Full wwPDB X-ray Structure Validation Report ⓘ

Aug 22, 2020 – 04:11 PM BST

PDB ID	:	4BIU
Title	:	Crystal structure of CpxAHDC (orthorhombic form 1)
Authors	:	Mechaly, A.E.; Sassoon, N.; Betton, J.M.; Alzari, P.M.
Deposited on	:	2013-04-13
Resolution	:	3.65 Å(reported)

This is a Full wwPDB X-ray Structure Validation 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 ⓘ symbol.

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

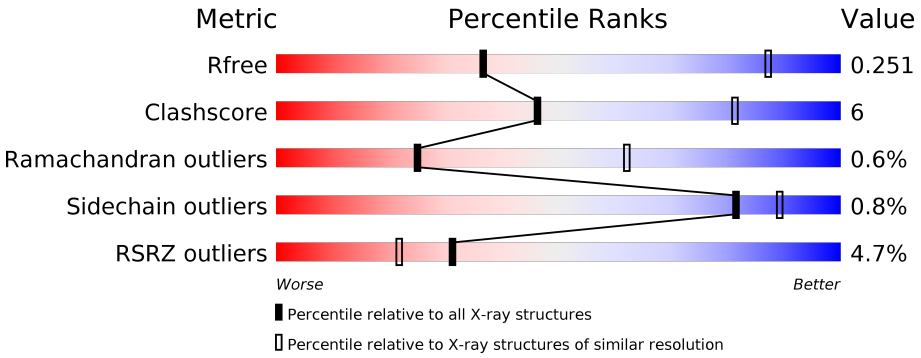
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.13.1
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.13.1

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 3.65 Å.

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



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	130704	1557 (3.82-3.50)
Clashscore	141614	1037 (3.80-3.52)
Ramachandran outliers	138981	1004 (3.80-3.52)
Sidechain outliers	138945	1002 (3.80-3.52)
RSRZ outliers	127900	1441 (3.82-3.50)

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 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	298	4% 72% 12% • 15%
1	B	298	6% 68% 15% 16%
1	C	298	2% 70% 15% • 14%
1	D	298	3% 76% 13% 10%
1	E	298	5% 69% 10% 20%
1	F	298	5% 69% 14% 16%

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
2	ADP	C	501	-	-	-	X

2 Entry composition (i)

There are 3 unique types of molecules in this entry. The entry contains 11993 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 SENSOR PROTEIN CPXA.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	252	Total	C	N	O	S	0	0	0
			1988	1244	359	379	6			
1	B	249	Total	C	N	O	S	0	0	0
			1962	1230	353	373	6			
1	C	256	Total	C	N	O	S	0	0	0
			2015	1262	364	383	6			
1	D	268	Total	C	N	O	S	0	0	0
			2104	1310	382	406	6			
1	E	237	Total	C	N	O	S	0	0	0
			1864	1172	332	354	6			
1	F	250	Total	C	N	O	S	0	0	0
			1964	1226	354	378	6			

There are 168 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	160	MET	-	expression tag	UNP P0AE82
A	161	GLY	-	expression tag	UNP P0AE82
A	162	SER	-	expression tag	UNP P0AE82
A	163	SER	-	expression tag	UNP P0AE82
A	164	HIS	-	expression tag	UNP P0AE82
A	165	HIS	-	expression tag	UNP P0AE82
A	166	HIS	-	expression tag	UNP P0AE82
A	167	HIS	-	expression tag	UNP P0AE82
A	168	HIS	-	expression tag	UNP P0AE82
A	169	HIS	-	expression tag	UNP P0AE82
A	170	SER	-	expression tag	UNP P0AE82
A	171	SER	-	expression tag	UNP P0AE82
A	172	GLY	-	expression tag	UNP P0AE82
A	173	LEU	-	expression tag	UNP P0AE82
A	174	VAL	-	expression tag	UNP P0AE82
A	175	PRO	-	expression tag	UNP P0AE82
A	176	ARG	-	expression tag	UNP P0AE82

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Chain	Residue	Modelled	Actual	Comment	Reference
A	177	GLY	-	expression tag	UNP P0AE82
A	178	SER	-	expression tag	UNP P0AE82
A	179	HIS	-	expression tag	UNP P0AE82
A	180	MET	-	expression tag	UNP P0AE82
A	181	GLU	-	expression tag	UNP P0AE82
A	182	ASN	-	expression tag	UNP P0AE82
A	183	LEU	-	expression tag	UNP P0AE82
A	184	TYR	-	expression tag	UNP P0AE82
A	185	PHE	-	expression tag	UNP P0AE82
A	186	GLN	-	expression tag	UNP P0AE82
A	187	GLY	-	expression tag	UNP P0AE82
B	160	MET	-	expression tag	UNP P0AE82
B	161	GLY	-	expression tag	UNP P0AE82
B	162	SER	-	expression tag	UNP P0AE82
B	163	SER	-	expression tag	UNP P0AE82
B	164	HIS	-	expression tag	UNP P0AE82
B	165	HIS	-	expression tag	UNP P0AE82
B	166	HIS	-	expression tag	UNP P0AE82
B	167	HIS	-	expression tag	UNP P0AE82
B	168	HIS	-	expression tag	UNP P0AE82
B	169	HIS	-	expression tag	UNP P0AE82
B	170	SER	-	expression tag	UNP P0AE82
B	171	SER	-	expression tag	UNP P0AE82
B	172	GLY	-	expression tag	UNP P0AE82
B	173	LEU	-	expression tag	UNP P0AE82
B	174	VAL	-	expression tag	UNP P0AE82
B	175	PRO	-	expression tag	UNP P0AE82
B	176	ARG	-	expression tag	UNP P0AE82
B	177	GLY	-	expression tag	UNP P0AE82
B	178	SER	-	expression tag	UNP P0AE82
B	179	HIS	-	expression tag	UNP P0AE82
B	180	MET	-	expression tag	UNP P0AE82
B	181	GLU	-	expression tag	UNP P0AE82
B	182	ASN	-	expression tag	UNP P0AE82
B	183	LEU	-	expression tag	UNP P0AE82
B	184	TYR	-	expression tag	UNP P0AE82
B	185	PHE	-	expression tag	UNP P0AE82
B	186	GLN	-	expression tag	UNP P0AE82
B	187	GLY	-	expression tag	UNP P0AE82
C	160	MET	-	expression tag	UNP P0AE82
C	161	GLY	-	expression tag	UNP P0AE82
C	162	SER	-	expression tag	UNP P0AE82

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Chain	Residue	Modelled	Actual	Comment	Reference
C	163	SER	-	expression tag	UNP P0AE82
C	164	HIS	-	expression tag	UNP P0AE82
C	165	HIS	-	expression tag	UNP P0AE82
C	166	HIS	-	expression tag	UNP P0AE82
C	167	HIS	-	expression tag	UNP P0AE82
C	168	HIS	-	expression tag	UNP P0AE82
C	169	HIS	-	expression tag	UNP P0AE82
C	170	SER	-	expression tag	UNP P0AE82
C	171	SER	-	expression tag	UNP P0AE82
C	172	GLY	-	expression tag	UNP P0AE82
C	173	LEU	-	expression tag	UNP P0AE82
C	174	VAL	-	expression tag	UNP P0AE82
C	175	PRO	-	expression tag	UNP P0AE82
C	176	ARG	-	expression tag	UNP P0AE82
C	177	GLY	-	expression tag	UNP P0AE82
C	178	SER	-	expression tag	UNP P0AE82
C	179	HIS	-	expression tag	UNP P0AE82
C	180	MET	-	expression tag	UNP P0AE82
C	181	GLU	-	expression tag	UNP P0AE82
C	182	ASN	-	expression tag	UNP P0AE82
C	183	LEU	-	expression tag	UNP P0AE82
C	184	TYR	-	expression tag	UNP P0AE82
C	185	PHE	-	expression tag	UNP P0AE82
C	186	GLN	-	expression tag	UNP P0AE82
C	187	GLY	-	expression tag	UNP P0AE82
D	160	MET	-	expression tag	UNP P0AE82
D	161	GLY	-	expression tag	UNP P0AE82
D	162	SER	-	expression tag	UNP P0AE82
D	163	SER	-	expression tag	UNP P0AE82
D	164	HIS	-	expression tag	UNP P0AE82
D	165	HIS	-	expression tag	UNP P0AE82
D	166	HIS	-	expression tag	UNP P0AE82
D	167	HIS	-	expression tag	UNP P0AE82
D	168	HIS	-	expression tag	UNP P0AE82
D	169	HIS	-	expression tag	UNP P0AE82
D	170	SER	-	expression tag	UNP P0AE82
D	171	SER	-	expression tag	UNP P0AE82
D	172	GLY	-	expression tag	UNP P0AE82
D	173	LEU	-	expression tag	UNP P0AE82
D	174	VAL	-	expression tag	UNP P0AE82
D	175	PRO	-	expression tag	UNP P0AE82
D	176	ARG	-	expression tag	UNP P0AE82

