Full wwPDB X-ray Structure Validation Report ⓘ

Feb 4, 2024 – 05:35 AM EST

PDB ID	:	1PTW
Title	:	The Crystal Structure of AMP-Bound PDE4 Suggests a Mechanism for Phosphodiesterase Catalysis
Authors	:	Huai, Q.; Colicelli, J.; Ke, H.
Deposited on	:	2003-06-23
Resolution	:	2.30 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:

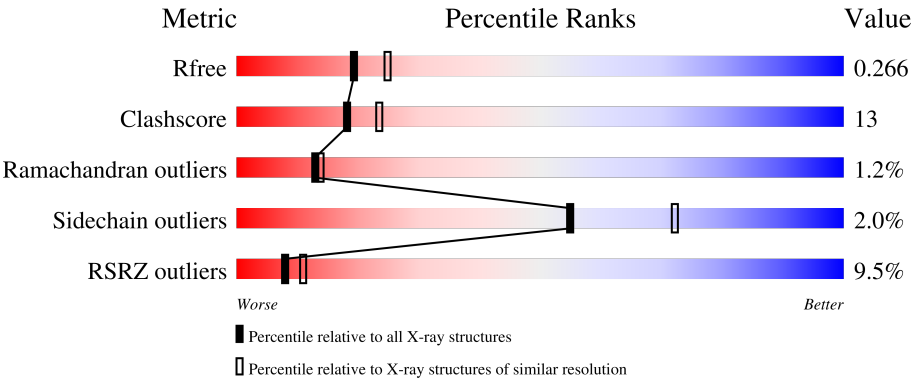
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.36
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.36

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 2.30 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	5042 (2.30-2.30)
Clashscore	141614	5643 (2.30-2.30)
Ramachandran outliers	138981	5575 (2.30-2.30)
Sidechain outliers	138945	5575 (2.30-2.30)
RSRZ outliers	127900	4938 (2.30-2.30)

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	360	8% 68% 23% • 7%
1	B	360	10% 60% 30% • 9%
1	C	360	10% 60% 29% • 9%
1	D	360	7% 66% 25% • 7%

2 Entry composition (i)

There are 4 unique types of molecules in this entry. The entry contains 10888 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.

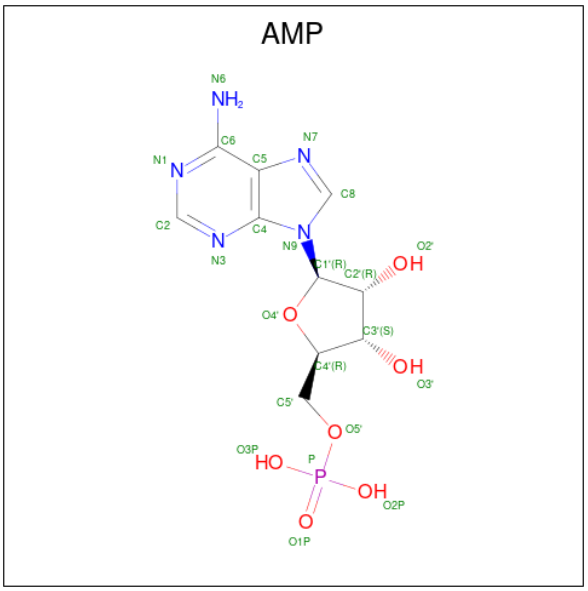
- Molecule 1 is a protein called cAMP-specific phosphodiesterase PDE4D2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	334	Total	C	N	O	S	0	0	0
			2704	1712	463	515	14			
1	B	327	Total	C	N	O	S	0	0	0
			2647	1673	452	508	14			
1	C	327	Total	C	N	O	S	0	0	0
			2647	1673	452	508	14			
1	D	334	Total	C	N	O	S	0	0	0
			2704	1712	463	515	14			

- Molecule 2 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	2	Total	Zn	0	0
			2	2		
2	B	2	Total	Zn	0	0
			2	2		
2	C	2	Total	Zn	0	0
			2	2		
2	D	2	Total	Zn	0	0
			2	2		

- Molecule 3 is ADENOSINE MONOPHOSPHATE (three-letter code: AMP) (formula: $C_{10}H_{14}N_5O_7P$).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
3	A	1	Total	C	N	O	P	0	0
			23	10	5	7	1		
3	B	1	Total	C	N	O	P	0	0
			23	10	5	7	1		
3	C	1	Total	C	N	O	P	0	0
			23	10	5	7	1		
3	D	1	Total	C	N	O	P	0	0
			23	10	5	7	1		

- Molecule 4 is water.

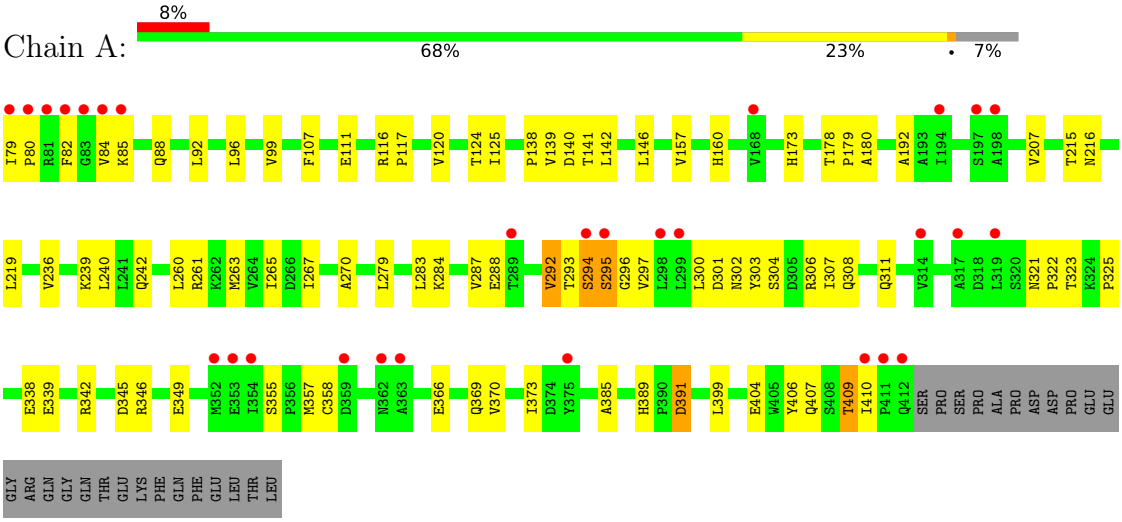
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	26	Total	O	0	0
			26	26		
4	B	13	Total	O	0	0
			13	13		
4	C	16	Total	O	0	0
			16	16		
4	D	31	Total	O	0	0
			31	31		

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.

