



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 1, 2026 – 06:34 AM UTC

PDB ID : 4BIZ / pdb_00004biz
Title : Crystal structure of CpxAHDC (orthorhombic form 2)
Authors : Mechaly, A.E.; Sassoon, N.; Betton, J.M.; Alzari, P.M.
Deposited on : 2013-04-13
Resolution : 2.65 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 types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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

MolProbity : 4-5-2 with Phenix2.0
Mogul : 2022.3.0, CSD as543be (2022)
Xtriage (Phenix) : 2.0
EDS : 3.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4 : 9.0.010 (Gargrove)
Density-Fitness : 1.0.12
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

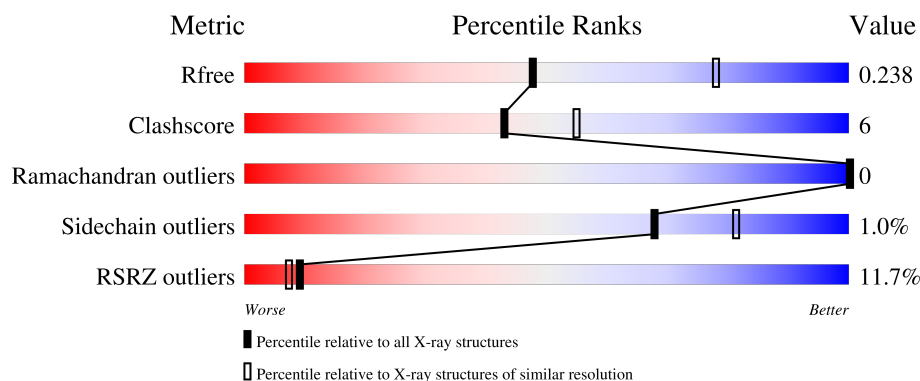
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.65 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}	180053	1110 (2.66-2.66)
Clashscore	190562	1141 (2.66-2.66)
Ramachandran outliers	187476	1126 (2.66-2.66)
Sidechain outliers	187428	1126 (2.66-2.66)
RSRZ outliers	180081	1110 (2.66-2.66)

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 $\leq 5\%$. 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	7% 64% 13% 22%
1	B	298	16% 64% 11% 24%
1	C	298	6% 69% 10% 20%
1	D	298	15% 60% 11% 28%
1	E	298	5% 65% 10% 23%

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Mol	Chain	Length	Quality of chain
1	F	298	5% 67% 8% 24%

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 11128 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	233	Total	C	N	O	S	0	0	0
			1838	1146	329	357	6			
1	B	227	Total	C	N	O	S	0	0	0
			1787	1120	317	344	6			
1	C	239	Total	C	N	O	S	0	0	0
			1881	1174	335	366	6			
1	D	214	Total	C	N	O	S	0	0	0
			1674	1049	297	322	6			
1	E	229	Total	C	N	O	S	0	0	0
			1809	1130	322	351	6			
1	F	225	Total	C	N	O	S	0	0	0
			1783	1116	318	343	6			

There are 174 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
A	248	GLU	HIS	engineered mutation	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
B	248	GLU	HIS	engineered mutation	UNP P0AE82
C	160	MET	-	expression tag	UNP P0AE82

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Chain	Residue	Modelled	Actual	Comment	Reference
C	161	GLY	-	expression tag	UNP P0AE82
C	162	SER	-	expression tag	UNP P0AE82
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
C	248	GLU	HIS	engineered mutation	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

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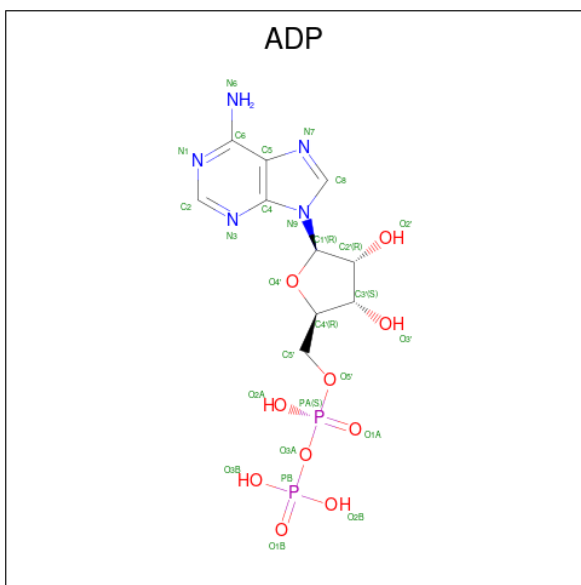
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D	174	VAL	-	expression tag	UNP P0AE82
D	175	PRO	-	expression tag	UNP P0AE82
D	176	ARG	-	expression tag	UNP P0AE82
D	177	GLY	-	expression tag	UNP P0AE82
D	178	SER	-	expression tag	UNP P0AE82
D	179	HIS	-	expression tag	UNP P0AE82
D	180	MET	-	expression 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
D	248	GLU	HIS	engineered mutation	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

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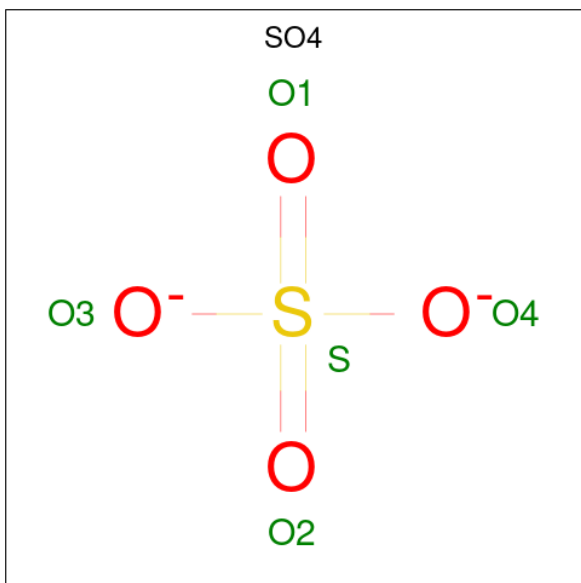
Chain	Residue	Modelled	Actual	Comment	Reference
E	187	GLY	-	expression tag	UNP P0AE82
E	248	GLU	HIS	engineered mutation	UNP P0AE82
F	160	MET	-	expression tag	UNP P0AE82
F	161	GLY	-	expression tag	UNP P0AE82
F	162	SER	-	expression tag	UNP P0AE82
F	163	SER	-	expression tag	UNP P0AE82
F	164	HIS	-	expression 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
F	248	GLU	HIS	engineered mutation	UNP P0AE82