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Chain	Residue	Modelled	Actual	Comment	Reference
D	177	GLY	-	expression tag	UNP P0AE82
D	178	SER	-	expression tag	UNP P0AE82
D	179	HIS	-	expression tag	UNP P0AE82
D	180	MET	-	expression tag	UNP P0AE82
D	181	GLU	-	expression tag	UNP P0AE82
D	182	ASN	-	expression tag	UNP P0AE82
D	183	LEU	-	expression tag	UNP P0AE82
D	184	TYR	-	expression tag	UNP P0AE82
D	185	PHE	-	expression tag	UNP P0AE82
D	186	GLN	-	expression tag	UNP P0AE82
D	187	GLY	-	expression tag	UNP P0AE82
E	160	MET	-	expression tag	UNP P0AE82
E	161	GLY	-	expression tag	UNP P0AE82
E	162	SER	-	expression tag	UNP P0AE82
E	163	SER	-	expression tag	UNP P0AE82
E	164	HIS	-	expression tag	UNP P0AE82
E	165	HIS	-	expression tag	UNP P0AE82
E	166	HIS	-	expression tag	UNP P0AE82
E	167	HIS	-	expression tag	UNP P0AE82
E	168	HIS	-	expression tag	UNP P0AE82
E	169	HIS	-	expression tag	UNP P0AE82
E	170	SER	-	expression tag	UNP P0AE82
E	171	SER	-	expression tag	UNP P0AE82
E	172	GLY	-	expression tag	UNP P0AE82
E	173	LEU	-	expression tag	UNP P0AE82
E	174	VAL	-	expression tag	UNP P0AE82
E	175	PRO	-	expression tag	UNP P0AE82
E	176	ARG	-	expression tag	UNP P0AE82
E	177	GLY	-	expression tag	UNP P0AE82
E	178	SER	-	expression tag	UNP P0AE82
E	179	HIS	-	expression tag	UNP P0AE82
E	180	MET	-	expression tag	UNP P0AE82
E	181	GLU	-	expression tag	UNP P0AE82
E	182	ASN	-	expression tag	UNP P0AE82
E	183	LEU	-	expression tag	UNP P0AE82
E	184	TYR	-	expression tag	UNP P0AE82
E	185	PHE	-	expression tag	UNP P0AE82
E	186	GLN	-	expression tag	UNP P0AE82
E	187	GLY	-	expression tag	UNP P0AE82
F	160	MET	-	expression tag	UNP P0AE82
F	161	GLY	-	expression tag	UNP P0AE82
F	162	SER	-	expression tag	UNP P0AE82

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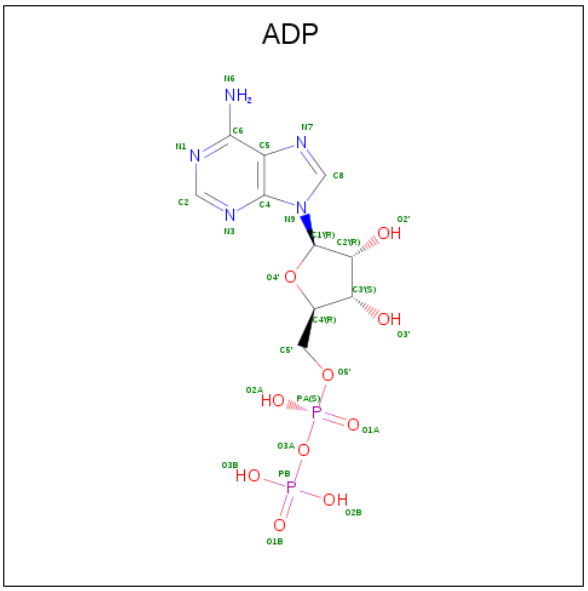
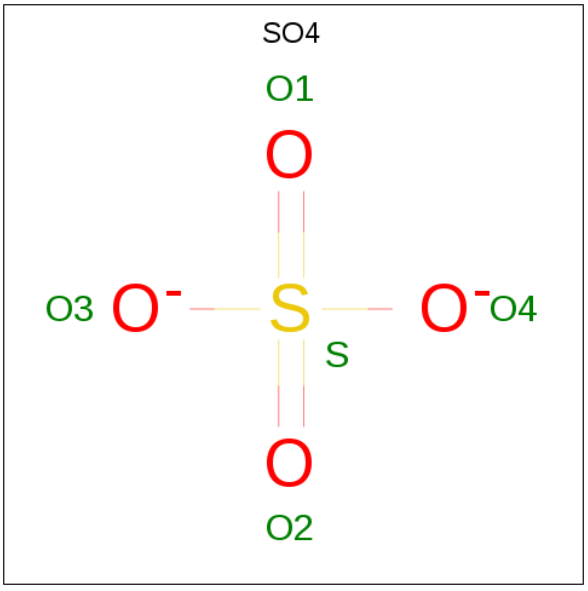
Chain	Residue	Modelled	Actual	Comment	Reference
F	163	SER	-	expression tag	UNP P0AE82
F	164	HIS	-	expression tag	UNP P0AE82
F	165	HIS	-	expression tag	UNP P0AE82
F	166	HIS	-	expression tag	UNP P0AE82
F	167	HIS	-	expression tag	UNP P0AE82
F	168	HIS	-	expression tag	UNP P0AE82
F	169	HIS	-	expression tag	UNP P0AE82
F	170	SER	-	expression tag	UNP P0AE82
F	171	SER	-	expression tag	UNP P0AE82
F	172	GLY	-	expression tag	UNP P0AE82
F	173	LEU	-	expression tag	UNP P0AE82
F	174	VAL	-	expression tag	UNP P0AE82
F	175	PRO	-	expression tag	UNP P0AE82
F	176	ARG	-	expression tag	UNP P0AE82
F	177	GLY	-	expression tag	UNP P0AE82
F	178	SER	-	expression tag	UNP P0AE82
F	179	HIS	-	expression tag	UNP P0AE82
F	180	MET	-	expression tag	UNP P0AE82
F	181	GLU	-	expression tag	UNP P0AE82
F	182	ASN	-	expression tag	UNP P0AE82
F	183	LEU	-	expression tag	UNP P0AE82
F	184	TYR	-	expression tag	UNP P0AE82
F	185	PHE	-	expression tag	UNP P0AE82
F	186	GLN	-	expression tag	UNP P0AE82
F	187	GLY	-	expression tag	UNP P0AE82

- Molecule 2 is ADENOSINE-5'-DIPHOSPHATE (three-letter code: ADP) (formula: $C_{10}H_{15}N_5O_{10}P_2$).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	C	1	Total	C	N	O	P	0	0
			27	10	5	10	2		
2	E	1	Total	C	N	O	P	0	0
			27	10	5	10	2		
2	F	1	Total	C	N	O	P	0	0
			27	10	5	10	2		