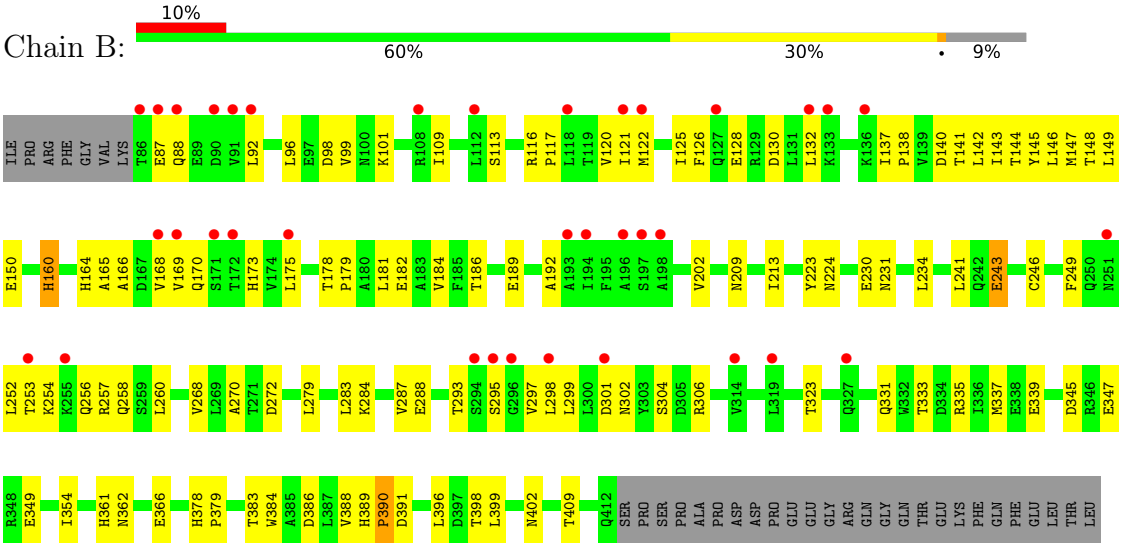
• Molecule 1: cAMP-specific phosphodiesterase PDE4D2

Chain A:



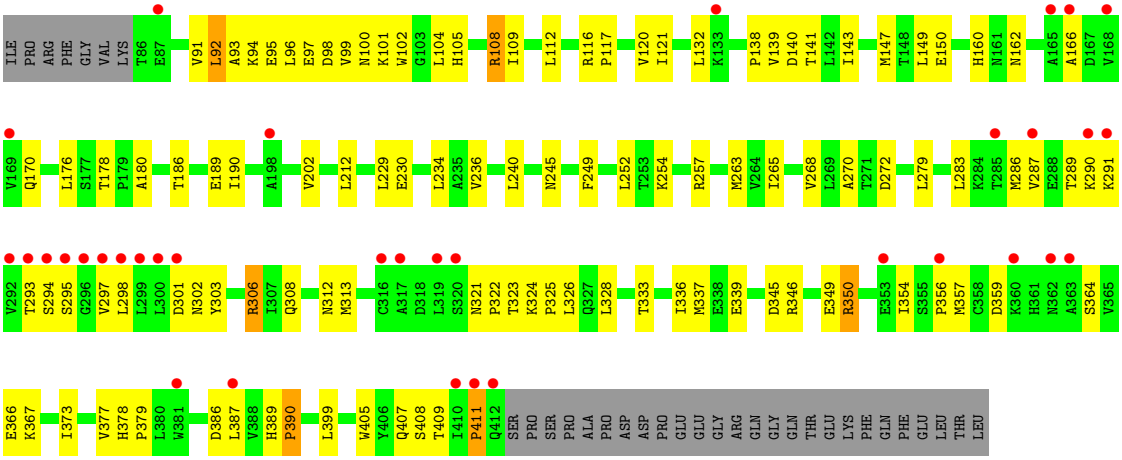
• Molecule 1: cAMP-specific phosphodiesterase PDE4D2

Chain B:



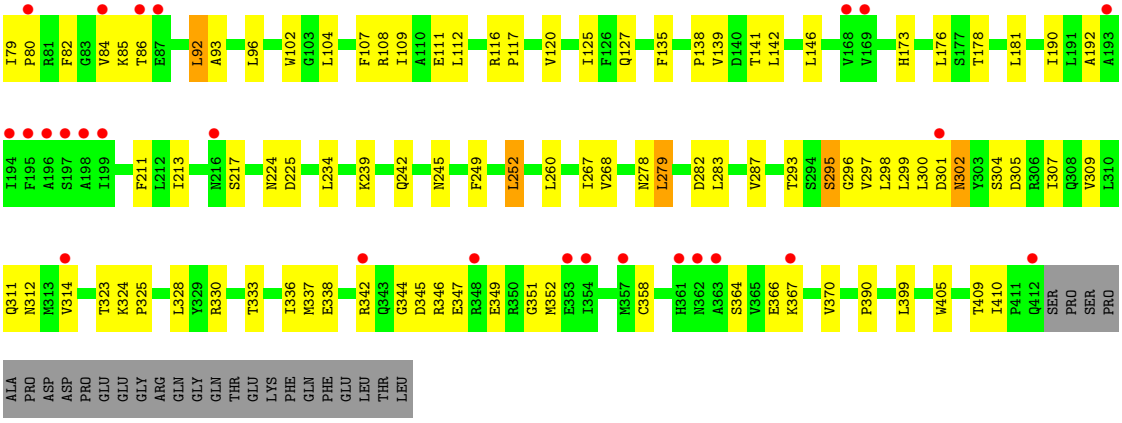
• Molecule 1: cAMP-specific phosphodiesterase PDE4D2

