:338:PHE:C	7:Q:381:TRP:N	2.24	0.90
7:H:338:PHE:C	7:P:380:CYS:C	2.32	0.88
7:P:338:PHE:C	7:Q:380:CYS:C	2.32	0.88
7:H:341:GLU:O	7:P:381:TRP:CA	2.22	0.88
7:H:381:TRP:CA	7:Q:341:GLU:O	2.22	0.88
7:H:380:CYS:C	7:Q:338:PHE:C	2.32	0.87
7:P:341:GLU:O	7:Q:381:TRP:CA	2.22	0.87
7:H:341:GLU:O	7:P:381:TRP:N	2.10	0.85
7:P:341:GLU:O	7:Q:381:TRP:N	2.10	0.85
7:H:381:TRP:N	7:Q:341:GLU:O	2.10	0.84
7:Q:296:GLU:CA	7:Q:368:THR:H	1.96	0.78
7:P:296:GLU:CA	7:P:368:THR:H	1.96	0.78
7:H:296:GLU:CA	7:H:368:THR:H	1.95	0.77
7:H:381:TRP:N	7:Q:338:PHE:O	2.22	0.72
7:H:338:PHE:O	7:P:381:TRP:N	2.22	0.72
7:P:338:PHE:O	7:Q:381:TRP:N	2.22	0.65
7:P:338:PHE:CA	7:Q:381:TRP:H	2.07	0.64
7:P:356:ASN:CA	7:P:362:LEU:H	2.10	0.64
7:H:381:TRP:H	7:Q:338:PHE:CA	2.07	0.64
7:Q:356:ASN:CA	7:Q:362:LEU:H	2.10	0.64
7:H:380:CYS:C	7:Q:341:GLU:O	2.36	0.64
7:H:356:ASN:CA	7:H:362:LEU:H	2.10	0.64
7:H:341:GLU:O	7:P:380:CYS:C	2.36	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:H:338:PHE:CA	7:P:381:TRP:H	2.07	0.63
7:P:341:GLU:O	7:Q:380:CYS:C	2.36	0.62
7:H:340:ALA:CA	7:P:379:ASN:N	2.58	0.61
7:P:340:ALA:CA	7:Q:379:ASN:N	2.58	0.61
7:H:379:ASN:N	7:Q:340:ALA:CA	2.58	0.57
7:P:341:GLU:H	7:Q:379:ASN:CA	2.18	0.56
7:H:379:ASN:CA	7:Q:341:GLU:H	2.18	0.56
7:H:341:GLU:H	7:P:379:ASN:CA	2.18	0.56
7:H:382:PRO:O	7:Q:336:LYS:O	0.56	0.56
7:P:336:LYS:O	7:Q:382:PRO:O	0.56	0.56
7:H:336:LYS:O	7:P:382:PRO:O	0.56	0.55
7:P:340:ALA:CA	7:Q:379:ASN:CA	2.05	0.53
7:H:340:ALA:CA	7:P:379:ASN:CA	2.04	0.52
7:H:379:ASN:CA	7:Q:341:GLU:N	2.71	0.51
7:H:341:GLU:N	7:P:379:ASN:CA	2.71	0.50
7:H:379:ASN:CA	7:Q:340:ALA:CA	2.04	0.49
7:P:341:GLU:N	7:Q:379:ASN:CA	2.71	0.47
7:H:356:ASN:C	7:H:362:LEU:H	2.20	0.45
7:P:356:ASN:C	7:P:362:LEU:H	2.20	0.45
7:Q:356:ASN:C	7:Q:362:LEU:H	2.20	0.44
4:M:249:SER:C	4:M:251:LEU:H	2.23	0.42
7:H:338:PHE:C	7:P:381:TRP:H	2.17	0.41
7:H:340:ALA:C	7:P:380:CYS:CA	2.82	0.41
7:H:356:ASN:CA	7:H:362:LEU:N	2.83	0.40
1:I:175:ASN:O	1:I:176:SER:C	2.60	0.40

There are no symmetry-related clashes.