- Molecule 3 is SULFATE ION (three-letter code: SO4) (formula: O_4S).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	D	1	Total	O	S	0	0
			5	4	1		

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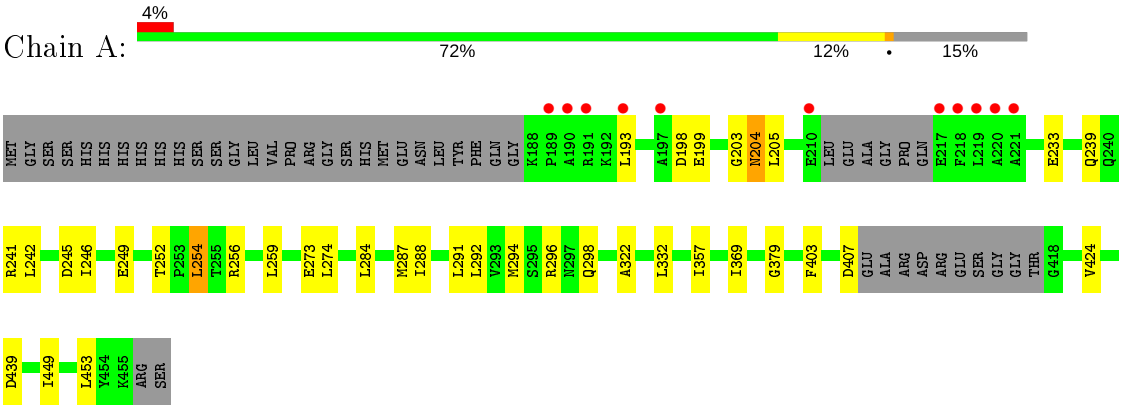
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	D	1	Total O S 5 4 1	0	0
3	F	1	Total O S 5 4 1	0	0

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.

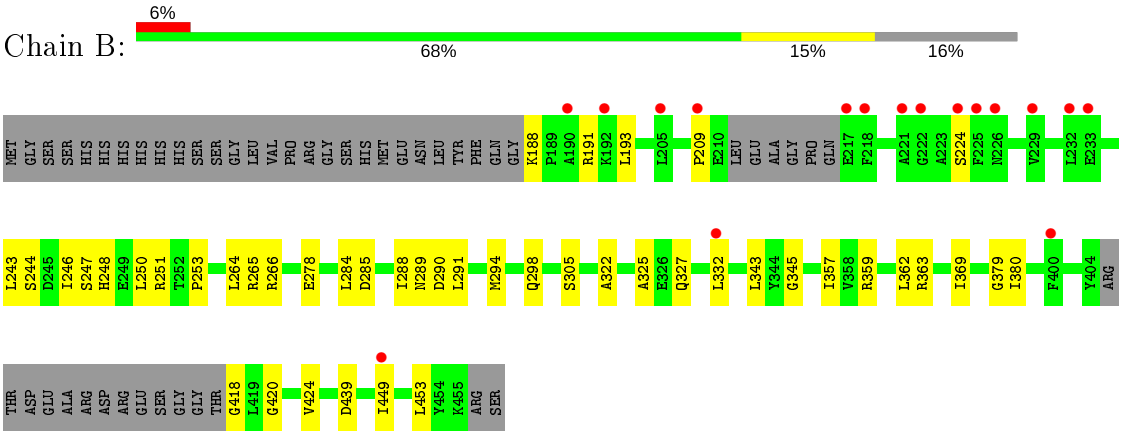
- Molecule 1: SENSOR PROTEIN CPXA

Chain A:



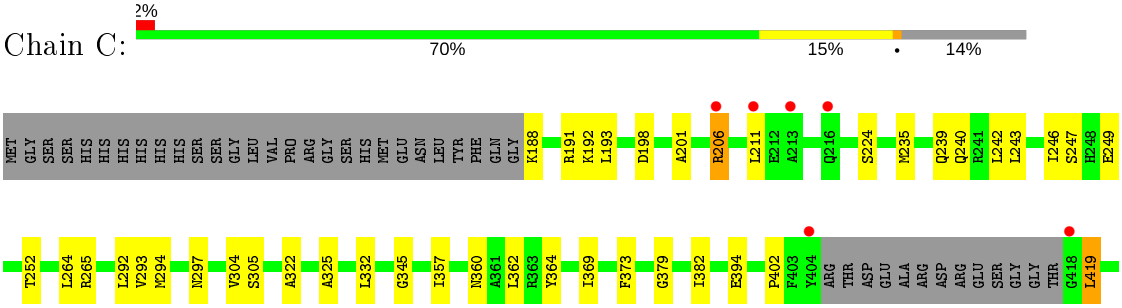
- Molecule 1: SENSOR PROTEIN CPXA

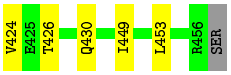
Chain B:



- Molecule 1: SENSOR PROTEIN CPXA

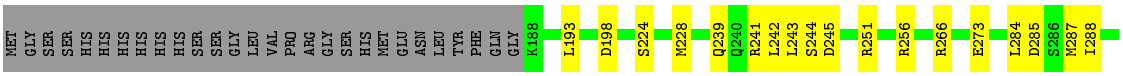
Chain C:

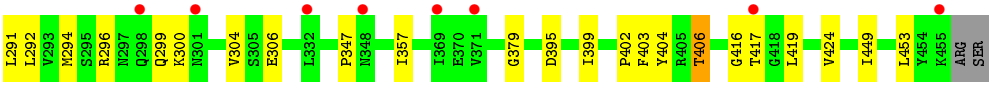




• Molecule 1: SENSOR PROTEIN CPXA

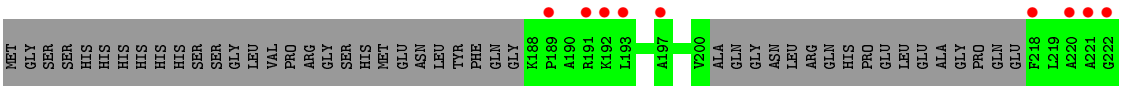
Chain D:

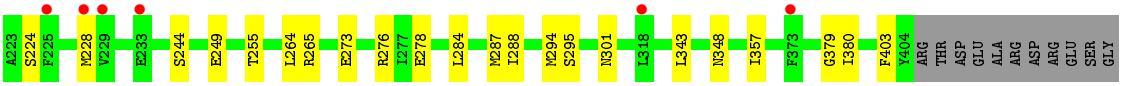


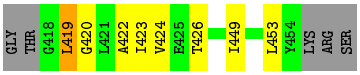


• Molecule 1: SENSOR PROTEIN CPXA

Chain E:

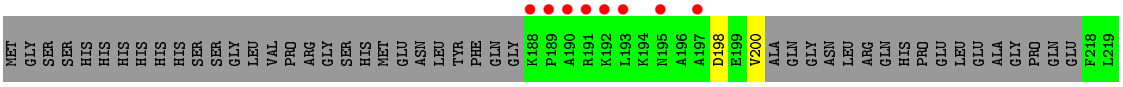


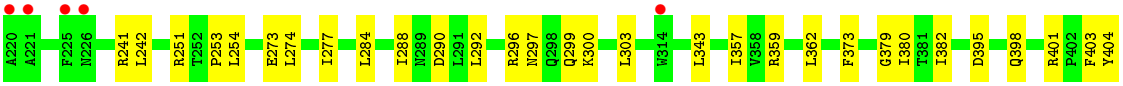


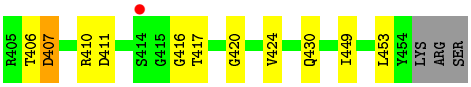


• Molecule 1: SENSOR PROTEIN CPXA

Chain F:







4 Data and refinement statistics (i)

Property	Value	Source
Space group	C 2 2 21	Depositor
Cell constants a, b, c, α, β, γ	143.27Å 191.70Å 205.01Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	47.92 – 3.65 47.92 – 3.65	Depositor EDS
% Data completeness (in resolution range)	100.0 (47.92-3.65) 100.0 (47.92-3.65)	Depositor EDS
R_{merge}	0.10	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	2.06 (at 3.67Å)	Xtriage
Refinement program	BUSTER 2.10.0	Depositor
R, R_{free}	0.211 , 0.227 0.229 , 0.251	Depositor DCC
R_{free} test set	1599 reflections (5.04%)	wwPDB-VP
Wilson B-factor (Å^2)	154.9	Xtriage
Anisotropy	0.280	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.33 , 158.1	EDS
L-test for twinning[2]	$< \|L\| > = 0.44$, $< L^2 > = 0.27$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.94	EDS
Total number of atoms	11993	wwPDB-VP
Average B, all atoms (Å^2)	188.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.51% of the height of the origin peak. No significant pseudotranslation is detected.*

[1] Intensities estimated from amplitudes.