Chain C:



• Molecule 1: cAMP-specific phosphodiesterase PDE4D2

Chain D:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α, β, γ	99.21Å 111.23Å 159.65Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	99.00 – 2.30 30.82 – 2.30	Depositor EDS
% Data completeness (in resolution range)	84.9 (99.00-2.30) 84.7 (30.82-2.30)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.07	Depositor
$< I/\sigma(I) >$ [1]	1.50 (at 2.29Å)	Xtriage
Refinement program	CNS 1.0	Depositor
R, R_{free}	0.229 , 0.274 0.222 , 0.266	Depositor DCC
R_{free} test set	7186 reflections (10.13%)	wwPDB-VP
Wilson B-factor (Å^2)	39.1	Xtriage
Anisotropy	0.131	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.35 , 40.9	EDS
L-test for twinning[2]	$< \|L\| > = 0.49$, $< L^2 > = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.94	EDS
Total number of atoms	10888	wwPDB-VP
Average B, all atoms (Å^2)	50.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.20% 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: AMP, ZN

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	0.37	0/2760	0.61	0/3749
1	B	0.34	0/2701	0.54	0/3670
1	C	0.33	0/2701	0.54	0/3670
1	D	0.38	0/2760	0.59	1/3749 (0.0%)
All	All	0.36	0/10922	0.57	1/14838 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	D	252	LEU	CA-CB-CG	5.17	127.19	115.30

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	2704	0	2664	62	0
1	B	2647	0	2599	79	0
1	C	2647	0	2599	83	0
1	D	2704	0	2664	68	0
2	A	2	0	0	0	0
2	B	2	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	C	2	0	0	0	0
2	D	2	0	0	0	0
3	A	23	0	12	1	0
3	B	23	0	12	1	0
3	C	23	0	12	2	0
3	D	23	0	12	0	0
4	A	26	0	0	1	0
4	B	13	0	0	0	0
4	C	16	0	0	0	0
4	D	31	0	0	0	0
All	All	10888	0	10574	286	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 13.