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



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

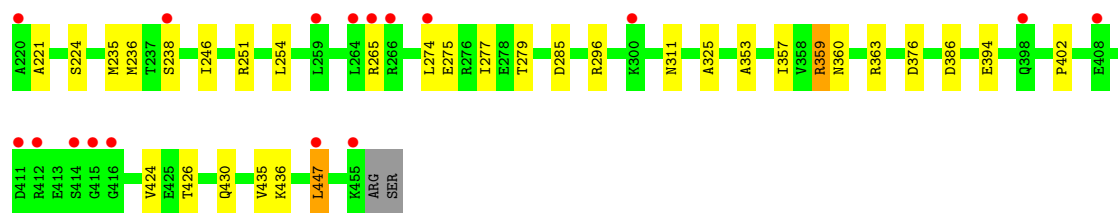
- Molecule 3 is SULFATE ION (CCD ID: SO4) (formula: O_4S).



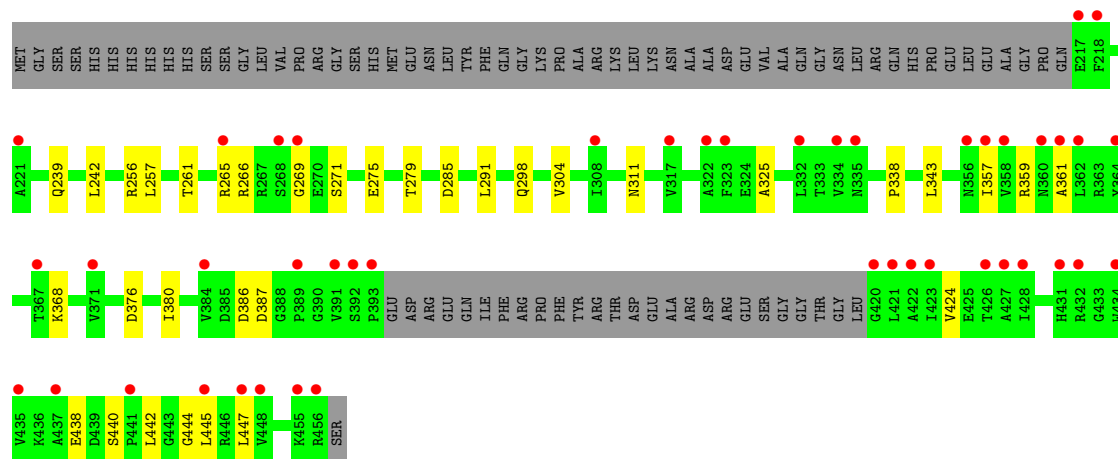
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	1	Total O S 5 4 1	0	0
3	B	1	Total O S 5 4 1	0	0
3	C	1	Total O S 5 4 1	0	0
3	D	1	Total O S 5 4 1	0	0
3	E	1	Total O S 5 4 1	0	0
3	F	1	Total O S 5 4 1	0	0

- Molecule 4 is water.

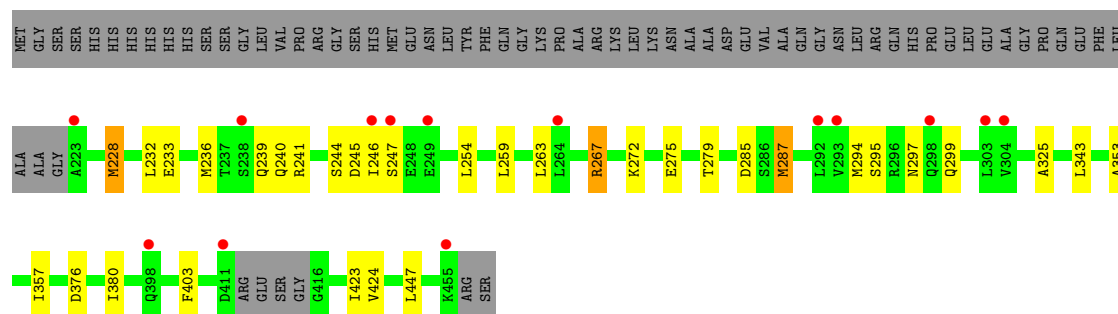
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	46	Total O 46 46	0	0
4	B	36	Total O 36 36	0	0
4	C	57	Total O 57 57	0	0
4	D	23	Total O 23 23	0	0
4	E	28	Total O 28 28	0	0
4	F	28	Total O 28 28	0	0



