wwPDB X-ray Structure Validation Summary Report (i)

Sep 29, 2024 – 09:17 AM EDT

PDB ID	:	3MV3
Title	:	Crystal Structure of a-COP in Complex with e-COP
Authors	:	Hoelz, A.; Hsia, K.C.
Deposited on	:	2010-05-03
Resolution	:	3.25 Å(reported)

This is a wwPDB X-ray Structure Validation Summary Report for a publicly released PDB entry.

We welcome your comments at *validation@mail.wwpdb.org*
A user guide is available at
https://www.wwpdb.org/validation/2017/XrayValidationReportHelp
with specific help available everywhere you see the (i) symbol.

The types of validation reports are described at
http://www.wwpdb.org/validation/2017/FAQs#types.

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

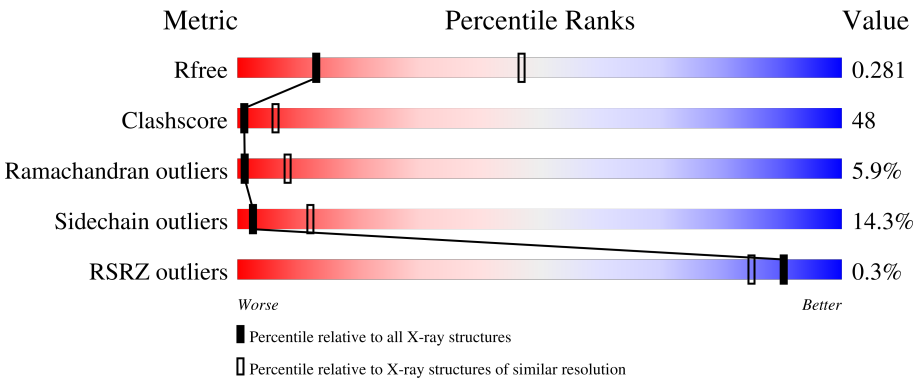
MolProbity	:	4.02b-467
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	1.20.1
EDS	:	3.0
Percentile statistics	:	20231227.v01 (using entries in the PDB archive December 27th 2023)
CCP4	:	9.0.003 (Gargrove)
Density-Fitness	:	1.0.11
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.39

1 Overall quality at a glance (i)

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

The reported resolution of this entry is 3.25 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	164625	1482 (3.30-3.22)
Clashscore	180529	1546 (3.30-3.22)
Ramachandran outliers	177936	1536 (3.30-3.22)
Sidechain outliers	177891	1535 (3.30-3.22)
RSRZ outliers	164620	1483 (3.30-3.22)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments of the lower bar indicate the fraction of residues that contain outliers for >=3, 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions <=5% The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	325	30% 54% 8% • 7%
1	C	325	31% 53% 8% • 7%
1	E	325	% 32% 53% 8% • 7%
2	B	310	36% 44% 14% • 5%
2	D	310	34% 45% 14% • 5%

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Mol	Chain	Length	Quality of chain
2	F	310	36% 44% 14% • 5%

2 Entry composition (i)

There are 2 unique types of molecules in this entry. The entry contains 14256 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the ZeroOcc column contains the number of atoms modelled with zero occupancy, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a protein called Coatomer subunit alpha.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
			Total	C	N	O	S	Se			
1	A	303	2388	1531	399	447	4	7	0	0	0
1	C	303	2388	1531	399	447	4	7	0	0	0
1	E	303	2388	1531	399	447	4	7	0	0	0

There are 69 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-22	MSE	-	expression tag	UNP P53622
A	-21	GLY	-	expression tag	UNP P53622
A	-20	SER	-	expression tag	UNP P53622
A	-19	SER	-	expression tag	UNP P53622
A	-18	HIS	-	expression tag	UNP P53622
A	-17	HIS	-	expression tag	UNP P53622
A	-16	HIS	-	expression tag	UNP P53622
A	-15	HIS	-	expression tag	UNP P53622
A	-14	HIS	-	expression tag	UNP P53622
A	-13	HIS	-	expression tag	UNP P53622
A	-12	SER	-	expression tag	UNP P53622
A	-11	SER	-	expression tag	UNP P53622
A	-10	GLY	-	expression tag	UNP P53622
A	-9	LEU	-	expression tag	UNP P53622
A	-8	GLU	-	expression tag	UNP P53622
A	-7	VAL	-	expression tag	UNP P53622
A	-6	LEU	-	expression tag	UNP P53622
A	-5	PHE	-	expression tag	UNP P53622
A	-4	GLN	-	expression tag	UNP P53622
A	-3	GLY	-	expression tag	UNP P53622
A	-2	PRO	-	expression tag	UNP P53622
A	-1	HIS	-	expression tag	UNP P53622
A	0	MSE	-	expression tag	UNP P53622