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

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: SO4, ADP

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	0.42	0/2021	0.58	0/2733
1	B	0.41	0/1995	0.58	0/2698
1	C	0.40	0/2050	0.58	0/2774
1	D	0.39	0/2140	0.58	0/2896
1	E	0.38	0/1895	0.54	0/2564
1	F	0.39	0/1995	0.58	0/2697
All	All	0.40	0/12096	0.57	0/16362

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	1988	0	1990	36	0
1	B	1962	0	1966	45	0
1	C	2015	0	2020	36	0
1	D	2104	0	2097	30	0
1	E	1864	0	1873	21	0
1	F	1964	0	1962	32	0
2	C	27	0	12	2	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	E	27	0	12	0	0
2	F	27	0	12	0	0
3	D	10	0	0	0	0
3	F	5	0	0	0	0
All	All	11993	0	11944	151	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 6.

All (151) 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:A:357:ILE:HG13	1:A:449:ILE:HD11	1.68	0.76
1:D:357:ILE:HG13	1:D:449:ILE:HD11	1.67	0.74
1:C:357:ILE:HG13	1:C:449:ILE:HD11	1.70	0.74
1:C:426:THR:HG21	1:D:242:LEU:HB2	1.70	0.73
1:B:247:SER:OG	1:B:291:LEU:HB3	1.87	0.73
1:A:256:ARG:NH1	1:B:359:ARG:HH12	1.89	0.71
1:C:430:GLN:OE1	1:D:239:GLN:NE2	2.25	0.70
1:B:357:ILE:HG13	1:B:449:ILE:HD11	1.72	0.69
1:F:357:ILE:HG13	1:F:449:ILE:HD11	1.76	0.67
1:C:247:SER:HB3	1:C:292:LEU:HD23	1.76	0.67
1:C:294:MET:HA	1:C:419:LEU:HD22	1.76	0.67
1:A:246:ILE:HD13	1:B:291:LEU:HG	1.76	0.67
1:D:294:MET:HE1	1:D:419:LEU:HD22	1.77	0.67
1:E:357:ILE:HG13	1:E:449:ILE:HD11	1.78	0.66
1:A:193:LEU:HD13	1:B:193:LEU:HD13	1.77	0.66
1:A:205:LEU:HD13	1:A:233:GLU:HG3	1.78	0.64
1:B:294:MET:O	1:B:298:GLN:HG3	1.97	0.64
1:C:360:ASN:ND2	2:C:501:ADP:N7	2.40	0.62
1:D:357:ILE:HD11	1:D:424:VAL:HG11	1.81	0.62
1:C:357:ILE:HD11	1:C:424:VAL:HG11	1.82	0.62
1:E:294:MET:HG3	1:E:423:ILE:HD11	1.82	0.62
1:C:243:LEU:HA	1:C:246:ILE:HD12	1.82	0.61
1:B:251:ARG:NH2	1:B:289:ASN:OD1	2.33	0.61
1:F:274:LEU:HD23	1:F:277:ILE:HD11	1.83	0.60
1:B:265:ARG:NH1	1:C:292:LEU:HD22	2.17	0.60
1:E:264:LEU:HG	1:F:273:GLU:HB2	1.85	0.59
1:B:363:ARG:HH22	1:B:418:GLY:N	2.00	0.59
1:F:274:LEU:HA	1:F:277:ILE:HG12	1.85	0.58
1:D:244:SER:HB2	1:D:299:GLN:OE1	2.03	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:357:ILE:HD11	1:A:424:VAL:HG11	1.87	0.57
1:B:357:ILE:HD11	1:B:424:VAL:HG11	1.87	0.57
1:C:242:LEU:HD13	1:D:402:PRO:HB3	1.87	0.57
1:F:357:ILE:HD11	1:F:424:VAL:HG11	1.87	0.56
1:F:241:ARG:HE	1:F:299:GLN:HE21	1.54	0.56
1:B:265:ARG:NH2	1:B:278:GLU:OE1	2.39	0.56
1:A:291:LEU:HD21	1:B:246:ILE:HG21	1.89	0.55
1:A:252:THR:HG22	1:B:359:ARG:HD2	1.87	0.55
1:E:357:ILE:HD11	1:E:424:VAL:HG11	1.88	0.55
1:C:394:GLU:HG3	1:F:401:ARG:HH22	1.72	0.54
1:A:273:GLU:HB2	1:B:264:LEU:HG	1.91	0.53
1:B:251:ARG:NH1	1:B:285:ASP:OD1	2.42	0.53
1:F:379:GLY:HA2	1:F:453:LEU:HG	1.90	0.53
1:C:198:ASP:OD1	1:D:224:SER:HB2	2.10	0.52
1:A:259:LEU:HD21	1:B:327:GLN:HG3	1.90	0.52
1:F:406:THR:HA	1:F:407:ASP:N	2.25	0.52
1:E:287:MET:HG2	1:E:403:PHE:CD1	2.45	0.52
1:D:395:ASP:HB3	1:D:404:TYR:OH	2.10	0.52
1:A:287:MET:CE	1:B:253:PRO:HG3	2.41	0.51
1:A:332:LEU:HD23	1:A:369:ILE:HB	1.93	0.51
1:B:379:GLY:HA2	1:B:453:LEU:HG	1.92	0.51
1:D:399:ILE:HG13	1:D:404:TYR:CE2	2.45	0.51
1:A:287:MET:HG2	1:A:403:PHE:CD1	2.45	0.51
1:A:274:LEU:HG	1:B:264:LEU:HD11	1.93	0.51
1:A:292:LEU:O	1:A:296:ARG:HG3	2.10	0.51
1:E:249:GLU:HG3	1:F:403:PHE:CG	2.46	0.50
1:E:287:MET:CE	1:F:253:PRO:HG3	2.40	0.50
1:D:287:MET:SD	1:D:417:THR:HG21	2.51	0.50
1:E:426:THR:HG21	1:F:242:LEU:HB2	1.92	0.50
1:E:379:GLY:HA2	1:E:453:LEU:HG	1.94	0.50
1:B:322:ALA:HA	1:B:332:LEU:HD12	1.92	0.50
1:D:379:GLY:HA2	1:D:453:LEU:HG	1.94	0.49
1:B:188:LYS:HB3	1:B:191:ARG:HD2	1.95	0.49
1:F:290:ASP:CB	1:F:417:THR:HG21	2.42	0.49
1:C:362:LEU:HD23	1:C:369:ILE:HD13	1.93	0.49
1:B:332:LEU:HD23	1:B:369:ILE:HB	1.95	0.49
1:D:251:ARG:NH1	1:D:285:ASP:OD1	2.44	0.49
1:A:245:ASP:O	1:A:249:GLU:HG2	2.13	0.48
1:B:251:ARG:HG2	1:C:265:ARG:HH22	1.77	0.48
1:E:228:MET:HG3	1:F:200:VAL:HB	1.94	0.48
1:D:404:TYR:CE2	1:D:406:THR:HB	2.49	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:235:MET:O	1:C:239:GLN:HG3	2.13	0.48