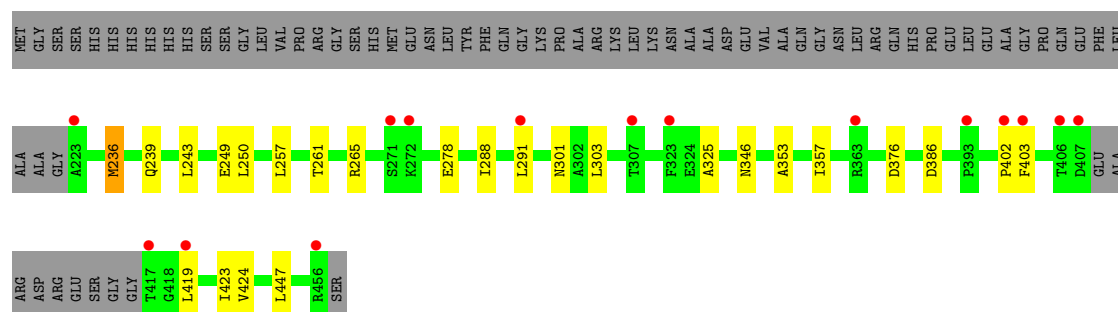
● Molecule 1: SENSOR PROTEIN CPXA



● Molecule 1: SENSOR PROTEIN CPXA



● Molecule 1: SENSOR PROTEIN CPXA



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 2	Depositor
Cell constants a, b, c, α , β , γ	120.45Å 125.11Å 159.79Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	49.01 – 2.65 49.01 – 2.65	Depositor EDS
% Data completeness (in resolution range)	100.0 (49.01-2.65) 100.0 (49.01-2.65)	Depositor EDS
R_{merge}	0.05	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.28 (at 2.65Å)	Xtriage
Refinement program	BUSTER 2.10.0	Depositor
R, R_{free}	0.206 , 0.235 0.212 , 0.238	Depositor DCC
R_{free} test set	3571 reflections (5.05%)	wwPDB-VP
Wilson B-factor (Å ²)	71.2	Xtriage
Anisotropy	0.185	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 67.7	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	0.014 for k,h,-l	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	11128	wwPDB-VP
Average B, all atoms (Å ²)	91.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.04% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ 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](#)

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

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	0.85	1/1867 (0.1%)	1.35	9/2526 (0.4%)
1	B	0.83	0/1816	1.35	5/2459 (0.2%)
1	C	0.83	1/1912 (0.1%)	1.37	13/2588 (0.5%)
1	D	0.85	0/1700	1.40	8/2302 (0.3%)
1	E	0.82	1/1838 (0.1%)	1.35	9/2488 (0.4%)
1	F	0.78	1/1812 (0.1%)	1.33	4/2453 (0.2%)
All	All	0.83	4/10945 (0.0%)	1.36	48/14816 (0.3%)

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	E	287	MET	SD-CE	-8.80	1.57	1.79
1	A	236	MET	SD-CE	-7.78	1.60	1.79
1	C	236	MET	SD-CE	-6.66	1.62	1.79
1	F	236	MET	SD-CE	-5.38	1.66	1.79

All (48) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	376	ASP	CA-CB-CG	7.67	120.27	112.60
1	B	376	ASP	CA-CB-CG	7.67	120.27	112.60
1	C	376	ASP	CA-CB-CG	7.65	120.25	112.60
1	E	376	ASP	CA-CB-CG	7.62	120.22	112.60
1	F	376	ASP	CA-CB-CG	7.46	120.06	112.60
1	A	376	ASP	CA-CB-CG	7.42	120.02	112.60
1	C	251	ARG	CA-C-N	6.96	127.56	119.83
1	C	251	ARG	C-N-CA	6.96	127.56	119.83
1	A	244	SER	CA-C-N	5.93	130.18	120.63
1	A	244	SER	C-N-CA	5.93	130.18	120.63
1	F	325	ALA	CA-C-N	5.91	128.20	120.28

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	F	325	ALA	C-N-CA	5.91	128.20	120.28
1	D	271	SER	CA-C-N	5.87	128.73	120.28
1	D	271	SER	C-N-CA	5.87	128.73	120.28
1	A	325	ALA	CA-C-N	5.79	128.04	120.28
1	A	325	ALA	C-N-CA	5.79	128.04	120.28
1	D	325	ALA	CA-C-N	5.65	127.85	120.28
1	D	325	ALA	C-N-CA	5.65	127.85	120.28
1	E	325	ALA	CA-C-N	5.61	127.79	120.28
1	E	325	ALA	C-N-CA	5.61	127.79	120.28
1	C	325	ALA	CA-C-N	5.60	127.78	120.28
1	C	325	ALA	C-N-CA	5.60	127.78	120.28
1	C	221	ALA	CA-C-N	5.55	126.11	120.00
1	C	221	ALA	C-N-CA	5.55	126.11	120.00
1	E	272	LYS	CA-C-N	5.55	127.66	120.44
1	E	272	LYS	C-N-CA	5.55	127.66	120.44
1	C	360	ASN	CA-CB-CG	5.54	118.14	112.60
1	B	423	ILE	CA-C-N	5.50	127.97	120.77
1	B	423	ILE	C-N-CA	5.50	127.97	120.77
1	D	304	VAL	N-CA-CB	-5.39	105.91	112.33
1	C	447	LEU	CD1-CG-CD2	-5.36	99.00	110.80
1	B	280	GLU	CB-CG-CD	5.36	121.71	112.60
1	C	218	PHE	CA-C-N	5.33	127.42	120.28
1	C	218	PHE	C-N-CA	5.33	127.42	120.28
1	F	386	ASP	CA-CB-CG	5.26	117.86	112.60
1	C	311	ASN	CA-CB-CG	5.22	117.82	112.60
1	A	379	GLY	N-CA-C	5.16	117.55	110.69
1	A	247	SER	CA-C-N	5.14	130.14	121.14
1	A	247	SER	C-N-CA	5.14	130.14	121.14
1	D	269	GLY	CA-C-N	5.11	127.64	120.28
1	D	269	GLY	C-N-CA	5.11	127.64	120.28
1	E	247	SER	CA-C-N	5.09	127.53	120.29
1	E	247	SER	C-N-CA	5.09	127.53	120.29
1	E	267	ARG	CA-C-N	5.08	130.49	121.80
1	E	267	ARG	C-N-CA	5.08	130.49	121.80
1	C	386	ASP	CA-CB-CG	5.08	117.68	112.60
1	A	386	ASP	CA-CB-CG	5.05	117.65	112.60
1	B	379	GLY	N-CA-C	5.03	117.90	110.80