All (286) 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:292:VAL:HG12	1:A:293:THR:H	1.15	1.04
1:C:306:ARG:HB3	1:C:306:ARG:HH11	1.23	1.03
1:D:302:ASN:HD22	1:D:302:ASN:H	1.15	0.88
1:C:306:ARG:HH11	1:C:306:ARG:CB	1.98	0.77
1:C:290:LYS:HE3	1:C:298:LEU:HD21	1.67	0.77
1:C:293:THR:HG22	1:C:294:SER:H	1.48	0.77
1:C:325:PRO:HD2	1:C:328:LEU:HD12	1.68	0.76
1:A:345:ASP:O	1:A:349:GLU:HG3	1.87	0.74
1:B:270:ALA:HB1	1:B:279:LEU:HD11	1.71	0.73
1:A:292:VAL:HG12	1:A:293:THR:N	1.98	0.72
1:D:366:GLU:HG2	1:D:409:THR:HB	1.71	0.72
1:D:338:GLU:O	1:D:342:ARG:HG2	1.90	0.72
1:A:346:ARG:HA	1:A:349:GLU:OE1	1.89	0.71
1:B:254:LYS:O	1:B:258:GLN:HG3	1.91	0.70
1:B:178:THR:HG23	1:B:181:LEU:HB2	1.74	0.70
1:B:87:GLU:HG3	1:B:88:GLN:H	1.57	0.70
1:C:104:LEU:HD11	1:C:109:ILE:HD11	1.75	0.69
1:D:79:ILE:N	1:D:80:PRO:HD2	2.08	0.68
1:C:143:ILE:O	1:C:147:MET:HG3	1.94	0.68
1:B:378:HIS:HB3	1:B:379:PRO:HD3	1.75	0.67
1:C:293:THR:HG22	1:C:294:SER:N	2.10	0.67
1:C:234:LEU:HD21	1:C:268:VAL:HB	1.77	0.67
1:D:302:ASN:H	1:D:302:ASN:ND2	1.91	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:302:ASN:HD22	1:D:302:ASN:N	1.90	0.66
1:D:84:VAL:HG12	1:D:85:LYS:H	1.60	0.66
1:B:230:GLU:HG2	1:B:272:ASP:HB2	1.78	0.66
1:B:345:ASP:O	1:B:349:GLU:HG3	1.95	0.65
1:A:96:LEU:O	1:A:99:VAL:HG23	1.96	0.65
1:C:354:ILE:HG21	1:C:359:ASP:HB2	1.79	0.64
1:B:87:GLU:HG3	1:B:88:GLN:N	2.12	0.63
1:B:116:ARG:HD3	1:B:150:GLU:OE1	1.98	0.63
1:B:323:THR:HG22	1:B:399:LEU:HD13	1.82	0.62
1:C:302:ASN:O	1:C:306:ARG:HG3	1.99	0.62
1:A:284:LYS:O	1:A:288:GLU:HG3	1.99	0.62
1:B:144:THR:HG22	1:B:246:CYS:SG	2.40	0.62
1:A:180:ALA:O	1:A:297:VAL:HG13	2.00	0.61
1:D:84:VAL:HG12	1:D:85:LYS:N	2.15	0.61
1:B:178:THR:HG21	1:B:181:LEU:HD12	1.82	0.61
1:B:253:THR:OG1	1:B:256:GLN:HG3	2.01	0.61
1:A:307:ILE:O	1:A:311:GLN:HG3	2.02	0.60
1:B:142:LEU:O	1:B:146:LEU:HG	2.01	0.60
1:C:236:VAL:O	1:C:240:LEU:HG	2.02	0.59
1:C:286:MET:HE1	1:C:308:GLN:HB3	1.84	0.59
1:C:102:TRP:NE1	1:C:324:LYS:HD3	2.17	0.59
1:C:270:ALA:HB1	1:C:279:LEU:HD11	1.84	0.58
1:A:96:LEU:O	1:A:99:VAL:CG2	2.51	0.58
1:A:239:LYS:NZ	1:D:239:LYS:NZ	2.52	0.58
1:A:79:ILE:N	1:A:80:PRO:HD2	2.18	0.57
1:B:122:MET:SD	1:B:169:VAL:HG11	2.44	0.57
1:A:82:PHE:O	1:A:84:VAL:HG23	2.05	0.57
1:C:116:ARG:HE	1:C:147:MET:HE2	1.69	0.57
1:C:287:VAL:HG22	1:C:387:LEU:HD13	1.87	0.57
1:D:302:ASN:OD1	1:D:304:SER:HB3	2.05	0.57
1:B:175:LEU:O	1:B:178:THR:HG22	2.06	0.56
1:D:79:ILE:N	1:D:79:ILE:HD12	2.20	0.56
1:A:160:HIS:ND1	1:A:339:GLU:OE2	2.29	0.56
1:C:373:ILE:HA	1:C:377:VAL:HB	1.88	0.56
1:B:143:ILE:O	1:B:147:MET:HG3	2.06	0.55
1:D:213:ILE:HG23	1:D:225:ASP:OD1	2.06	0.55
1:A:302:ASN:O	1:A:306:ARG:HG3	2.07	0.55
1:B:165:ALA:O	1:B:169:VAL:HG23	2.06	0.55
1:A:79:ILE:N	1:A:80:PRO:CD	2.69	0.55
1:D:142:LEU:O	1:D:146:LEU:HG	2.07	0.55
1:A:304:SER:O	1:A:308:GLN:HB2	2.06	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:234:LEU:HD21	1:B:268:VAL:HB	1.89	0.55
1:B:361:HIS:C	1:B:362:ASN:HD22	2.10	0.54
1:D:344:GLY:HA3	1:D:358:CYS:O	2.07	0.54
1:B:383:THR:O	1:B:386:ASP:HB2	2.08	0.54
1:C:306:ARG:HB3	1:C:306:ARG:NH1	2.07	0.54
1:A:192:ALA:HB2	1:A:260:LEU:HD12	1.90	0.54
1:B:331:GLN:O	1:B:335:ARG:HG3	2.08	0.54
1:C:230:GLU:HG2	1:C:272:ASP:HB2	1.90	0.54
1:C:409:THR:O	1:C:411:PRO:HD3	2.07	0.54
1:B:178:THR:CG2	1:B:181:LEU:HD12	2.38	0.54
1:C:121:ILE:HD12	1:C:166:ALA:HB1	1.90	0.54
3:C:509:AMP:O1P	3:C:509:AMP:H3'	2.08	0.53
1:C:120:VAL:HG23	1:C:121:ILE:N	2.23	0.53
1:B:409:THR:O	1:B:409:THR:HG22	2.08	0.53
1:D:104:LEU:HD11	1:D:109:ILE:HD11	1.90	0.53
1:D:370:VAL:HG21	1:D:410:ILE:HD11	1.91	0.53
1:A:242:GLN:OE1	1:D:242:GLN:OE1	2.27	0.53
1:A:366:GLU:HG2	1:A:409:THR:HG22	1.91	0.53
1:B:284:LYS:HE2	1:B:383:THR:OG1	2.09	0.53
1:C:378:HIS:HB3	1:C:379:PRO:HD3	1.91	0.53
1:D:345:ASP:O	1:D:349:GLU:HG3	2.08	0.53
1:B:96:LEU:O	1:B:99:VAL:HG23	2.09	0.52
1:C:139:VAL:HG23	1:C:140:ASP:N	2.23	0.52
1:B:116:ARG:NH2	1:D:349:GLU:OE1	2.43	0.52
1:C:263:MET:HG2	1:C:303:TYR:OH	2.10	0.52
1:D:295:SER:O	1:D:297:VAL:N	2.40	0.52
1:B:302:ASN:O	1:B:306:ARG:HG3	2.09	0.52
1:A:142:LEU:O	1:A:146:LEU:HG	2.10	0.52
1:D:330:ARG:HH11	1:D:405:TRP:HH2	1.57	0.52
1:C:356:PRO:O	1:C:357:MET:HB2	2.10	0.52
1:D:346:ARG:HA	1:D:349:GLU:OE1	2.10	0.51
1:A:292:VAL:CG1	1:A:293:THR:H	1.92	0.51
1:A:349:GLU:HB3	1:C:147:MET:SD	2.51	0.51
1:D:96:LEU:HD11	1:D:120:VAL:CG1	2.40	0.51