## 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 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

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	B	157/181 (87%)	153 (98%)	4 (2%)	0	100	100
1	I	157/181 (87%)	153 (98%)	4 (2%)	0	100	100
1	J	157/181 (87%)	153 (98%)	4 (2%)	0	100	100
2	C	811/1262 (64%)	671 (83%)	97 (12%)	43 (5%)	2	25
2	K	811/1262 (64%)	671 (83%)	97 (12%)	43 (5%)	2	25
3	D	801/905 (88%)	700 (87%)	64 (8%)	37 (5%)	2	27
3	L	801/905 (88%)	700 (87%)	64 (8%)	37 (5%)	2	27
4	E	548/874 (63%)	491 (90%)	28 (5%)	29 (5%)	2	25
4	M	820/874 (94%)	749 (91%)	40 (5%)	31 (4%)	3	31
5	F	137/177 (77%)	128 (93%)	7 (5%)	2 (2%)	11	51
5	N	137/177 (77%)	128 (93%)	7 (5%)	2 (2%)	11	51
6	G	809/968 (84%)	658 (81%)	84 (10%)	67 (8%)	1	15
6	O	809/968 (84%)	658 (81%)	84 (10%)	67 (8%)	1	15
7	H	376/511 (74%)	336 (89%)	31 (8%)	9 (2%)	6	40
7	P	376/511 (74%)	336 (89%)	31 (8%)	9 (2%)	6	40
7	Q	243/511 (48%)	220 (90%)	15 (6%)	8 (3%)	4	33
All	All	8107/10629 (76%)	7058 (87%)	665 (8%)	384 (5%)	5	27

All (384) 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
3	D	6	ASP
3	D	284	ASN
3	D	329	ALA
3	D	336	LYS
3	D	350	SER
3	D	484	SER
3	D	513	ALA
3	D	615	LYS
3	D	791	PRO
3	D	795	GLU

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Mol	Chain	Res	Type
4	E	117	GLU
4	E	280	CYS
4	E	309	ARG
4	E	323	THR
4	E	324	ALA
4	E	391	PRO
4	E	393	LYS
4	E	413	TYR
4	E	448	PHE
4	E	549	ASN
5	F	36	PRO
6	G	55	LEU
6	G	69	LEU
6	G	85	VAL
6	G	90	PRO
6	G	173	ALA
6	G	181	LEU
6	G	197	LEU
6	G	237	ALA
6	G	253	LEU
6	G	275	PRO
6	G	331	THR
6	G	499	GLU
6	G	506	ILE
6	G	508	VAL
6	G	523	THR
6	G	543	ARG
6	G	770	ASN
6	G	785	GLU
6	G	792	LEU
6	G	814	ILE
6	G	826	ALA
6	G	939	THR
6	G	959	ILE
7	H	326	GLN
7	H	361	VAL
2	K	11	ARG
2	K	227	ARG
2	K	526	GLU
2	K	572	ARG
2	K	686	ASN
3	L	6	ASP

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Mol	Chain	Res	Type
3	L	284	ASN
3	L	329	ALA
3	L	336	LYS
3	L	350	SER
3	L	484	SER
3	L	513	ALA
3	L	615	LYS
3	L	791	PRO
3	L	795	GLU
4	M	117	GLU
4	M	280	CYS
4	M	309	ARG
4	M	323	THR
4	M	324	ALA
4	M	391	PRO
4	M	393	LYS
4	M	413	TYR
4	M	448	PHE
4	M	549	ASN
5	N	36	PRO
6	O	55	LEU
6	O	69	LEU
6	O	85	VAL
6	O	90	PRO
6	O	173	ALA
6	O	181	LEU
6	O	197	LEU
6	O	237	ALA
6	O	253	LEU
6	O	275	PRO
6	O	331	THR
6	O	499	GLU
6	O	506	ILE
6	O	508	VAL
6	O	523	THR
6	O	543	ARG
6	O	770	ASN
6	O	785	GLU
6	O	792	LEU
6	O	814	ILE
6	O	826	ALA
6	O	939	THR