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	1838	0	1832	40	0
1	B	1787	0	1791	37	0
1	C	1881	0	1872	25	0
1	D	1674	0	1686	26	0
1	E	1809	0	1805	28	0
1	F	1783	0	1787	22	0
2	A	27	0	12	0	0
2	C	27	0	12	0	0
2	E	27	0	12	0	0
2	F	27	0	12	0	0
3	A	5	0	0	0	0
3	B	5	0	0	0	0
3	C	5	0	0	0	0
3	D	5	0	0	0	0
3	E	5	0	0	0	0
3	F	5	0	0	0	0
4	A	46	0	0	0	0
4	B	36	0	0	0	0
4	C	57	0	0	1	0
4	D	23	0	0	0	0
4	E	28	0	0	0	0
4	F	28	0	0	0	0
All	All	11128	0	10821	135	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 (135) 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:357:ILE:HD12	1:C:447:LEU:CD2	1.52	1.37
1:C:357:ILE:HD12	1:C:447:LEU:HD23	1.28	1.14
1:A:251:ARG:NH2	1:A:289:ASN:OD1	1.83	1.10
1:A:246:ILE:HB	1:B:291:LEU:HD21	1.39	1.02
1:D:368:LYS:HG2	1:D:387:ASP:OD2	1.61	1.00