1:F:300:LYS:HE2	1:F:303:LEU:HD23	1.96	0.48
1:A:259:LEU:HD21	1:B:327:GLN:CB	2.43	0.48
1:E:301:ASN:OD1	1:E:348:ASN:HB3	2.14	0.48
1:C:322:ALA:HA	1:C:332:LEU:HD12	1.96	0.48
1:B:265:ARG:HH11	1:C:292:LEU:HD22	1.79	0.47
1:B:290:ASP:O	1:B:294:MET:HB2	2.14	0.47
1:C:305:SER:HB2	1:C:345:GLY:HA2	1.97	0.47
1:C:402:PRO:HG2	1:D:245:ASP:HB3	1.97	0.47
1:D:241:ARG:HA	1:D:299:GLN:NE2	2.30	0.47
1:C:379:GLY:HA2	1:C:453:LEU:HG	1.96	0.47
1:A:322:ALA:HA	1:A:332:LEU:HD12	1.96	0.47
1:A:379:GLY:HA2	1:A:453:LEU:HG	1.97	0.46
1:C:264:LEU:HG	1:D:273:GLU:CB	2.45	0.46
1:F:290:ASP:HB2	1:F:417:THR:HG21	1.98	0.46
1:A:259:LEU:HD11	1:B:327:GLN:HB3	1.97	0.46
1:A:199:GLU:HG2	1:A:204:ASN:HB2	1.98	0.46
1:D:306:GLU:OE2	1:D:347:PRO:HG2	2.16	0.46
1:E:419:LEU:HD22	1:E:422:ALA:HB3	1.98	0.45
1:C:188:LYS:HD3	1:C:191:ARG:HG3	1.99	0.45
1:C:224:SER:HB2	1:D:198:ASP:OD1	2.16	0.45
1:C:240:GLN:HE21	1:D:239:GLN:HE22	1.64	0.45
1:E:343:LEU:HD21	1:E:380:ILE:HD12	1.97	0.45
1:E:224:SER:HB2	1:F:198:ASP:OD1	2.17	0.45
1:A:252:THR:HB	1:B:359:ARG:HH11	1.81	0.45
1:C:193:LEU:HD13	1:D:193:LEU:HD13	1.99	0.45
1:A:291:LEU:HD11	1:B:250:LEU:HD11	1.98	0.45
1:B:359:ARG:HA	1:B:362:LEU:HD12	1.99	0.45
1:C:264:LEU:HG	1:D:273:GLU:HB2	1.98	0.45
1:D:256:ARG:HG2	1:E:255:THR:HG21	1.99	0.45
1:A:239:GLN:HG2	1:B:298:GLN:OE1	2.17	0.44
1:A:256:ARG:HH12	1:B:359:ARG:HH12	1.62	0.44
1:E:287:MET:HE3	1:F:253:PRO:HG3	1.98	0.44
1:F:398:GLN:O	1:F:404:TYR:HD2	1.99	0.44
1:B:325:ALA:HB2	1:B:362:LEU:HD21	2.00	0.44
1:F:292:LEU:O	1:F:296:ARG:HG3	2.16	0.44
1:A:252:THR:HB	1:B:359:ARG:NH1	2.32	0.44
1:B:305:SER:HB2	1:B:345:GLY:HA2	1.99	0.44
1:F:292:LEU:HB3	1:F:296:ARG:HE	1.82	0.44
1:B:244:SER:O	1:B:248:HIS:CD2	2.71	0.44
1:F:241:ARG:NE	1:F:299:GLN:HE21	2.15	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:287:MET:HE3	1:B:253:PRO:HG3	1.99	0.43
1:F:284:LEU:O	1:F:288:ILE:HG12	2.18	0.43
1:C:293:VAL:HG12	1:C:419:LEU:HD23	2.01	0.43
1:E:265:ARG:HD2	1:E:278:GLU:OE2	2.18	0.43
1:A:198:ASP:OD1	1:B:224:SER:HB2	2.19	0.43
1:A:242:LEU:HD22	1:B:298:GLN:HE21	1.83	0.43
1:C:249:GLU:HG3	1:D:403:PHE:CD1	2.53	0.43
1:A:284:LEU:O	1:A:288:ILE:HG12	2.19	0.43
1:D:300:LYS:NZ	1:F:411:ASP:OD2	2.51	0.43
1:E:244:SER:HA	1:E:295:SER:HB2	2.00	0.43
1:E:284:LEU:O	1:E:288:ILE:HG12	2.18	0.43
1:F:395:ASP:CG	1:F:406:THR:HG21	2.40	0.43
1:C:192:LYS:HB3	1:C:211:LEU:HD23	2.00	0.42
1:E:273:GLU:HA	1:E:276:ARG:HD2	2.00	0.42
1:F:297:ASN:HB3	1:F:430:GLN:NE2	2.34	0.42
1:F:251:ARG:NH2	1:F:292:LEU:HD13	2.34	0.42
1:F:373:PHE:CE2	1:F:382:ILE:HG12	2.54	0.42
1:C:364:TYR:CZ	2:C:501:ADP:H2'	2.54	0.42
1:A:259:LEU:HD21	1:B:327:GLN:CG	2.49	0.42
1:D:266:ARG:HH11	1:D:266:ARG:HG3	1.85	0.42
1:C:201:ALA:HB2	1:D:228:MET:HA	2.02	0.42
1:A:241:ARG:HG2	1:A:245:ASP:OD2	2.20	0.42
1:B:343:LEU:HD21	1:B:380:ILE:HD12	2.02	0.41
1:A:246:ILE:HG21	1:B:291:LEU:HG	2.02	0.41
1:C:206:ARG:HD2	1:C:304:VAL:HG13	2.03	0.41
1:D:292:LEU:O	1:D:296:ARG:HG3	2.20	0.41
1:C:325:ALA:HB2	1:C:362:LEU:HD21	2.02	0.41
1:A:242:LEU:HD23	1:B:243:LEU:HD13	2.03	0.41
1:B:284:LEU:O	1:B:288:ILE:HG12	2.20	0.41
1:D:243:LEU:HD11	1:D:291:LEU:HD22	2.03	0.41
1:A:254:LEU:HD12	1:A:288:ILE:HG13	2.04	0.40
1:F:359:ARG:HA	1:F:362:LEU:HD12	2.03	0.40
1:F:407:ASP:HA	1:F:410:ARG:HB2	2.03	0.40
1:A:294:MET:O	1:A:298:GLN:NE2	2.44	0.40
1:D:284:LEU:O	1:D:288:ILE:HG12	2.21	0.40
1:E:264:LEU:HD11	1:F:274:LEU:HG	2.02	0.40
1:C:297:ASN:OD1	1:C:419:LEU:HD21	2.22	0.40
1:B:266:ARG:HD2	1:C:252:THR:HG21	2.03	0.40
1:C:373:PHE:CE2	1:C:382:ILE:HG12	2.57	0.40
1:F:343:LEU:HD21	1:F:380:ILE:HD12	2.03	0.40

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	246/298 (83%)	237 (96%)	8 (3%)	1 (0%)	34	69
1	B	243/298 (82%)	234 (96%)	7 (3%)	2 (1%)	19	56
1	C	252/298 (85%)	249 (99%)	2 (1%)	1 (0%)	34	69
1	D	266/298 (89%)	254 (96%)	10 (4%)	2 (1%)	19	56
1	E	231/298 (78%)	225 (97%)	5 (2%)	1 (0%)	34	69
1	F	244/298 (82%)	234 (96%)	8 (3%)	2 (1%)	19	56
All	All	1482/1788 (83%)	1433 (97%)	40 (3%)	9 (1%)	25	62