1:A:292:VAL:CG1	1:A:293:THR:N	2.67	0.51
1:A:338:GLU:OE2	1:A:342:ARG:NH2	2.44	0.51
1:D:181:LEU:HD21	1:D:298:LEU:HD22	1.93	0.51
1:C:336:ILE:HG23	1:C:337:MET:N	2.26	0.51
1:B:121:ILE:HG21	1:B:170:GLN:HB2	1.93	0.50
1:C:254:LYS:HD2	1:C:257:ARG:HH12	1.75	0.50
1:C:321:ASN:CG	1:C:322:PRO:HD3	2.32	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:345:ASP:O	1:C:349:GLU:HG3	2.10	0.50
1:A:404:GLU:O	1:A:407:GLN:N	2.45	0.50
1:C:407:GLN:C	1:C:409:THR:H	2.15	0.50
1:D:249:PHE:CZ	1:D:260:LEU:HD21	2.46	0.50
1:D:279:LEU:HD22	1:D:312:ASN:OD1	2.11	0.50
1:B:92:LEU:HD23	1:B:92:LEU:O	2.11	0.50
1:A:406:TYR:O	1:A:410:ILE:HG13	2.12	0.50
1:A:321:ASN:CG	1:A:322:PRO:HD3	2.32	0.50
1:A:366:GLU:O	1:A:370:VAL:HG23	2.12	0.50
1:B:145:TYR:CE1	1:B:241:LEU:HD23	2.47	0.50
1:C:94:LYS:HA	1:C:97:GLU:OE2	2.12	0.50
1:A:300:LEU:HD13	1:A:306:ARG:HA	1.93	0.49
1:B:178:THR:CG2	1:B:181:LEU:HB2	2.42	0.49
1:C:333:THR:O	1:C:336:ILE:HG22	2.12	0.49
1:A:270:ALA:HB1	1:A:279:LEU:HD11	1.93	0.49
1:B:186:THR:OG1	1:B:189:GLU:HG3	2.12	0.49
1:B:366:GLU:HG2	1:B:409:THR:CG2	2.43	0.49
1:C:93:ALA:O	1:C:97:GLU:HG3	2.13	0.49
1:B:148:THR:HG21	1:B:243:GLU:HG3	1.94	0.49
1:C:308:GLN:O	1:C:312:ASN:ND2	2.41	0.49
1:D:141:THR:HG23	1:D:245:ASN:O	2.13	0.49
1:B:109:ILE:O	1:B:113:SER:HB3	2.13	0.49
1:D:192:ALA:HB2	1:D:260:LEU:HD12	1.95	0.49
1:D:302:ASN:ND2	1:D:302:ASN:N	2.54	0.49
1:B:302:ASN:OD1	1:B:304:SER:HB3	2.13	0.49
1:C:346:ARG:O	1:C:350:ARG:HD2	2.13	0.48
1:D:127:GLN:HE21	1:D:127:GLN:HA	1.79	0.48
1:C:116:ARG:HG2	1:C:116:ARG:HH11	1.78	0.48
1:D:307:ILE:O	1:D:311:GLN:HG3	2.14	0.48
1:B:120:VAL:HG23	1:B:121:ILE:N	2.29	0.48
1:B:366:GLU:HG2	1:B:409:THR:HB	1.95	0.47
1:C:212:LEU:HD11	1:C:229:LEU:HD21	1.96	0.47
1:C:336:ILE:CG2	1:C:337:MET:N	2.76	0.47
1:D:138:PRO:HG2	1:D:141:THR:OG1	2.15	0.47
1:C:326:LEU:HD21	1:C:405:TRP:CE2	2.48	0.47
1:A:215:THR:O	1:A:216:ASN:HB2	2.14	0.47
1:A:236:VAL:O	1:A:240:LEU:HG	2.15	0.47
1:C:293:THR:CG2	1:C:294:SER:H	2.24	0.47
1:C:160:HIS:NE2	3:C:509:AMP:O1P	2.37	0.47
1:D:234:LEU:HD21	1:D:268:VAL:HB	1.96	0.47
1:D:300:LEU:HD11	1:D:309:VAL:HG21	1.96	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:333:THR:O	1:B:337:MET:HG2	2.15	0.47
1:C:160:HIS:ND1	1:C:339:GLU:OE2	2.48	0.47
1:D:333:THR:O	1:D:337:MET:HG2	2.15	0.47
1:B:160:HIS:ND1	1:B:339:GLU:OE2	2.42	0.47
1:B:192:ALA:HB2	1:B:260:LEU:HD12	1.97	0.47
1:A:179:PRO:HD2	1:A:391:ASP:OD2	2.15	0.46
1:B:132:LEU:HA	1:B:137:ILE:HB	1.96	0.46
1:A:116:ARG:N	1:A:117:PRO:CD	2.78	0.46
1:B:179:PRO:O	1:B:182:GLU:HB2	2.14	0.46
1:B:249:PHE:HA	1:B:252:LEU:HD13	1.97	0.46
1:A:157:VAL:HG13	1:A:339:GLU:OE1	2.15	0.46
1:B:283:LEU:O	1:B:287:VAL:HG23	2.16	0.46
1:C:289:THR:O	1:C:289:THR:HG22	2.16	0.46
1:C:323:THR:HG22	1:C:399:LEU:HD13	1.97	0.46
1:D:104:LEU:HD11	1:D:109:ILE:CD1	2.46	0.46
1:D:333:THR:HA	1:D:336:ILE:HG22	1.97	0.46
1:D:364:SER:HB3	1:D:367:LYS:HB3	1.97	0.46
1:A:207:VAL:HG13	1:A:346:ARG:HH21	1.80	0.46
1:C:104:LEU:HD12	1:C:105:HIS:H	1.80	0.46
1:D:108:ARG:CZ	1:D:112:LEU:HD21	2.46	0.46
1:C:94:LYS:HD2	1:C:97:GLU:OE2	2.16	0.46
1:A:283:LEU:O	1:A:287:VAL:HG23	2.16	0.45
1:B:243:GLU:OE2	1:D:217:SER:HA	2.17	0.45
1:D:323:THR:HG22	1:D:399:LEU:HD13	1.99	0.45
1:B:398:THR:HG22	1:B:402:ASN:ND2	2.31	0.45
1:C:306:ARG:HH11	1:C:306:ARG:CG	2.29	0.45
1:B:252:LEU:HA	1:B:256:GLN:OE1	2.16	0.45
1:C:176:LEU:HD23	1:C:313:MET:SD	2.57	0.45
1:D:301:ASP:OD2	1:D:301:ASP:C	2.54	0.45
1:A:357:MET:HE1	4:A:514:HOH:O	2.16	0.45
1:D:135:PHE:CD1	1:D:252:LEU:HD22	2.52	0.45
1:A:160:HIS:NE2	3:A:507:AMP:O2P	2.50	0.45
1:B:98:ASP:OD1	1:B:101:LYS:HD2	2.17	0.45
1:B:295:SER:OG	1:B:297:VAL:HG23	2.17	0.45
1:A:207:VAL:HG13	1:A:346:ARG:NH2	2.32	0.44
1:A:369:GLN:O	1:A:373:ILE:HG13	2.16	0.44
1:C:116:ARG:N	1:C:117:PRO:CD	2.79	0.44
1:C:283:LEU:O	1:C:287:VAL:HG23	2.17	0.44
1:B:116:ARG:N	1:B:117:PRO:CD	2.81	0.44
1:B:223:TYR:CE1	1:B:231:ASN:HB3	2.53	0.44
1:B:284:LYS:O	1:B:288:GLU:HG3	2.17	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:366:GLU:CD	1:C:366:GLU:H	2.20	0.44
1:C:249:PHE:HB3	1:C:252:LEU:HD12	2.00	0.44
1:D:325:PRO:HD2	1:D:328:LEU:HD12	2.00	0.44
1:B:138:PRO:HG2	1:B:141:THR:HB	2.00	0.44
3:B:508:AMP:O1P	3:B:508:AMP:H3'	2.17	0.44
1:C:139:VAL:CG2	1:C:140:ASP:N	2.81	0.44
1:B:137:ILE:CG2	1:B:142:LEU:HB2	2.48	0.43
1:C:104:LEU:HD23	1:C:170:GLN:HG3	1.99	0.43