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:357:ILE:CD1	1:C:447:LEU:CD2	2.41	0.98
1:E:246:ILE:HD13	1:F:291:LEU:HB3	1.48	0.95
1:C:357:ILE:CD1	1:C:447:LEU:HD23	2.07	0.84
1:A:302:ALA:HB1	1:A:303:LEU:HA	1.57	0.83
1:A:246:ILE:CG2	1:B:403:PHE:HE2	1.90	0.83
1:C:426:THR:HG22	4:C:2049:HOH:O	1.79	0.83
1:C:357:ILE:HD12	1:C:447:LEU:HD21	1.59	0.81
1:A:426:THR:HG21	1:B:242:LEU:HB2	1.65	0.79
1:E:245:ASP:HB3	1:F:402:PRO:HD2	1.63	0.79
1:C:357:ILE:HD12	1:C:447:LEU:HD22	1.65	0.78
1:E:246:ILE:HG21	1:F:291:LEU:HD23	1.63	0.78
1:A:302:ALA:HB1	1:A:303:LEU:CA	2.14	0.77
1:E:357:ILE:HD11	1:E:424:VAL:HG11	1.67	0.76
1:A:251:ARG:NH1	1:A:285:ASP:OD1	2.17	0.75
1:C:357:ILE:HD11	1:C:424:VAL:HG11	1.72	0.72
1:D:361:ALA:HA	1:D:386:ASP:OD2	1.90	0.72
1:A:357:ILE:HD11	1:A:424:VAL:HG11	1.73	0.71
1:A:246:ILE:HG21	1:B:403:PHE:HE2	1.55	0.71
1:A:343:LEU:HD11	1:A:380:ILE:HD12	1.72	0.71
1:A:246:ILE:CB	1:B:291:LEU:HD21	2.17	0.70
1:E:343:LEU:HD11	1:E:380:ILE:HD12	1.74	0.70
1:F:357:ILE:HD11	1:F:424:VAL:HG11	1.74	0.69
1:A:241:ARG:NH1	1:B:426:THR:HG22	2.07	0.69
1:E:246:ILE:HG12	1:F:403:PHE:HE2	1.57	0.68
1:F:243:LEU:HD22	1:F:291:LEU:HD13	1.75	0.68
1:D:440:SER:HB3	1:D:444:GLY:O	1.94	0.67
1:B:343:LEU:HD11	1:B:380:ILE:HD12	1.78	0.66
1:C:265:ARG:HA	1:C:274:LEU:HD21	1.79	0.64
1:E:263:LEU:HD22	1:E:267:ARG:CZ	2.27	0.64
1:A:302:ALA:HA	1:A:346:ASN:HD21	1.62	0.63
1:E:259:LEU:O	1:E:263:LEU:HG	1.99	0.63
1:E:228:MET:HA	1:E:228:MET:HE2	1.82	0.62
1:C:357:ILE:CD1	1:C:447:LEU:HD21	2.22	0.61
1:D:343:LEU:HD11	1:D:380:ILE:HD12	1.83	0.61
1:C:426:THR:HG21	1:D:242:LEU:HB2	1.84	0.60
1:A:288:ILE:O	1:A:292:LEU:HG	2.01	0.60
1:F:236:MET:HE1	1:F:303:LEU:HG	1.82	0.59
1:A:246:ILE:HG23	1:B:403:PHE:HE2	1.64	0.59
1:B:357:ILE:HD11	1:B:424:VAL:HG11	1.82	0.59
1:A:227:GLN:HB3	1:D:266:ARG:NH1	2.19	0.58
1:B:265:ARG:HD3	1:B:274:LEU:HB3	1.87	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:233:GLU:HA	1:E:236:MET:HE2	1.86	0.57
1:C:254:LEU:HD21	1:C:285:ASP:HA	1.86	0.57
1:B:230:THR:HG22	1:D:256:ARG:HH12	1.70	0.56
1:C:436:LYS:O	1:C:447:LEU:HD12	2.05	0.55
1:B:365:SER:HA	1:B:388:GLY:HA3	1.88	0.55
1:E:287:MET:HE1	1:F:249:GLU:C	2.31	0.55
1:E:246:ILE:HG12	1:F:403:PHE:CE2	2.38	0.55
1:A:302:ALA:HB1	1:A:303:LEU:CB	2.37	0.54
1:A:362:LEU:HD23	1:A:369:ILE:HD13	1.89	0.54
1:A:254:LEU:HD21	1:A:285:ASP:HA	1.90	0.54
1:C:402:PRO:HG3	1:D:242:LEU:HD12	1.89	0.54
1:D:311:ASN:HA	1:D:338:PRO:HB2	1.88	0.54
1:A:235:MET:HE1	1:B:236:MET:HA	1.89	0.54
1:A:264:LEU:HD23	1:A:274:LEU:HD13	1.89	0.53
1:C:246:ILE:HD13	1:D:291:LEU:HB2	1.90	0.53
1:A:273:GLU:HG2	1:B:264:LEU:HD21	1.90	0.53
1:B:266:ARG:HB2	1:C:224:SER:HB2	1.89	0.53
1:A:240:GLN:HE21	1:A:298:GLN:HB3	1.73	0.53
1:B:357:ILE:HD12	1:B:447:LEU:HD13	1.91	0.53
1:E:287:MET:HE2	1:F:250:LEU:HD23	1.91	0.53
1:E:275:GLU:O	1:E:279:THR:HG23	2.09	0.53
1:F:243:LEU:CD2	1:F:291:LEU:HD13	2.39	0.53
1:D:357:ILE:HD12	1:D:447:LEU:HD13	1.90	0.52
1:A:357:ILE:HD12	1:A:447:LEU:HD13	1.91	0.52
1:B:305:SER:O	1:D:265:ARG:NH2	2.41	0.52
1:E:254:LEU:HD21	1:E:285:ASP:HA	1.89	0.52
1:E:241:ARG:HD2	1:E:299:GLN:HE22	1.74	0.52
1:B:275:GLU:O	1:B:279:THR:HG23	2.10	0.51
1:A:246:ILE:CG2	1:B:403:PHE:CE2	2.82	0.51
1:C:353:ALA:O	1:C:357:ILE:HG12	2.12	0.50
1:C:430:GLN:OE1	1:D:239:GLN:HG2	2.12	0.50
1:B:257:LEU:O	1:B:261:THR:HG23	2.12	0.50
1:E:240:GLN:HG3	1:F:239:GLN:HE21	1.76	0.49
1:E:357:ILE:HG23	1:E:447:LEU:HD12	1.93	0.49
1:E:244:SER:HA	1:E:295:SER:HB2	1.94	0.49
1:C:357:ILE:CG1	1:C:447:LEU:HD23	2.42	0.49
1:C:275:GLU:O	1:C:279:THR:HG23	2.12	0.49
1:A:302:ALA:HA	1:A:346:ASN:ND2	2.27	0.49
1:B:261:THR:O	1:B:265:ARG:HG2	2.13	0.48
1:B:276:ARG:O	1:B:280:GLU:HG2	2.14	0.48
1:A:275:GLU:O	1:A:279:THR:HG23	2.14	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:246:ILE:HG21	1:B:403:PHE:CE2	2.43	0.48
1:D:357:ILE:HD11	1:D:424:VAL:HG11	1.96	0.47
1:C:357:ILE:CG2	1:C:447:LEU:HD23	2.44	0.47
1:F:265:ARG:NH1	1:F:278:GLU:OE1	2.47	0.47
1:A:246:ILE:HD12	1:B:291:LEU:HD23	1.97	0.47
1:A:273:GLU:HB3	1:B:264:LEU:HD11	1.95	0.47
1:E:245:ASP:CB	1:F:402:PRO:HD2	2.40	0.47
1:B:353:ALA:O	1:B:357:ILE:HG12	2.15	0.47
1:D:275:GLU:O	1:D:279:THR:HG23	2.15	0.47
1:E:232:LEU:O	1:E:236:MET:HG3	2.15	0.47
1:B:361:ALA:O	1:B:365:SER:HB3	2.15	0.47
1:C:359:ARG:HH21	1:C:363:ARG:NH2	2.13	0.47
1:E:357:ILE:HD12	1:E:447:LEU:HD13	1.95	0.47
1:B:345:GLY:HA3	1:B:431:HIS:CD2	2.50	0.46
1:D:368:LYS:HG2	1:D:387:ASP:CG	2.38	0.46
1:A:239:GLN:HG3	1:B:298:GLN:OE1	2.15	0.46
1:E:287:MET:HE3	1:E:403:PHE:CD2	2.51	0.46
1:A:246:ILE:HG23	1:B:403:PHE:CE2	2.46	0.45
1:A:353:ALA:O	1:A:357:ILE:HG12	2.17	0.45
1:B:230:THR:CG2	1:D:256:ARG:HH12	2.28	0.45
1:A:344:TYR:CE2	1:B:219:LEU:HD21	2.51	0.45
1:F:288:ILE:O	1:F:291:LEU:HG	2.17	0.45
1:E:294:MET:HG3	1:E:423:ILE:HD11	1.99	0.44
1:B:296:ARG:NH1	1:D:285:ASP:OD2	2.50	0.44
1:F:353:ALA:O	1:F:357:ILE:HG12	2.17	0.44
1:A:224:SER:HB2	1:D:266:ARG:HB2	1.99	0.44
1:A:227:GLN:HB3	1:D:266:ARG:HH11	1.82	0.44
1:D:438:GLU:O	1:D:445:LEU:HD12	2.17	0.44
1:B:301:ASN:HA	1:B:346:ASN:HD22	1.83	0.44
1:E:357:ILE:HG23	1:E:447:LEU:CD1	2.47	0.44
1:C:238:SER:HB2	1:D:298:GLN:HG2	2.00	0.43
1:E:246:ILE:CD1	1:F:291:LEU:HB3	2.34	0.43
1:E:353:ALA:O	1:E:357:ILE:HG12	2.19	0.43
1:A:241:ARG:HH11	1:B:426:THR:HG22	1.82	0.42
1:A:246:ILE:HD12	1:B:291:LEU:CD2	2.49	0.42
1:C:435:VAL:HG12	1:C:447:LEU:HD11	2.01	0.42
1:E:236:MET:HB3	1:F:239:GLN:HE22	1.84	0.42
1:D:257:LEU:O	1:D:261:THR:HG23	2.19	0.42
1:D:368:LYS:CG	1:D:387:ASP:OD2	2.49	0.41
1:F:301:ASN:HA	1:F:346:ASN:HD22	1.85	0.41
1:A:235:MET:HE3	1:A:239:GLN:OE1	2.19	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:359:ARG:CZ	1:A:359:ARG:HB3	2.51	0.41
1:F:257:LEU:O	1:F:261:THR:HG23	2.21	0.41
1:C:235:MET:HG3	1:D:298:GLN:HB3	2.03	0.40
1:F:357:ILE:HD12	1:F:447:LEU:HD13	2.02	0.40
1:F:419:LEU:O	1:F:423:ILE:HG12	2.21	0.40
1:B:301:ASN:HD22	1:B:430:GLN:NE2	2.19	0.40
1:D:387:ASP:OD1	1:D:442:LEU:HB3	2.21	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	229/298 (77%)	222 (97%)	7 (3%)	0	100	100
1	B	223/298 (75%)	215 (96%)	8 (4%)	0	100	100
1	C	237/298 (80%)	234 (99%)	3 (1%)	0	100	100
1	D	210/298 (70%)	203 (97%)	7 (3%)	0	100	100
1	E	225/298 (76%)	220 (98%)	5 (2%)	0	100	100
1	F	221/298 (74%)	215 (97%)	6 (3%)	0	100	100
All	All	1345/1788 (75%)	1309 (97%)	36 (3%)	0	100	100