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Mol	Chain	Res	Type
6	O	959	ILE
7	P	326	GLN
7	P	361	VAL
7	Q	326	GLN
7	Q	361	VAL
2	C	137	TYR
2	C	226	ASP
2	C	425	ARG
2	C	441	LYS
2	C	498	ALA
2	C	538	SER
2	C	546	SER
2	C	621	VAL
2	C	630	GLN
2	C	642	VAL
3	D	17	ARG
3	D	59	PRO
3	D	273	ARG
3	D	410	SER
3	D	426	PRO
3	D	630	PHE
3	D	739	ASP
4	E	263	HIS
4	E	310	THR
4	E	313	LYS
4	E	373	ASP
4	E	442	PHE
4	E	484	HIS
4	E	551	LEU
6	G	83	GLU
6	G	103	ASP
6	G	174	PRO
6	G	307	GLU
6	G	554	ALA
6	G	558	ALA
6	G	879	ASP
7	H	351	LYS
2	K	137	TYR
2	K	226	ASP
2	K	425	ARG
2	K	441	LYS
2	K	498	ALA

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Mol	Chain	Res	Type
2	K	538	SER
2	K	546	SER
2	K	621	VAL
2	K	642	VAL
3	L	17	ARG
3	L	59	PRO
3	L	273	ARG
3	L	410	SER
3	L	426	PRO
3	L	630	PHE
3	L	739	ASP
4	M	263	HIS
4	M	310	THR
4	M	313	LYS
4	M	373	ASP
4	M	442	PHE
4	M	484	HIS
4	M	551	LEU
4	M	739	THR
4	M	741	GLU
6	O	83	GLU
6	O	103	ASP
6	O	174	PRO
6	O	307	GLU
6	O	554	ALA
6	O	558	ALA
6	O	879	ASP
7	P	351	LYS
7	Q	351	LYS
2	C	205	ASP
2	C	337	LYS
2	C	345	ASP
2	C	348	SER
2	C	349	SER
2	C	387	GLU
2	C	469	ALA
2	C	594	PRO
2	C	619	LYS
2	C	624	SER
2	C	627	ALA
2	C	790	PRO
3	D	140	GLY

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Mol	Chain	Res	Type
3	D	260	THR
3	D	272	GLU
3	D	571	ASN
3	D	601	ARG
3	D	662	VAL
3	D	694	GLN
3	D	735	GLN
4	E	256	GLU
4	E	353	SER
4	E	522	ASN
4	E	569	PRO
5	F	55	THR
6	G	18	SER
6	G	22	SER
6	G	194	PHE
6	G	257	SER
6	G	259	ALA
6	G	308	LEU
6	G	318	LEU
6	G	487	PRO
6	G	501	LYS
6	G	528	SER
6	G	817	ASN
6	G	904	GLY
7	H	45	GLN
7	H	358	ASP
7	H	398	GLN
7	H	447	ALA
2	K	205	ASP
2	K	337	LYS
2	K	345	ASP
2	K	348	SER
2	K	349	SER
2	K	387	GLU
2	K	469	ALA
2	K	594	PRO
2	K	619	LYS
2	K	624	SER
2	K	627	ALA
2	K	630	GLN
2	K	790	PRO
3	L	140	GLY