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Chain	Residue	Modelled	Actual	Comment	Reference
C	-22	MSE	-	expression tag	UNP P53622
C	-21	GLY	-	expression tag	UNP P53622
C	-20	SER	-	expression tag	UNP P53622
C	-19	SER	-	expression tag	UNP P53622
C	-18	HIS	-	expression tag	UNP P53622
C	-17	HIS	-	expression tag	UNP P53622
C	-16	HIS	-	expression tag	UNP P53622
C	-15	HIS	-	expression tag	UNP P53622
C	-14	HIS	-	expression tag	UNP P53622
C	-13	HIS	-	expression tag	UNP P53622
C	-12	SER	-	expression tag	UNP P53622
C	-11	SER	-	expression tag	UNP P53622
C	-10	GLY	-	expression tag	UNP P53622
C	-9	LEU	-	expression tag	UNP P53622
C	-8	GLU	-	expression tag	UNP P53622
C	-7	VAL	-	expression tag	UNP P53622
C	-6	LEU	-	expression tag	UNP P53622
C	-5	PHE	-	expression tag	UNP P53622
C	-4	GLN	-	expression tag	UNP P53622
C	-3	GLY	-	expression tag	UNP P53622
C	-2	PRO	-	expression tag	UNP P53622
C	-1	HIS	-	expression tag	UNP P53622
C	0	MSE	-	expression tag	UNP P53622
E	-22	MSE	-	expression tag	UNP P53622
E	-21	GLY	-	expression tag	UNP P53622
E	-20	SER	-	expression tag	UNP P53622
E	-19	SER	-	expression tag	UNP P53622
E	-18	HIS	-	expression tag	UNP P53622
E	-17	HIS	-	expression tag	UNP P53622
E	-16	HIS	-	expression tag	UNP P53622
E	-15	HIS	-	expression tag	UNP P53622
E	-14	HIS	-	expression tag	UNP P53622
E	-13	HIS	-	expression tag	UNP P53622
E	-12	SER	-	expression tag	UNP P53622
E	-11	SER	-	expression tag	UNP P53622
E	-10	GLY	-	expression tag	UNP P53622
E	-9	LEU	-	expression tag	UNP P53622
E	-8	GLU	-	expression tag	UNP P53622
E	-7	VAL	-	expression tag	UNP P53622
E	-6	LEU	-	expression tag	UNP P53622
E	-5	PHE	-	expression tag	UNP P53622
E	-4	GLN	-	expression tag	UNP P53622

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Chain	Residue	Modelled	Actual	Comment	Reference
E	-3	GLY	-	expression tag	UNP P53622
E	-2	PRO	-	expression tag	UNP P53622
E	-1	HIS	-	expression tag	UNP P53622
E	0	MSE	-	expression tag	UNP P53622

- Molecule 2 is a protein called Coatomer subunit epsilon.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
			Total	C	N	O	S	Se			
2	B	293	2364	1508	371	480	2	3	0	0	0
			Total	C	N	O	S	Se			
2	D	293	2364	1508	371	480	2	3	0	0	0
			Total	C	N	O	S	Se			
2	F	293	2364	1508	371	480	2	3	0	0	0