There are no Ramachandran outliers to report.

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	199/251 (79%)	197 (99%)	2 (1%)	68	81
1	B	194/251 (77%)	192 (99%)	2 (1%)	68	81
1	C	203/251 (81%)	199 (98%)	4 (2%)	48	69
1	D	182/251 (72%)	181 (100%)	1 (0%)	81	91
1	E	197/251 (78%)	194 (98%)	3 (2%)	57	75
1	F	195/251 (78%)	195 (100%)	0	100	100
All	All	1170/1506 (78%)	1158 (99%)	12 (1%)	68	81

All (12) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	246	ILE
1	A	394	GLU
1	B	236	MET
1	B	279	THR
1	C	277	ILE
1	C	296	ARG
1	C	359	ARG
1	C	394	GLU
1	D	359	ARG
1	E	228	MET
1	E	239	GLN
1	E	297	ASN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (20) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	226	ASN
1	A	240	GLN
1	A	282	GLN
1	A	298	GLN
1	A	346	ASN
1	B	282	GLN
1	B	346	ASN
1	B	430	GLN
1	C	282	GLN
1	C	346	ASN
1	D	346	ASN

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Mol	Chain	Res	Type
1	E	282	GLN
1	E	299	GLN
1	E	301	ASN
1	E	312	GLN
1	E	346	ASN
1	F	239	GLN
1	F	282	GLN
1	F	346	ASN
1	F	366	HIS

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](#)

10 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	E	501	-	28,29,29	0.56	0	43,45,45	0.48	0
2	ADP	A	501	-	28,29,29	0.42	0	43,45,45	0.56	0
3	SO4	A	1456	-	4,4,4	0.31	0	6,6,6	0.20	0
3	SO4	C	1456	-	4,4,4	0.33	0	6,6,6	0.15	0
3	SO4	B	1456	-	4,4,4	0.29	0	6,6,6	0.10	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
3	SO4	D	1457	-	4,4,4	0.30	0	6,6,6	0.16	0
3	SO4	F	1457	-	4,4,4	0.31	0	6,6,6	0.27	0
2	ADP	F	501	-	28,29,29	0.50	0	43,45,45	0.50	0
3	SO4	E	1456	-	4,4,4	0.17	0	6,6,6	0.18	0
2	ADP	C	501	-	28,29,29	0.57	0	43,45,45	0.49	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	A	501	-	-	0/16/32/32	0/3/3/3
2	ADP	E	501	-	-	0/16/32/32	0/3/3/3
2	ADP	F	501	-	-	3/16/32/32	0/3/3/3
2	ADP	C	501	-	-	0/16/32/32	0/3/3/3

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (3) torsion outliers are listed below:

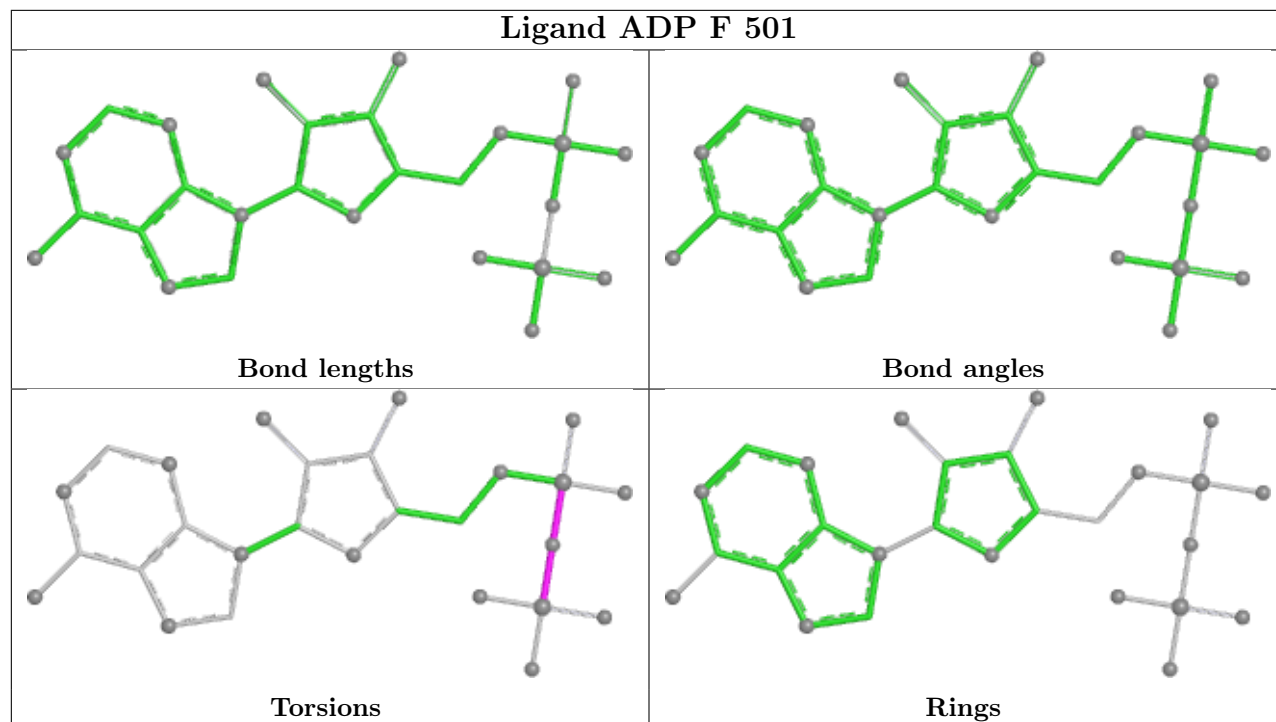
Mol	Chain	Res	Type	Atoms
2	F	501	ADP	PA-O3A-PB-O2B
2	F	501	ADP	PB-O3A-PA-O1A
2	F	501	ADP	PB-O3A-PA-O2A