1:D:82:PHE:CZ	1:D:93:ALA:HA	2.53	0.43
1:A:265:ILE:HD13	1:B:224:ASN:O	2.18	0.43
1:B:396:LEU:O	1:B:396:LEU:HD23	2.17	0.43
1:D:107:PHE:O	1:D:111:GLU:HG3	2.18	0.43
1:D:181:LEU:CD2	1:D:298:LEU:HD22	2.48	0.43
1:A:107:PHE:O	1:A:111:GLU:HG3	2.18	0.43
1:B:99:VAL:O	1:B:170:GLN:NE2	2.50	0.43
1:B:209:ASN:O	1:B:213:ILE:HG13	2.17	0.43
1:B:362:ASN:HD22	1:B:362:ASN:N	2.15	0.43
1:D:108:ARG:O	1:D:112:LEU:HG	2.17	0.43
1:A:293:THR:O	1:A:294:SER:CB	2.66	0.43
1:D:116:ARG:N	1:D:117:PRO:CD	2.82	0.43
1:D:305:ASP:O	1:D:309:VAL:HG23	2.17	0.43
1:A:116:ARG:O	1:A:120:VAL:HG22	2.18	0.43
1:A:125:ILE:HD13	1:A:173:HIS:HB2	2.01	0.43
1:C:364:SER:HB3	1:C:367:LYS:HD2	2.01	0.43
1:B:126:PHE:HB3	1:B:132:LEU:HD11	2.00	0.43
1:B:249:PHE:CZ	1:B:260:LEU:HD21	2.53	0.43
1:C:150:GLU:HG3	1:C:162:ASN:HB3	2.01	0.43
1:A:139:VAL:HG23	1:A:140:ASP:N	2.34	0.43
1:A:385:ALA:O	1:A:389:HIS:HB2	2.19	0.43
1:C:132:LEU:HD12	1:C:132:LEU:H	1.83	0.43
1:A:355:SER:O	1:A:358:CYS:HB2	2.19	0.43
1:B:347:GLU:OE1	1:B:354:ILE:HA	2.19	0.43
1:C:99:VAL:HG13	1:C:100:ASN:OD1	2.19	0.43
1:C:389:HIS:HA	1:C:390:PRO:HA	1.83	0.42
1:D:349:GLU:C	1:D:351:GLY:H	2.22	0.42
1:B:164:HIS:O	1:B:168:VAL:HG23	2.19	0.42
1:B:181:LEU:O	1:B:184:VAL:HG23	2.19	0.42
1:C:104:LEU:HD11	1:C:109:ILE:CD1	2.46	0.42
1:D:86:THR:HG21	1:D:92:LEU:HD12	2.01	0.42
1:C:138:PRO:HG2	1:C:141:THR:OG1	2.20	0.42
1:C:180:ALA:O	1:C:297:VAL:HG13	2.19	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:150:GLU:HG3	1:C:162:ASN:CB	2.49	0.42
1:A:138:PRO:HG2	1:A:141:THR:OG1	2.20	0.42
1:B:120:VAL:HG23	1:B:121:ILE:H	1.85	0.42
1:B:149:LEU:HD12	1:B:202:VAL:HG21	2.01	0.42
1:C:293:THR:CG2	1:C:294:SER:N	2.80	0.42
1:A:99:VAL:HG21	1:A:124:THR:HG21	2.01	0.42
1:A:404:GLU:O	1:A:407:GLN:HB2	2.19	0.42
1:D:135:PHE:HD1	1:D:252:LEU:HD22	1.85	0.42
1:A:219:LEU:HD12	1:A:219:LEU:HA	1.89	0.42
1:A:349:GLU:HB3	1:C:147:MET:HE1	2.01	0.42
1:C:176:LEU:HD13	1:C:190:ILE:HG23	2.02	0.42
1:D:79:ILE:N	1:D:80:PRO:CD	2.80	0.42
1:A:303:TYR:O	1:A:307:ILE:HG22	2.19	0.41
1:B:113:SER:OG	1:B:116:ARG:HB2	2.19	0.41
1:C:139:VAL:O	1:C:143:ILE:HG13	2.21	0.41
1:C:289:THR:O	1:C:291:LYS:HG3	2.20	0.41
1:D:347:GLU:O	1:D:352:MET:HB2	2.20	0.41
1:C:326:LEU:HD21	1:C:405:TRP:CD2	2.56	0.41
1:D:125:ILE:HD13	1:D:173:HIS:HB2	2.02	0.41
1:D:336:ILE:HG23	1:D:337:MET:N	2.35	0.41
1:B:389:HIS:HA	1:B:390:PRO:HA	1.86	0.41
1:C:91:VAL:O	1:C:95:GLU:HG2	2.20	0.41
1:A:323:THR:HG22	1:A:399:LEU:HD13	2.03	0.41
1:B:257:ARG:NH1	1:B:257:ARG:HB2	2.35	0.41
1:A:139:VAL:HG23	1:A:140:ASP:OD1	2.21	0.41
1:C:138:PRO:HG2	1:C:141:THR:CB	2.51	0.41
1:D:283:LEU:O	1:D:287:VAL:HG23	2.20	0.41
1:B:306:ARG:HH11	1:B:306:ARG:HG2	1.86	0.41
1:C:92:LEU:HD22	1:C:96:LEU:HD11	2.01	0.41
1:C:108:ARG:NH1	1:C:112:LEU:HD21	2.36	0.41
1:D:84:VAL:CG1	1:D:85:LYS:H	2.32	0.41
1:A:261:ARG:O	1:A:265:ILE:HG13	2.21	0.41
1:A:263:MET:O	1:A:267:ILE:HG13	2.20	0.41
1:A:293:THR:HA	1:A:296:GLY:H	1.86	0.41
1:B:384:TRP:O	1:B:388:VAL:HG22	2.21	0.41
1:C:230:GLU:H	1:C:230:GLU:CD	2.24	0.41
1:C:265:ILE:HD13	1:D:224:ASN:HB3	2.03	0.41
1:A:293:THR:HB	1:A:294:SER:H	1.65	0.41
1:A:370:VAL:HG21	1:A:410:ILE:HD11	2.03	0.41
1:D:92:LEU:HD22	1:D:96:LEU:CD1	2.51	0.41
1:D:330:ARG:NH1	1:D:405:TRP:HH2	2.19	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:121:ILE:HD12	1:B:166:ALA:HB1	2.03	0.41
1:D:102:TRP:CE2	1:D:324:LYS:HE2	2.55	0.41
1:B:128:GLU:C	1:B:130:ASP:H	2.23	0.40
1:C:98:ASP:OD1	1:C:101:LYS:HD2	2.20	0.40
1:C:186:THR:OG1	1:C:189:GLU:HG3	2.21	0.40
1:C:295:SER:C	1:C:297:VAL:H	2.25	0.40
1:C:322:PRO:HG2	1:C:377:VAL:HG21	2.03	0.40
1:D:84:VAL:CG1	1:D:85:LYS:N	2.84	0.40
1:B:125:ILE:HG23	1:B:173:HIS:ND1	2.36	0.40
1:D:267:ILE:HG21	1:D:314:VAL:HG21	2.02	0.40
1:C:149:LEU:HD12	1:C:202:VAL:HG21	2.02	0.40
1:D:176:LEU:HD13	1:D:190:ILE:HG23	2.02	0.40
1:B:125:ILE:HG23	1:B:173:HIS:CE1	2.57	0.40
1:B:287:VAL:HG11	1:B:386:ASP:HB3	2.03	0.40
1:B:293:THR:HG22	1:B:299:LEU:HD23	2.04	0.40
1:D:211:PHE:CD1	1:D:211:PHE:C	2.94	0.40
1:D:293:THR:HG22	1:D:299:LEU:HD23	2.04	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	332/360 (92%)	304 (92%)	20 (6%)	8 (2%)	6	4
1	B	325/360 (90%)	287 (88%)	34 (10%)	4 (1%)	13	14
1	C	325/360 (90%)	297 (91%)	25 (8%)	3 (1%)	17	20
1	D	332/360 (92%)	311 (94%)	20 (6%)	1 (0%)	41	50
All	All	1314/1440 (91%)	1199 (91%)	99 (8%)	16 (1%)	13	14