All (9) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	E	420	GLY
1	F	420	GLY
1	D	304	VAL
1	F	416	GLY
1	A	203	GLY
1	B	209	PRO
1	C	206	ARG
1	B	420	GLY
1	D	416	GLY

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	214/251 (85%)	210 (98%)	4 (2%)	57 76
1	B	211/251 (84%)	210 (100%)	1 (0%)	88 94
1	C	216/251 (86%)	215 (100%)	1 (0%)	88 94
1	D	225/251 (90%)	224 (100%)	1 (0%)	91 95
1	E	201/251 (80%)	200 (100%)	1 (0%)	88 94
1	F	211/251 (84%)	209 (99%)	2 (1%)	78 88
All	All	1278/1506 (85%)	1268 (99%)	10 (1%)	81 89

All (10) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	204	ASN
1	A	254	LEU
1	A	407	ASP
1	A	439	ASP
1	B	439	ASP
1	C	419	LEU
1	D	406	THR
1	E	419	LEU
1	F	254	LEU
1	F	407	ASP

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (4) such sidechains are listed below:

Mol	Chain	Res	Type
1	D	239	GLN
1	E	239	GLN
1	F	298	GLN
1	F	299	GLN

5.3.3 RNA (i)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates (i)

There are no monosaccharides in this entry.

5.6 Ligand geometry (i)

6 ligands are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. 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 $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\| > 2$	Counts	RMSZ	$\#\|Z\| > 2$
2	ADP	F	501	-	24,29,29	0.90	1 (4%)	29,45,45	1.10	1 (3%)
3	SO4	D	1456	-	4,4,4	0.17	0	6,6,6	0.22	0
3	SO4	F	1455	-	4,4,4	0.11	0	6,6,6	0.24	0
2	ADP	C	501	-	24,29,29	0.84	0	29,45,45	1.10	3 (10%)
2	ADP	E	501	-	24,29,29	0.85	1 (4%)	29,45,45	1.08	1 (3%)
3	SO4	D	1457	-	4,4,4	0.18	0	6,6,6	0.13	0

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	ADP	C	501	-	-	1/12/32/32	0/3/3/3
2	ADP	F	501	-	-	2/12/32/32	0/3/3/3
2	ADP	E	501	-	-	3/12/32/32	0/3/3/3

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	F	501	ADP	C8-N7	-2.44	1.30	1.34
2	E	501	ADP	C8-N7	-2.16	1.30	1.34

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	F	501	ADP	C5-C6-N6	3.92	126.31	120.35
2	E	501	ADP	C5-C6-N6	3.63	125.88	120.35
2	C	501	ADP	C5-C6-N6	3.47	125.62	120.35
2	C	501	ADP	C4-C5-N7	2.26	111.76	109.40
2	C	501	ADP	C3'-C2'-C1'	2.05	104.06	100.98

There are no chirality outliers.

All (6) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	E	501	ADP	C3'-C4'-C5'-O5'
2	F	501	ADP	O4'-C4'-C5'-O5'
2	F	501	ADP	C3'-C4'-C5'-O5'
2	E	501	ADP	O4'-C4'-C5'-O5'
2	E	501	ADP	PB-O3A-PA-O1A
2	C	501	ADP	PA-O3A-PB-O2B

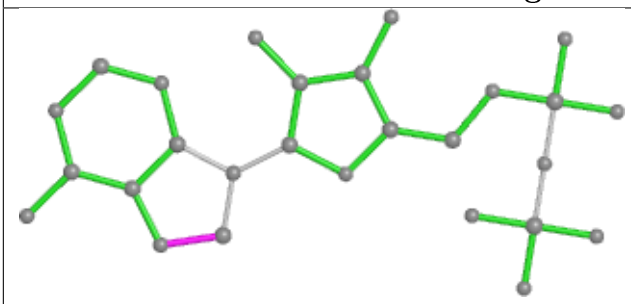
There are no ring outliers.

1 monomer is involved in 2 short contacts:

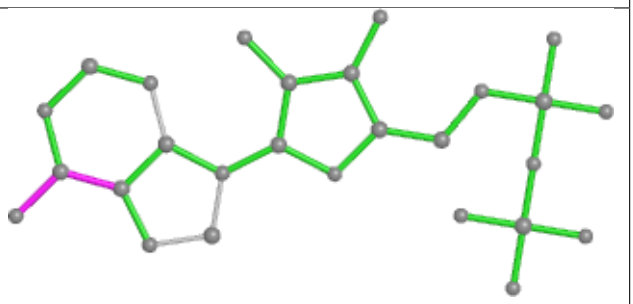
Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	C	501	ADP	2	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less then 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.