There are 42 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	-13	MSE	-	expression tag	UNP P40509
B	-12	GLY	-	expression tag	UNP P40509
B	-11	SER	-	expression tag	UNP P40509
B	-10	SER	-	expression tag	UNP P40509
B	-9	HIS	-	expression tag	UNP P40509
B	-8	HIS	-	expression tag	UNP P40509
B	-7	HIS	-	expression tag	UNP P40509
B	-6	HIS	-	expression tag	UNP P40509
B	-5	HIS	-	expression tag	UNP P40509
B	-4	HIS	-	expression tag	UNP P40509
B	-3	SER	-	expression tag	UNP P40509
B	-2	GLN	-	expression tag	UNP P40509
B	-1	ASP	-	expression tag	UNP P40509
B	0	PRO	-	expression tag	UNP P40509
D	-13	MSE	-	expression tag	UNP P40509
D	-12	GLY	-	expression tag	UNP P40509
D	-11	SER	-	expression tag	UNP P40509
D	-10	SER	-	expression tag	UNP P40509
D	-9	HIS	-	expression tag	UNP P40509
D	-8	HIS	-	expression tag	UNP P40509
D	-7	HIS	-	expression tag	UNP P40509
D	-6	HIS	-	expression tag	UNP P40509
D	-5	HIS	-	expression tag	UNP P40509
D	-4	HIS	-	expression tag	UNP P40509

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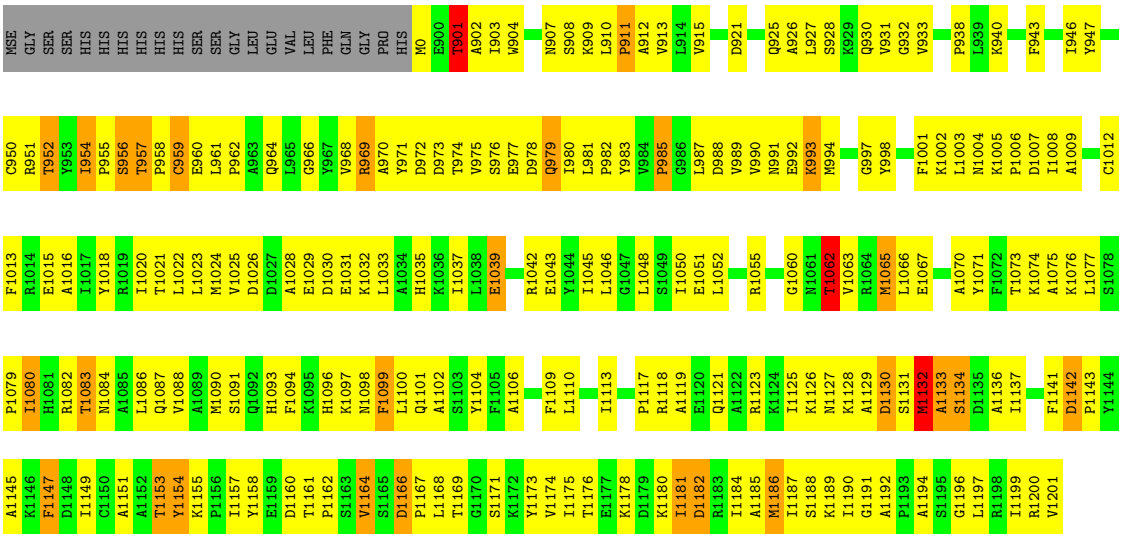
Chain	Residue	Modelled	Actual	Comment	Reference
D	-3	SER	-	expression tag	UNP P40509
D	-2	GLN	-	expression tag	UNP P40509
D	-1	ASP	-	expression tag	UNP P40509
D	0	PRO	-	expression tag	UNP P40509
F	-13	MSE	-	expression tag	UNP P40509
F	-12	GLY	-	expression tag	UNP P40509
F	-11	SER	-	expression tag	UNP P40509
F	-10	SER	-	expression tag	UNP P40509
F	-9	HIS	-	expression tag	UNP P40509
F	-8	HIS	-	expression tag	UNP P40509
F	-7	HIS	-	expression tag	UNP P40509
F	-6	HIS	-	expression tag	UNP P40509
F	-5	HIS	-	expression tag	UNP P40509
F	-4	HIS	-	expression tag	UNP P40509
F	-3	SER	-	expression tag	UNP P40509
F	-2	GLN	-	expression tag	UNP P40509
F	-1	ASP	-	expression tag	UNP P40509
F	0	PRO	-	expression tag	UNP P40509

3 Residue-property plots (i)

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red dot above a residue indicates a poor fit to the electron density (RSRZ > 2). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