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Mol	Chain	Res	Type
3	L	260	THR
3	L	272	GLU
3	L	571	ASN
3	L	601	ARG
3	L	662	VAL
3	L	694	GLN
3	L	735	GLN
4	M	256	GLU
4	M	353	SER
4	M	522	ASN
4	M	569	PRO
5	N	55	THR
6	O	18	SER
6	O	22	SER
6	O	194	PHE
6	O	257	SER
6	O	259	ALA
6	O	308	LEU
6	O	318	LEU
6	O	487	PRO
6	O	501	LYS
6	O	528	SER
6	O	817	ASN
6	O	904	GLY
7	P	45	GLN
7	P	358	ASP
7	P	398	GLN
7	P	447	ALA
7	Q	358	ASP
7	Q	398	GLN
7	Q	447	ALA
2	C	133	GLY
2	C	193	THR
2	C	271	LYS
2	C	423	ARG
2	C	452	ASN
2	C	731	GLY
3	D	89	LEU
3	D	318	LYS
3	D	734	LEU
3	D	740	ALA
3	D	787	SER

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Mol	Chain	Res	Type
3	D	788	LEU
4	E	40	ASN
4	E	251	LEU
4	E	464	PRO
6	G	332	PRO
6	G	446	PHE
6	G	537	GLU
6	G	583	ALA
6	G	876	ASP
6	G	916	PHE
7	H	309	LYS
7	H	359	VAL
2	K	133	GLY
2	K	193	THR
2	K	271	LYS
2	K	423	ARG
2	K	452	ASN
2	K	731	GLY
3	L	89	LEU
3	L	318	LYS
3	L	577	ASP
3	L	734	LEU
3	L	740	ALA
3	L	787	SER
3	L	788	LEU
4	M	40	ASN
4	M	251	LEU
4	M	464	PRO
6	O	332	PRO
6	O	446	PHE
6	O	537	GLU
6	O	583	ALA
6	O	876	ASP
6	O	916	PHE
7	P	309	LYS
7	P	359	VAL
7	Q	309	LYS
7	Q	359	VAL
2	C	470	ASP
2	C	698	LYS
2	C	793	LYS
2	C	812	THR

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Mol	Chain	Res	Type
3	D	577	ASP
4	E	221	HIS
4	E	311	LEU
4	E	410	GLY
6	G	32	LYS
6	G	99	ILE
6	G	262	TYR
6	G	330	SER
6	G	372	GLU
6	G	794	PRO
6	G	894	THR
6	G	898	ALA
6	G	900	SER
6	G	962	SER
2	K	470	ASP
2	K	698	LYS
2	K	793	LYS
2	K	812	THR
4	M	221	HIS
4	M	311	LEU
4	M	410	GLY
6	O	32	LYS
6	O	99	ILE
6	O	262	TYR
6	O	330	SER
6	O	372	GLU
6	O	794	PRO
6	O	894	THR
6	O	898	ALA
6	O	900	SER
6	O	962	SER
2	C	442	ASN
2	C	781	GLU
3	D	391	ALA
6	G	21	PRO
6	G	102	CYS
6	G	230	LEU
6	G	503	GLU
2	K	442	ASN
2	K	781	GLU
3	L	391	ALA
6	O	21	PRO

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Mol	Chain	Res	Type
6	O	102	CYS
6	O	230	LEU
6	O	503	GLU
3	D	790	ASP
6	G	216	VAL
6	G	238	ASN
3	L	790	ASP
6	O	216	VAL
6	O	238	ASN
2	C	780	PRO
2	C	799	ALA
3	D	355	PRO
6	G	540	PRO
2	K	780	PRO
2	K	799	ALA
3	L	355	PRO
6	O	540	PRO
3	D	762	LEU
4	E	278	PRO
6	G	531	ARG
4	M	278	PRO
6	O	531	ARG
4	E	556	PRO
6	G	317	VAL
3	L	200	PRO
3	L	762	LEU
4	M	556	PRO
6	O	317	VAL
2	C	247	GLY
2	C	488	ILE
3	D	200	PRO
2	K	247	GLY
2	K	488	ILE

### 5.3.2 Protein sidechains ⓘ

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

### 5.3.3 RNA ⓘ

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 carbohydrates 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.