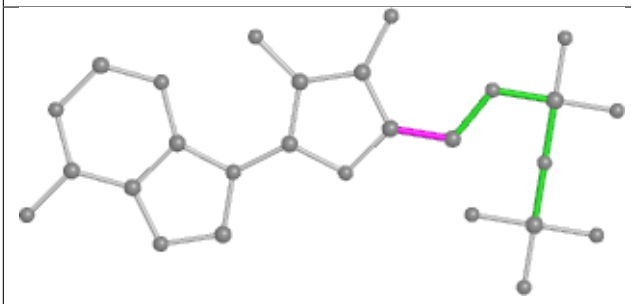
Ligand ADP F 501



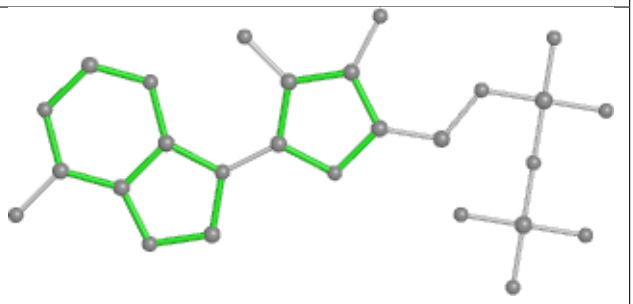
Bond lengths



Bond angles

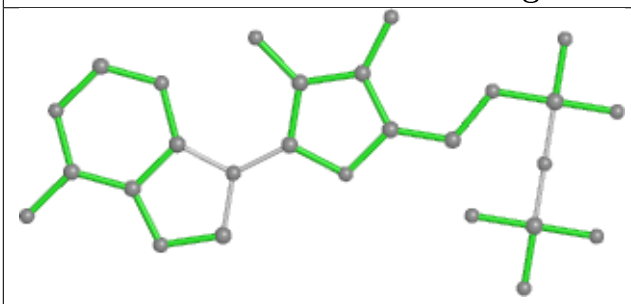


Torsions

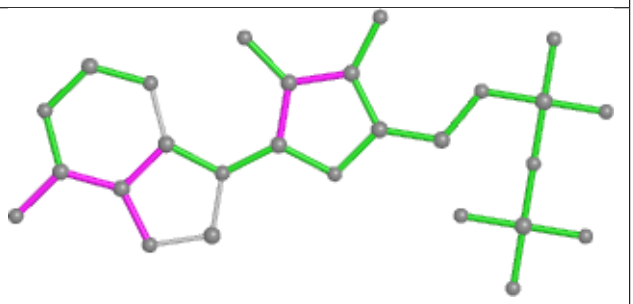


Rings

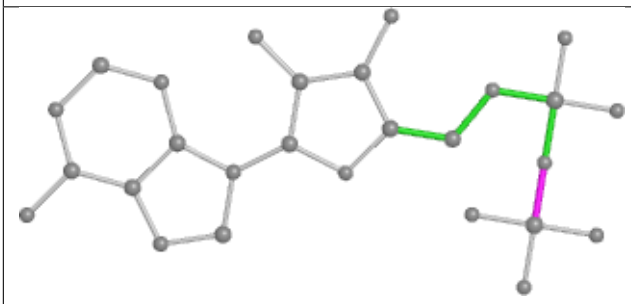
Ligand ADP C 501



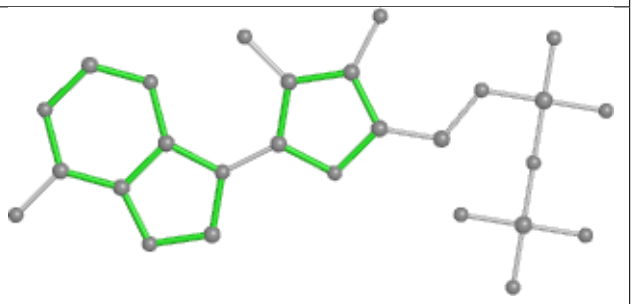
Bond lengths



Bond angles

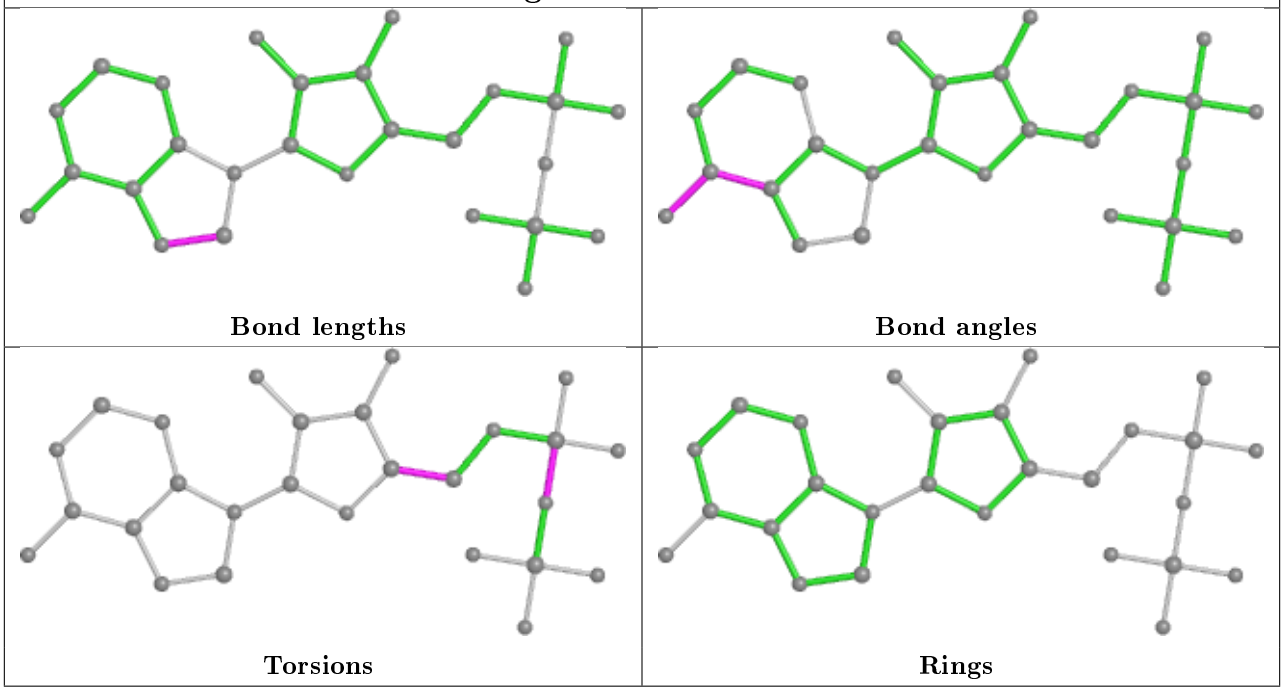


Torsions



Rings

Ligand ADP E 501



5.7 Other polymers

There are no such residues in this entry.

5.8 Polymer linkage issues

The following chains have linkage breaks:

Mol	Chain	Number of breaks
1	F	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	F	406:THR	C	407:ASP	N	3.32

6 Fit of model and data

6.1 Protein, DNA and RNA chains

In the following table, the column labelled '#RSRZ> 2' contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95^{th} percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled 'Q< 0.9' lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2			OWAB(Å^2)	Q<0.9
1	A	252/298 (84%)	0.27	11 (4%)	34	23	123, 185, 269, 299	0
1	B	249/298 (83%)	0.35	17 (6%)	17	11	112, 166, 258, 295	0
1	C	256/298 (85%)	0.23	6 (2%)	60	46	113, 151, 210, 280	0
1	D	268/298 (89%)	0.28	8 (2%)	50	36	116, 183, 271, 300	0
1	E	237/298 (79%)	0.39	15 (6%)	20	12	123, 204, 298, 300	0
1	F	250/298 (83%)	0.46	14 (5%)	24	16	124, 190, 282, 299	0
All	All	1512/1788 (84%)	0.33	71 (4%)	31	22	112, 181, 274, 300	0

All (71) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	F	188	LYS	6.6
1	E	193	LEU	6.2
1	F	189	PRO	6.1
1	B	222	GLY	5.9
1	F	191	ARG	5.7
1	A	193	LEU	5.0
1	F	193	LEU	4.6
1	F	225	PHE	4.5
1	F	197	ALA	4.2
1	C	206	ARG	4.1
1	C	404	TYR	4.1
1	F	414	SER	4.0
1	B	229	VAL	4.0
1	A	218	PHE	3.9
1	F	190	ALA	3.9
1	B	221	ALA	3.9
1	A	189	PRO	3.8
1	A	197	ALA	3.8
1	C	418	GLY	3.7

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Mol	Chain	Res	Type	RSRZ
1	A	190	ALA	3.5
1	F	221	ALA	3.4
1	E	222	GLY	3.3
1	C	216	GLN	3.3
1	A	221	ALA	3.3
1	E	225	PHE	3.3
1	E	228	MET	3.1
1	E	221	ALA	3.1
1	F	195	ASN	3.0
1	A	220	ALA	3.0
1	E	233	GLU	3.0
1	B	232	LEU	3.0
1	F	192	LYS	2.9
1	D	369	ILE	2.8
1	E	191	ARG	2.8
1	B	225	PHE	2.8
1	F	314	TRP	2.7
1	F	226	ASN	2.6
1	A	191	ARG	2.6
1	D	298	GLN	2.6
1	D	417	THR	2.6
1	E	220	ALA	2.6
1	D	348	ASN	2.6
1	E	189	PRO	2.6
1	B	190	ALA	2.6
1	E	229	VAL	2.5
1	B	217	GLU	2.5
1	B	192	LYS	2.4
1	A	217	GLU	2.4
1	B	209	PRO	2.4
1	B	218	PHE	2.3
1	E	373	PHE	2.3
1	B	224	SER	2.3
1	C	213	ALA	2.3
1	B	205	LEU	2.2
1	C	211	LEU	2.2
1	E	318	LEU	2.2
1	B	400	PHE	2.2
1	B	226	ASN	2.2
1	D	455	LYS	2.2
1	E	192	LYS	2.2
1	A	219	LEU	2.2

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Mol	Chain	Res	Type	RSRZ
1	B	449	ILE	2.2
1	E	218	PHE	2.2
1	D	371	VAL	2.1
1	F	220	ALA	2.1
1	E	197	ALA	2.1
1	D	332	LEU	2.0
1	A	210	GLU	2.0
1	D	301	ASN	2.0
1	B	332	LEU	2.0
1	B	233	GLU	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)