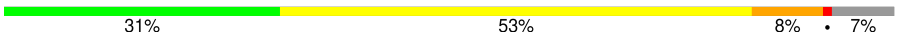
• Molecule 1: Coatomer subunit alpha

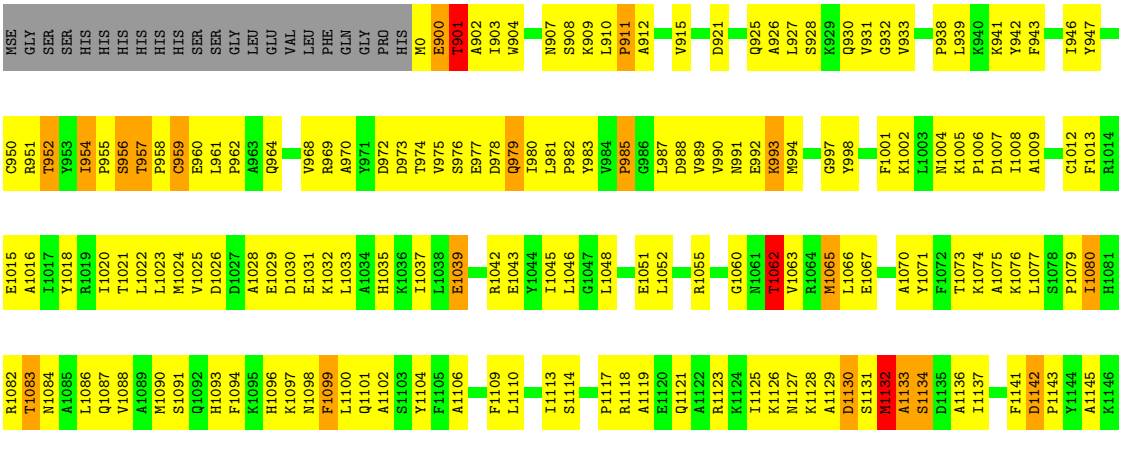
Chain A:



• Molecule 1: Coatomer subunit alpha

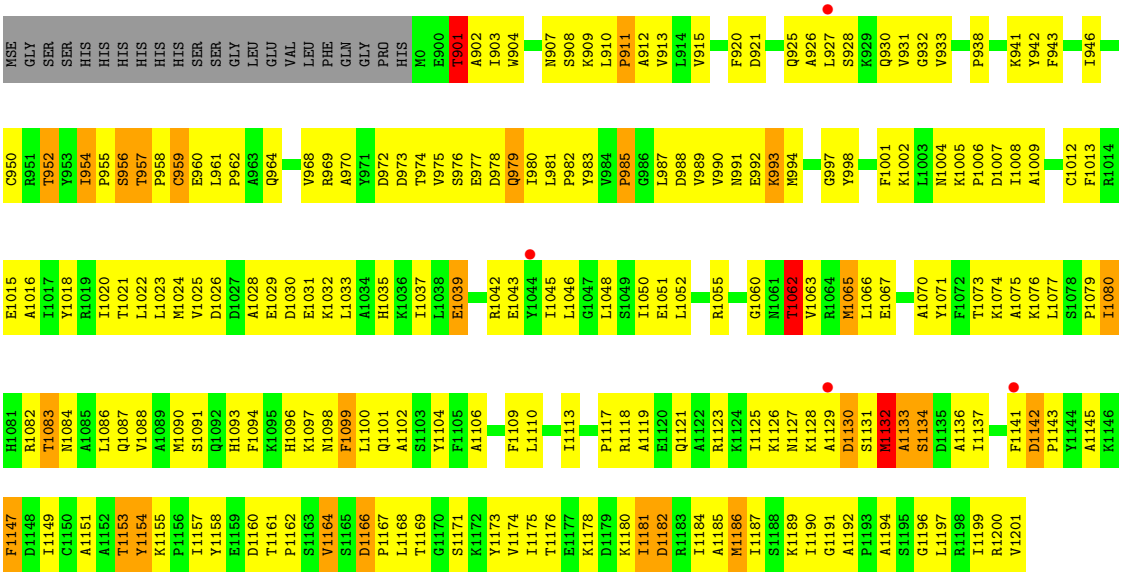
Chain C:





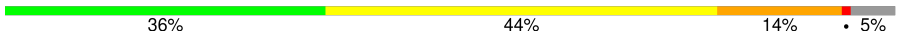
• Molecule 1: Coatomer subunit alpha

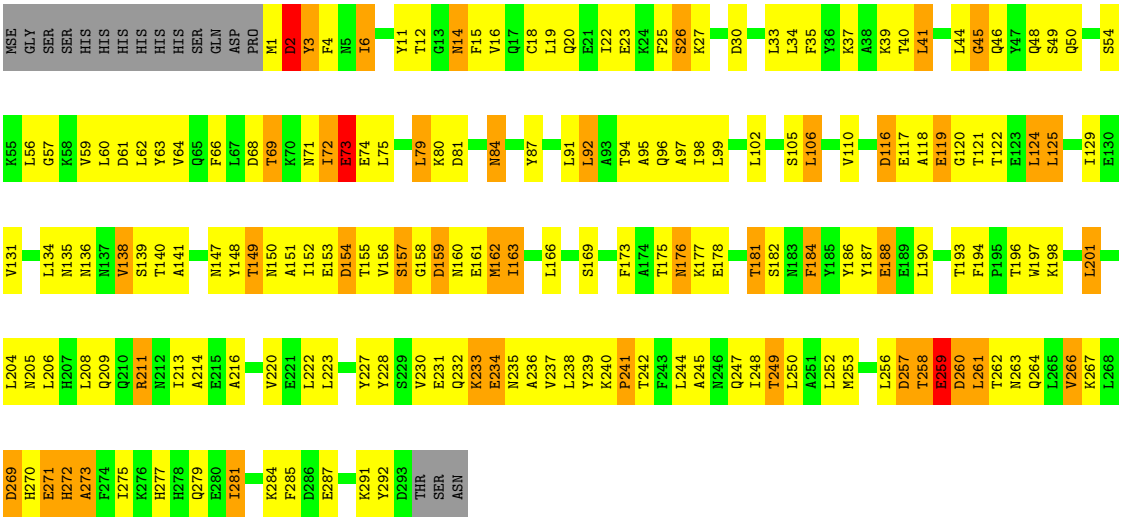
Chain E:



• Molecule 2: Coatomer subunit epsilon

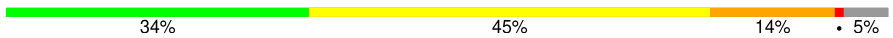
Chain B:

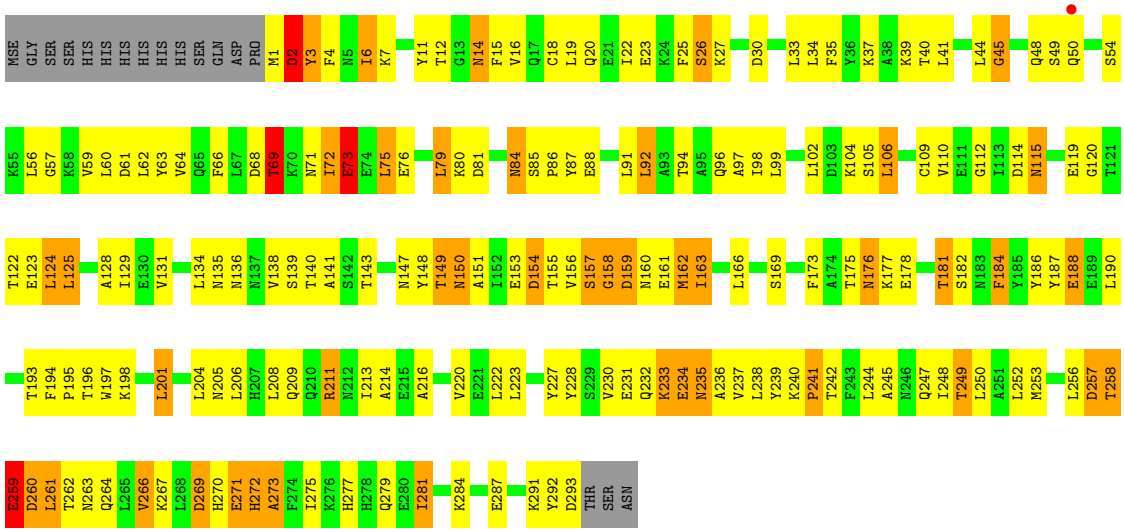




• Molecule 2: Coatomer subunit epsilon

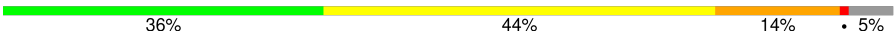
Chain D:

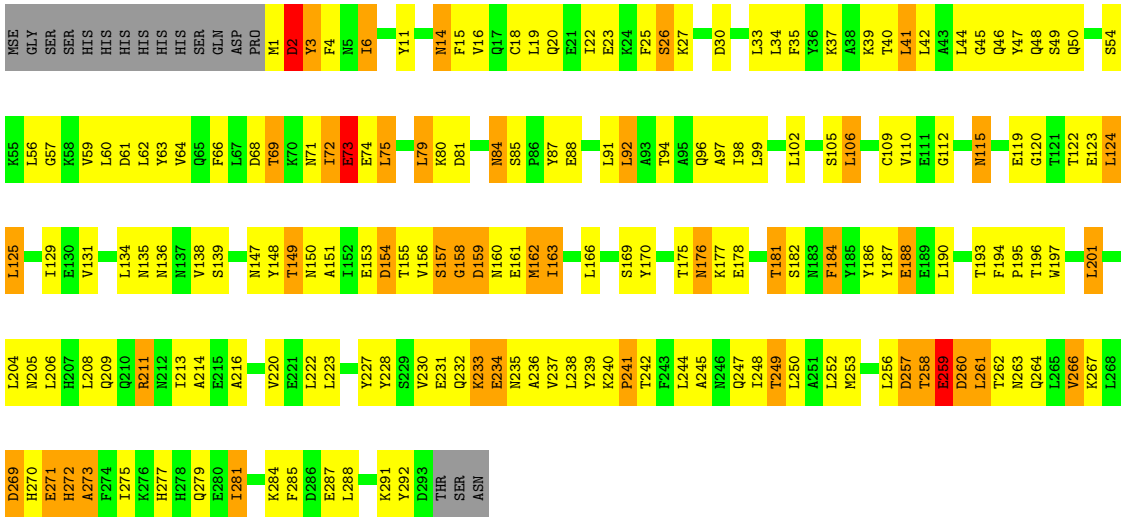




- Molecule 2: Coatomer subunit epsilon

Chain F:





4 Data and refinement statistics (i)

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α, β, γ	328.13Å 74.31Å 96.40Å 90.00° 101.98° 90.00°	Depositor
Resolution (Å)	50.00 – 3.25 50.00 – 3.25	Depositor EDS
% Data completeness (in resolution range)	89.7 (50.00-3.25) 91.0 (50.00-3.25)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.10	Depositor
$< I/\sigma(I) >$ [1]	1.88 (at 3.25Å)	Xtriage
Refinement program	CNS	Depositor
R, R_{free}	0.241 , 0.287 0.244 , 0.281	Depositor DCC
R_{free} test set	1758 reflections (4.86%)	wwPDB-VP
Wilson B-factor (Å^2)	85.9	Xtriage
Anisotropy	0.537	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.33 , 131.9	EDS
L-test for twinning[2]	$< \|L\| > = 0.48$, $< L^2 > = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.92	EDS
Total number of atoms	14256	wwPDB-VP
Average B, all atoms (Å^2)	129.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.05% of the height of the origin peak. No significant pseudotranslation is detected.*

[1]Intensities estimated from amplitudes.

[2]Theoretical values of $< |L| >$, $< L^2 >$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality (i)

5.1 Standard geometry (i)

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	0.50	0/2429	0.79	1/3273 (0.0%)
1	C	0.49	0/2429	0.79	1/3273 (0.0%)
1	E	0.47	0/2429	0.78	1/3273 (0.0%)
2	B	0.51	0/2401	0.76	1/3255 (0.0%)
2	D	0.51	0/2401	0.76	1/3255 (0.0%)
2	F	0.49	0/2401	0.75	1/3255 (0.0%)
All	All	0.49	0/14490	0.77	6/19584 (0.0%)

There are no bond length outliers.