There are no ring outliers.

No monomer is involved in short contacts.

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 than 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.



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 ⓘ

6.1 Protein, DNA and RNA chains ⓘ

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

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	A	233/298 (78%)	0.48	20 (8%) 16 12	51, 76, 127, 158	0
1	B	227/298 (76%)	0.92	47 (20%) 2 1	48, 91, 161, 193	0
1	C	239/298 (80%)	0.29	19 (7%) 18 14	52, 71, 126, 173	0
1	D	214/298 (71%)	1.00	45 (21%) 2 1	51, 96, 163, 173	0
1	E	229/298 (76%)	0.35	14 (6%) 27 20	56, 81, 137, 172	0
1	F	225/298 (75%)	0.46	15 (6%) 24 18	58, 88, 150, 186	0
All	All	1367/1788 (76%)	0.58	160 (11%) 9 7	48, 82, 151, 193	0

All (160) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	E	455	LYS	6.5
1	A	292	LEU	5.6
1	D	393	PRO	5.4
1	A	247	SER	5.4
1	F	223	ALA	5.4
1	A	303	LEU	5.4
1	A	301	ASN	5.3
1	A	246	ILE	5.2
1	B	220	ALA	5.2
1	D	391	VAL	4.8
1	E	223	ALA	4.7
1	A	245	ASP	4.7
1	D	421	LEU	4.5
1	B	219	LEU	4.4
1	D	445	LEU	4.3
1	A	298	GLN	4.3
1	C	266	ARG	4.1
1	D	218	PHE	4.0
1	B	221	ALA	4.0

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Mol	Chain	Res	Type	RSRZ
1	C	412	ARG	4.0
1	B	317	VAL	4.0
1	C	415	GLY	3.9
1	F	407	ASP	3.9
1	D	437	ALA	3.9
1	B	418	GLY	3.9
1	C	218	PHE	3.9
1	B	222	GLY	3.8
1	B	364	TYR	3.7
1	B	455	LYS	3.6
1	D	361	ALA	3.6
1	D	435	VAL	3.6
1	C	259	LEU	3.6
1	A	302	ALA	3.5
1	D	420	GLY	3.4
1	B	404	TYR	3.3
1	D	422	ALA	3.3
1	B	400	PHE	3.3
1	D	423	ILE	3.3
1	D	447	LEU	3.3
1	D	317	VAL	3.3
1	C	408	GLU	3.3
1	E	247	SER	3.2
1	F	272	LYS	3.2
1	A	221	ALA	3.2
1	C	220	ALA	3.2
1	B	360	ASN	3.2
1	E	298	GLN	3.1
1	D	357	ILE	3.1
1	B	328	MET	3.1
1	D	364	TYR	3.1
1	D	456	ARG	3.1
1	D	360	ASN	3.1
1	B	393	PRO	3.0
1	A	455	LYS	3.0
1	C	414	SER	3.0
1	D	269	GLY	3.0
1	C	447	LEU	3.0
1	D	268	SER	3.0
1	B	405	ARG	3.0
1	B	437	ALA	3.0
1	F	307	THR	2.9

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Mol	Chain	Res	Type	RSRZ
1	D	322	ALA	2.9
1	D	332	LEU	2.9
1	B	406	THR	2.9
1	E	303	LEU	2.9
1	C	264	LEU	2.8
1	A	241	ARG	2.8
1	D	308	ILE	2.8
1	E	411	ASP	2.8
1	F	323	PHE	2.8
1	D	389	PRO	2.8
1	B	399	ILE	2.8
1	A	295	SER	2.8
1	C	455	LYS	2.7
1	E	246	ILE	2.7
1	A	300	LYS	2.7
1	D	432	ARG	2.7
1	D	426	THR	2.7
1	F	403	PHE	2.7
1	A	412	ARG	2.6
1	C	238	SER	2.6
1	F	393	PRO	2.6
1	D	431	HIS	2.6
1	B	270	GLU	2.6
1	A	238	SER	2.5
1	B	268	SER	2.5
1	B	304	VAL	2.5
1	E	293	VAL	2.5
1	A	413	GLU	2.5
1	B	407	ASP	2.5
1	F	419	LEU	2.4
1	D	217	GLU	2.4
1	B	398	GLN	2.4
1	F	417	THR	2.4
1	F	271	SER	2.4
1	D	323	PHE	2.4
1	B	369	ILE	2.4
1	A	304	VAL	2.4
1	E	264	LEU	2.4
1	A	249	GLU	2.4
1	B	395	ASP	2.4
1	D	441	PRO	2.4
1	F	291	LEU	2.3