All (16) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	160	HIS
1	B	243	GLU
1	B	301	ASP
1	A	85	LYS
1	A	301	ASP
1	A	391	ASP
1	A	294	SER
1	A	409	THR
1	A	88	GLN
1	B	140	ASP
1	C	408	SER
1	A	295	SER
1	C	301	ASP
1	D	296	GLY
1	C	411	PRO
1	A	292	VAL

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	305/328 (93%)	301 (99%)	4 (1%)	69	82
1	B	299/328 (91%)	296 (99%)	3 (1%)	76	87
1	C	299/328 (91%)	291 (97%)	8 (3%)	44	61
1	D	305/328 (93%)	296 (97%)	9 (3%)	41	57
All	All	1208/1312 (92%)	1184 (98%)	24 (2%)	55	72

All (24) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	92	LEU
1	A	178	THR
1	A	295	SER
1	A	325	PRO
1	B	298	LEU
1	B	390	PRO

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Mol	Chain	Res	Type
1	B	391	ASP
1	C	92	LEU
1	C	108	ARG
1	C	178	THR
1	C	245	ASN
1	C	306	ARG
1	C	350	ARG
1	C	386	ASP
1	C	390	PRO
1	D	92	LEU
1	D	139	VAL
1	D	178	THR
1	D	278	ASN
1	D	279	LEU
1	D	282	ASP
1	D	295	SER
1	D	302	ASN
1	D	390	PRO

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	245	ASN
1	A	312	ASN
1	A	393	GLN
1	A	407	GLN
1	B	245	ASN
1	B	308	GLN
1	B	362	ASN
1	B	369	GLN
1	C	231	ASN
1	C	242	GLN
1	C	245	ASN
1	C	308	GLN
1	C	362	ASN
1	D	123	HIS
1	D	127	GLN
1	D	216	ASN
1	D	224	ASN
1	D	245	ASN
1	D	278	ASN
1	D	302	ASN

5.3.3 RNA

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates

There are no monosaccharides in this entry.

5.6 Ligand geometry

Of 12 ligands modelled in this entry, 8 are monoatomic - leaving 4 for Mogul analysis.

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	$\#\|Z\| > 2$
3	AMP	B	508	2	22,25,25	0.77	0	25,38,38	0.88	1 (4%)
3	AMP	D	510	2	22,25,25	0.73	0	25,38,38	0.93	1 (4%)
3	AMP	C	509	2	22,25,25	0.75	0	25,38,38	0.91	1 (4%)
3	AMP	A	507	2	22,25,25	0.77	0	25,38,38	0.90	1 (4%)

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
3	AMP	B	508	2	-	5/6/26/26	0/3/3/3
3	AMP	D	510	2	-	3/6/26/26	0/3/3/3
3	AMP	C	509	2	-	2/6/26/26	0/3/3/3
3	AMP	A	507	2	-	5/6/26/26	0/3/3/3

There are no bond length outliers.

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
3	A	507	AMP	C5-C6-N6	2.42	124.03	120.35
3	D	510	AMP	C5-C6-N6	2.38	123.96	120.35
3	C	509	AMP	C5-C6-N6	2.24	123.76	120.35
3	B	508	AMP	C5-C6-N6	2.19	123.68	120.35

There are no chirality outliers.