The worst 5 of 6 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	C	1155	LYS	N-CA-C	-5.69	95.63	111.00
1	A	1155	LYS	N-CA-C	-5.69	95.65	111.00
1	E	1155	LYS	N-CA-C	-5.68	95.67	111.00
2	F	125	LEU	CA-CB-CG	-5.21	103.31	115.30
2	B	125	LEU	CA-CB-CG	-5.18	103.37	115.30

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts (i)

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	2388	0	2441	281	0
1	C	2388	0	2441	246	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	E	2388	0	2441	249	0
2	B	2364	0	2319	214	0
2	D	2364	0	2319	239	0
2	F	2364	0	2319	215	0
All	All	14256	0	14280	1363	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 48.

The worst 5 of 1363 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:1090:MSE:HE2	1:C:1106:ALA:HA	1.30	1.12
1:E:1090:MSE:HE2	1:E:1106:ALA:HA	1.29	1.12
2:B:211:ARG:HH11	2:B:211:ARG:HB2	1.11	1.10
1:C:1028:ALA:HB2	1:C:1200:ARG:CZ	1.80	1.10
1:A:1090:MSE:HE2	1:A:1106:ALA:HA	1.30	1.08

There are no symmetry-related clashes.

5.3 Torsion angles (i)

5.3.1 Protein backbone (i)

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
1	A	301/325 (93%)	233 (77%)	53 (18%)	15 (5%)	1 10
1	C	301/325 (93%)	232 (77%)	53 (18%)	16 (5%)	1 9
1	E	301/325 (93%)	233 (77%)	53 (18%)	15 (5%)	1 10
2	B	291/310 (94%)	211 (72%)	59 (20%)	21 (7%)	1 6
2	D	291/310 (94%)	215 (74%)	56 (19%)	20 (7%)	1 6
2	F	291/310 (94%)	212 (73%)	61 (21%)	18 (6%)	1 7

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
All	All	1776/1905 (93%)	1336 (75%)	335 (19%)	105 (6%)	1 8

5 of 105 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	957	THR
1	A	973	ASP
1	A	977	GLU
1	A	979	GLN
1	A	985	PRO

5.3.2 Protein sidechains (i)

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
1	A	257/268 (96%)	226 (88%)	31 (12%)	4 16
1	C	257/268 (96%)	226 (88%)	31 (12%)	4 16
1	E	257/268 (96%)	226 (88%)	31 (12%)	4 16
2	B	263/275 (96%)	221 (84%)	42 (16%)	2 8
2	D	263/275 (96%)	218 (83%)	45 (17%)	1 7
2	F	263/275 (96%)	220 (84%)	43 (16%)	2 8
All	All	1560/1629 (96%)	1337 (86%)	223 (14%)	2 12

5 of 223 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	D	73	GLU
2	F	272	HIS
2	D	260	ASP
2	F	266	VAL
2	F	124	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (5) such sidechains are listed below:

Mol	Chain	Res	Type
2	B	50	GLN
1	C	1093	HIS
1	C	1101	GLN
2	D	50	GLN
2	F	50	GLN

5.3.3 RNA (i)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates (i)

There are no oligosaccharides in this entry.

5.6 Ligand geometry (i)

There are no ligands in this entry.

5.7 Other polymers (i)

There are no such residues in this entry.

5.8 Polymer linkage issues (i)

There are no chain breaks in this entry.

6 Fit of model and data (i)

6.1 Protein, DNA and RNA chains (i)

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	296/325 (91%)	-0.40	0	100	100	47, 89, 147, 193	0
1	C	296/325 (91%)	-0.40	0	100	100	56, 111, 179, 201	0
1	E	296/325 (91%)	-0.04	4 (1%)	73	60	113, 171, 201, 201	0
2	B	290/310 (93%)	-0.42	0	100	100	44, 96, 169, 188	0
2	D	290/310 (93%)	-0.32	1 (0%)	90	85	59, 110, 173, 201	0
2	F	290/310 (93%)	-0.10	0	100	100	92, 177, 201, 201	0
All	All	1758/1905 (92%)	-0.28	5 (0%)	90	85	44, 127, 196, 201	0

All (5) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	E	1141	PHE	3.0
1	E	1129	ALA	2.5
1	E	1044	TYR	2.2
2	D	50	GLN	2.2
1	E	927	LEU	2.0

6.2 Non-standard residues in protein, DNA, RNA chains (i)

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

6.3 Carbohydrates (i)

There are no monosaccharides in this entry.

6.4 Ligands (i)

There are no ligands in this entry.

6.5 Other polymers (i)

There are no such residues in this entry.