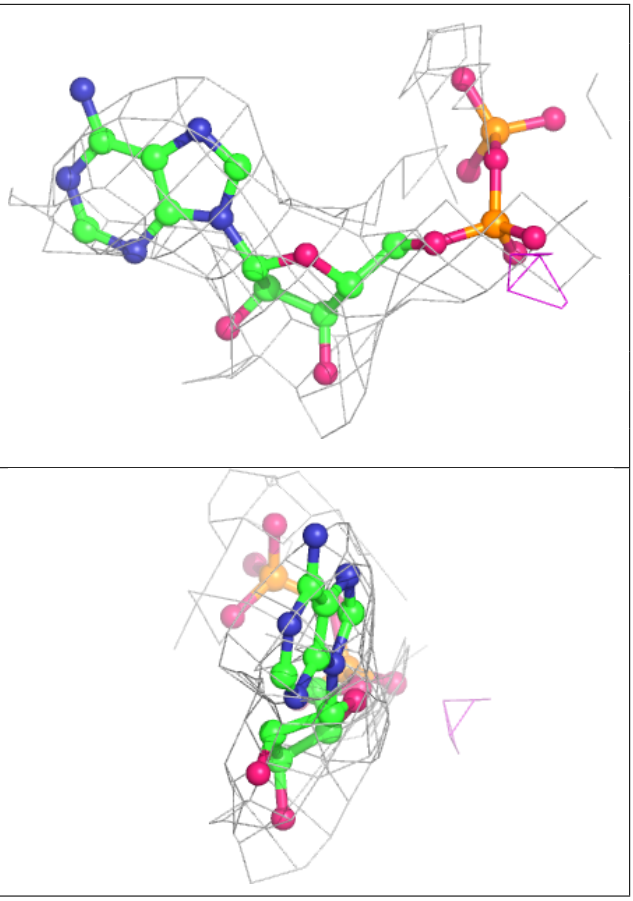
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95^{th} percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
2	ADP	E	501	27/27	0.53	0.36	193,246,280,285	0
2	ADP	C	501	27/27	0.61	0.44	184,211,222,226	0
2	ADP	F	501	27/27	0.74	0.31	217,249,284,285	0
3	SO4	D	1457	5/5	0.74	0.27	190,201,203,205	0
3	SO4	D	1456	5/5	0.83	0.23	177,189,191,198	0
3	SO4	F	1455	5/5	0.90	0.20	136,146,161,169	0

The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation to approximate a three-dimensional view.

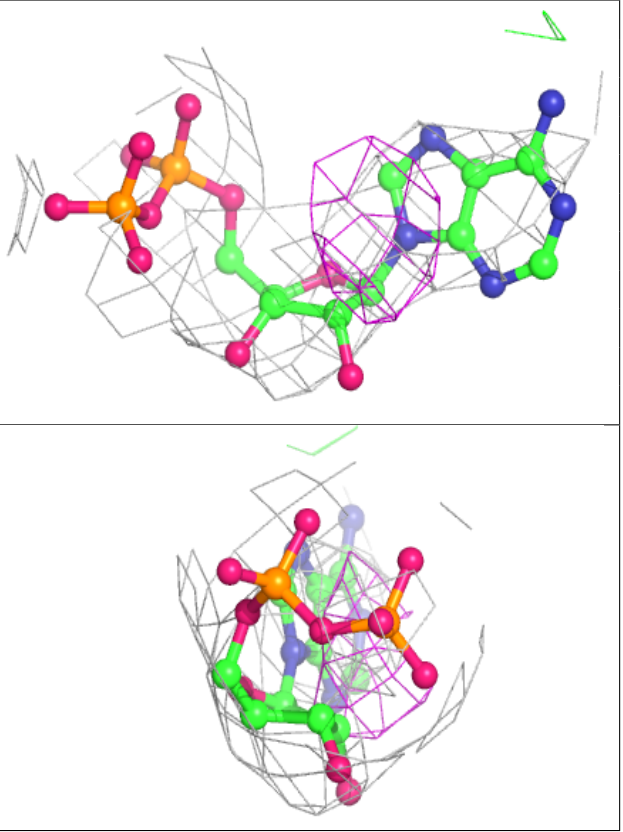
Electron density around ADP E 501:

$2mF_o$-DF_c (at 0.7 rmsd) in gray
mF_o-DF_c (at 3 rmsd) in purple (negative) and green (positive)



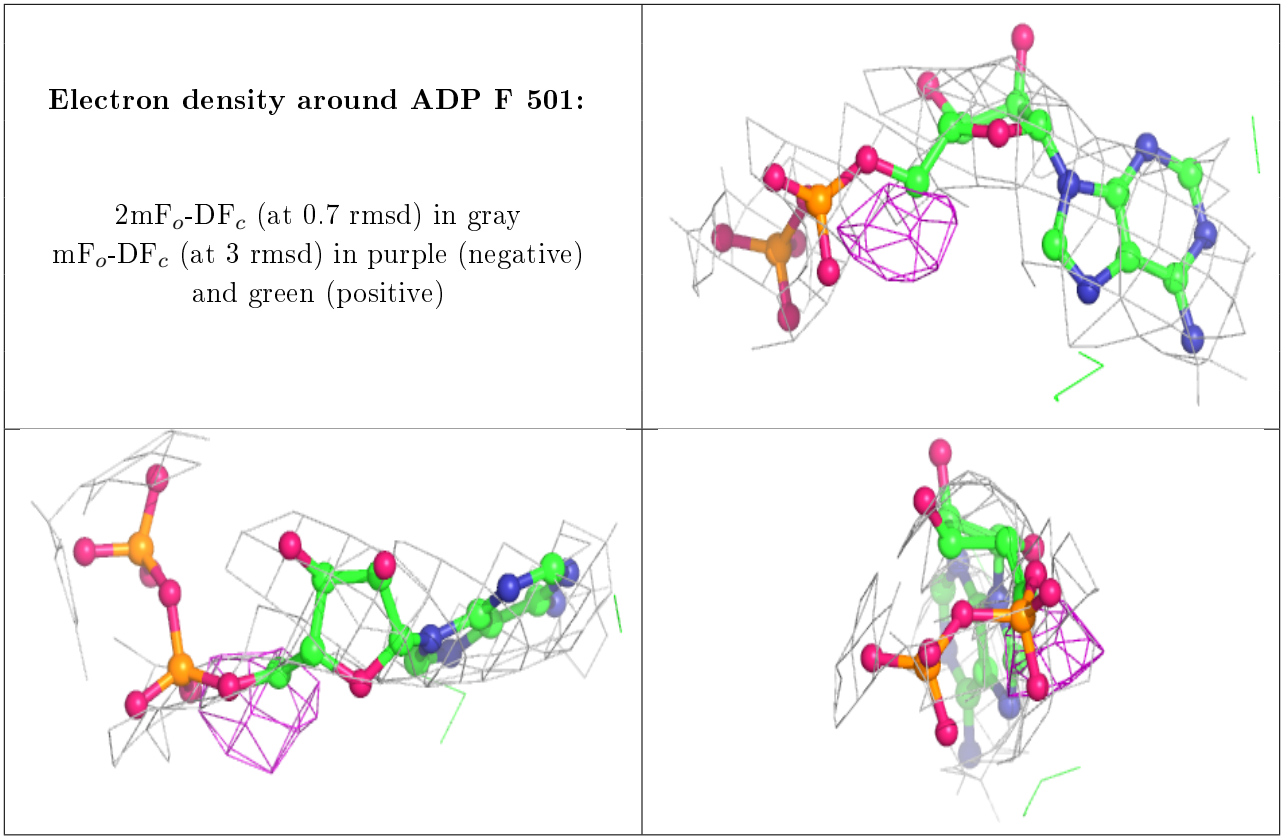
Electron density around ADP C 501:

$2mF_o$-DF_c (at 0.7 rmsd) in gray
mF_o-DF_c (at 3 rmsd) in purple (negative) and green (positive)



Electron density around ADP F 501:

$2mF_o$-DF_c (at 0.7 rmsd) in gray
mF_o-DF_c (at 3 rmsd) in purple (negative) and green (positive)



6.5 Other polymers (i)

There are no such residues in this entry.