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Mol	Chain	Res	Type	RSRZ
1	B	423	ILE	2.3
1	D	362	LEU	2.3
1	E	304	VAL	2.3
1	D	427	ALA	2.3
1	B	315	SER	2.3
1	D	265	ARG	2.3
1	B	424	VAL	2.3
1	B	447	LEU	2.3
1	B	419	LEU	2.3
1	B	403	PHE	2.3
1	F	406	THR	2.2
1	C	217	GLU	2.2
1	F	402	PRO	2.2
1	B	329	GLY	2.2
1	B	323	PHE	2.2
1	B	389	PRO	2.2
1	C	411	ASP	2.2
1	D	334	VAL	2.2
1	B	357	ILE	2.2
1	B	394	GLU	2.2
1	E	249	GLU	2.2
1	B	365	SER	2.2
1	D	371	VAL	2.2
1	D	448	VAL	2.2
1	D	428	ILE	2.2
1	F	363	ARG	2.2
1	B	441	PRO	2.2
1	C	398	GLN	2.2
1	B	362	LEU	2.2
1	B	420	GLY	2.2
1	D	392	SER	2.2
1	B	322	ALA	2.1
1	D	221	ALA	2.1
1	C	265	ARG	2.1
1	C	300	LYS	2.1
1	D	455	LYS	2.1
1	A	243	LEU	2.1
1	D	356	ASN	2.1
1	E	292	LEU	2.1
1	B	358	VAL	2.1
1	B	396	ARG	2.1
1	B	327	GLN	2.1

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Mol	Chain	Res	Type	RSRZ
1	B	361	ALA	2.1
1	B	401	ARG	2.1
1	C	274	LEU	2.1
1	D	335	ASN	2.1
1	C	416	GLY	2.1
1	D	358	VAL	2.1
1	F	456	ARG	2.0
1	E	238	SER	2.0
1	D	434	TRP	2.0
1	D	367	THR	2.0
1	B	291	LEU	2.0
1	E	398	GLN	2.0
1	B	308	ILE	2.0
1	A	293	VAL	2.0
1	D	384	VAL	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 oligosaccharides 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, 95th 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.

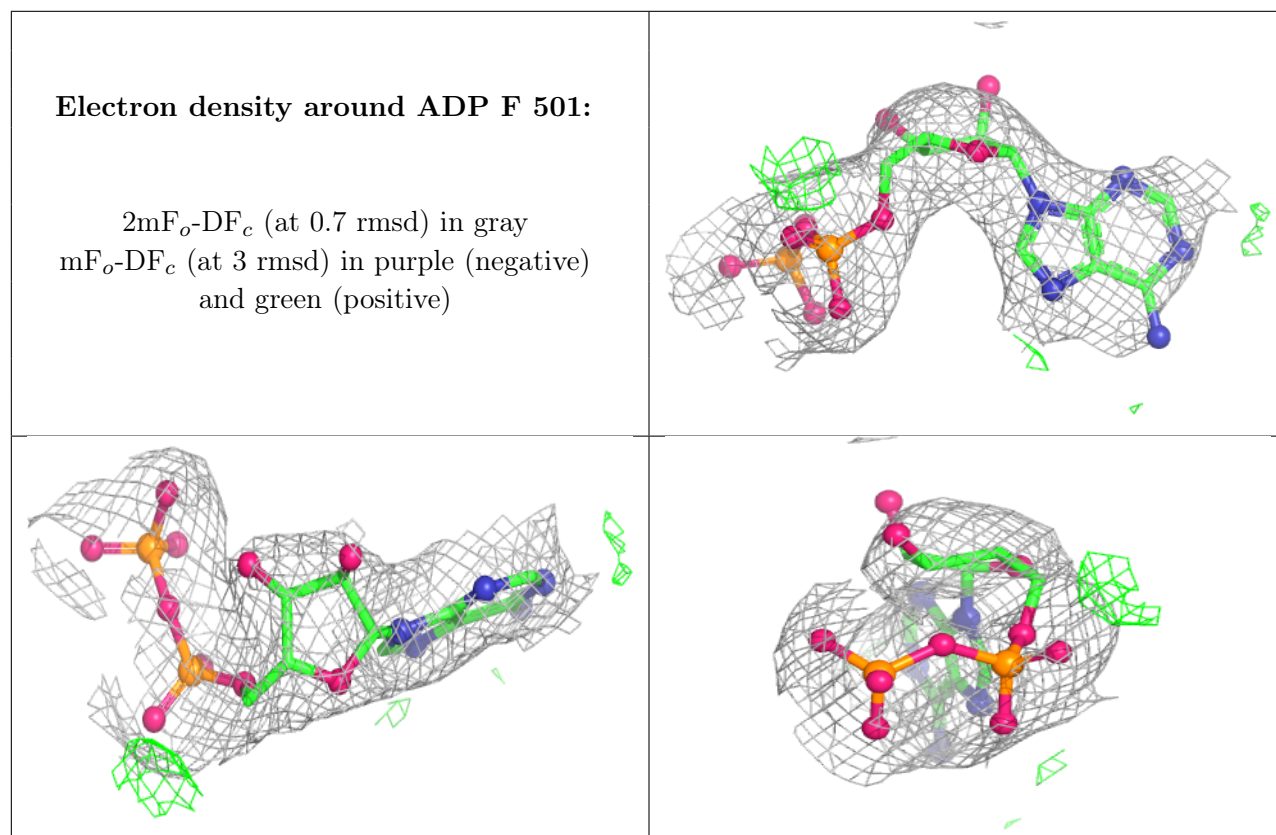
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
3	SO4	D	1457	5/5	0.71	0.15	147,148,149,150	0
3	SO4	B	1456	5/5	0.75	0.11	157,159,159,159	0
3	SO4	C	1456	5/5	0.81	0.09	119,120,121,121	0
3	SO4	E	1456	5/5	0.84	0.10	114,114,115,117	0
2	ADP	F	501	27/27	0.90	0.10	118,131,137,139	0
3	SO4	A	1456	5/5	0.91	0.08	98,101,101,103	0
3	SO4	F	1457	5/5	0.91	0.15	91,94,95,96	0
2	ADP	A	501	27/27	0.95	0.09	60,75,87,91	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
2	ADP	E	501	27/27	0.96	0.08	62,76,89,92	0
2	ADP	C	501	27/27	0.97	0.07	54,66,80,82	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.



6.5 Other polymers ⓘ

There are no such residues in this entry.