All (15) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	507	AMP	C5'-O5'-P-O1P
3	A	507	AMP	C5'-O5'-P-O2P
3	A	507	AMP	C5'-O5'-P-O3P
3	B	508	AMP	C5'-O5'-P-O1P
3	B	508	AMP	C5'-O5'-P-O2P
3	B	508	AMP	C5'-O5'-P-O3P
3	D	510	AMP	C5'-O5'-P-O2P
3	C	509	AMP	C4'-C5'-O5'-P
3	D	510	AMP	C5'-O5'-P-O3P
3	B	508	AMP	C4'-C5'-O5'-P
3	A	507	AMP	C4'-C5'-O5'-P
3	A	507	AMP	O4'-C4'-C5'-O5'
3	D	510	AMP	O4'-C4'-C5'-O5'
3	B	508	AMP	O4'-C4'-C5'-O5'
3	C	509	AMP	O4'-C4'-C5'-O5'

There are no ring outliers.

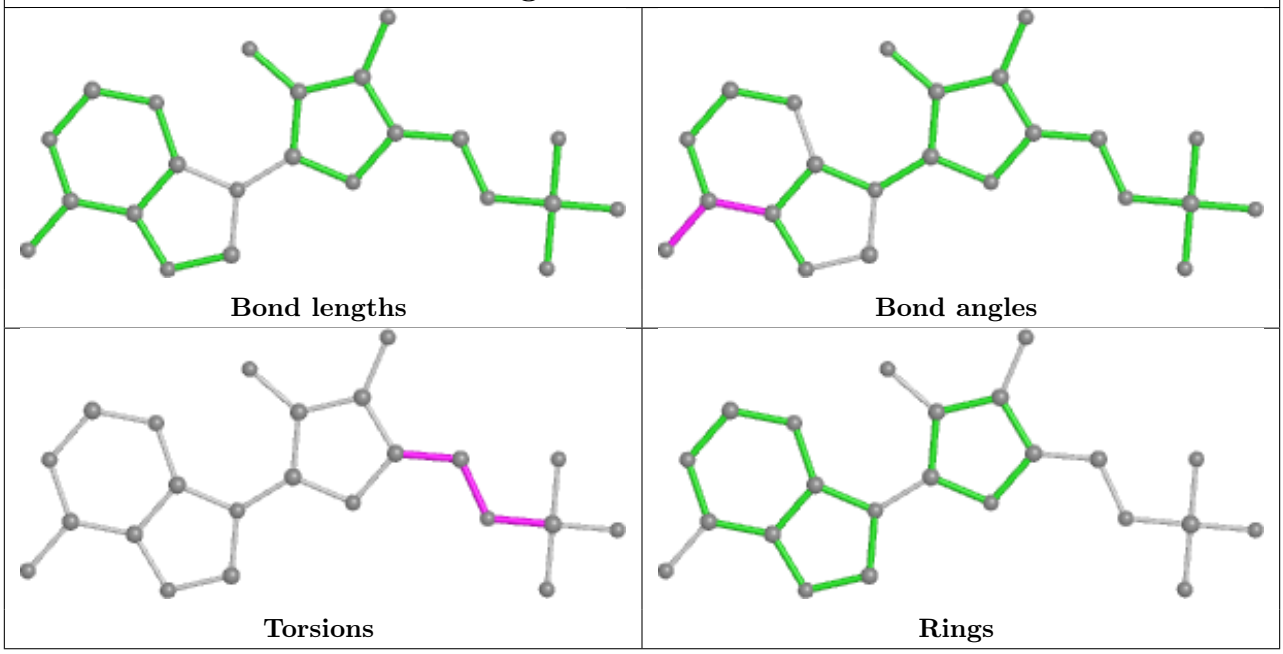
3 monomers are involved in 4 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	B	508	AMP	1	0
3	C	509	AMP	2	0
3	A	507	AMP	1	0

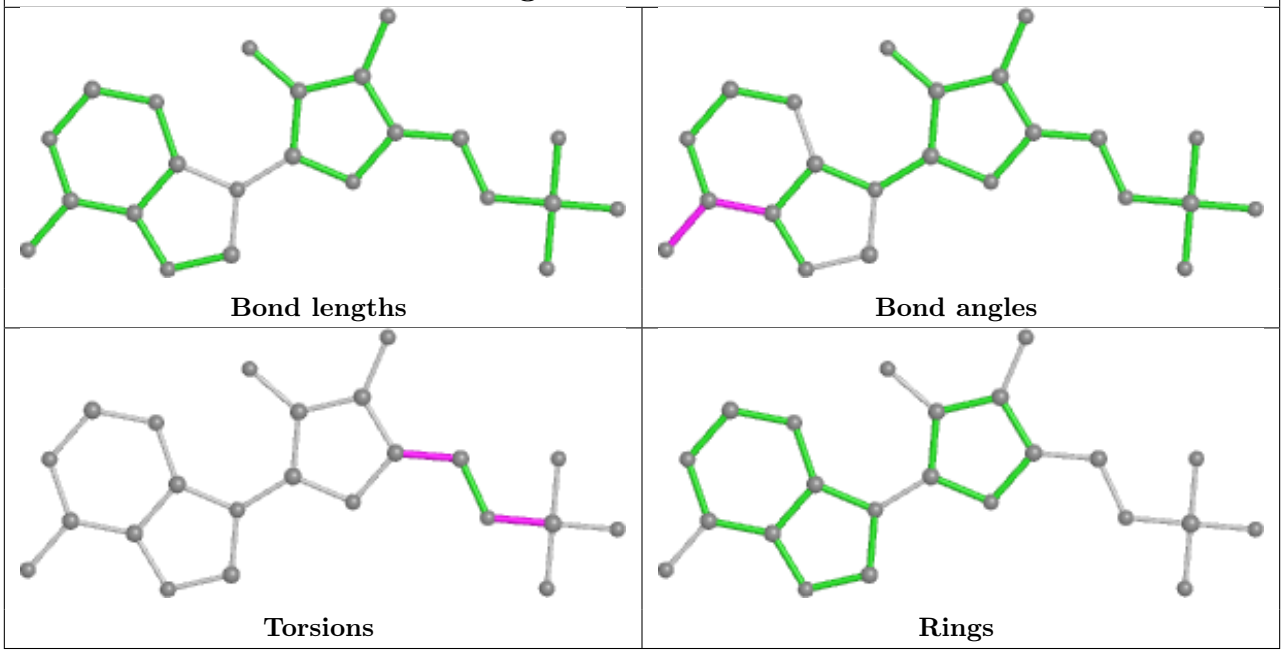
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. 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.

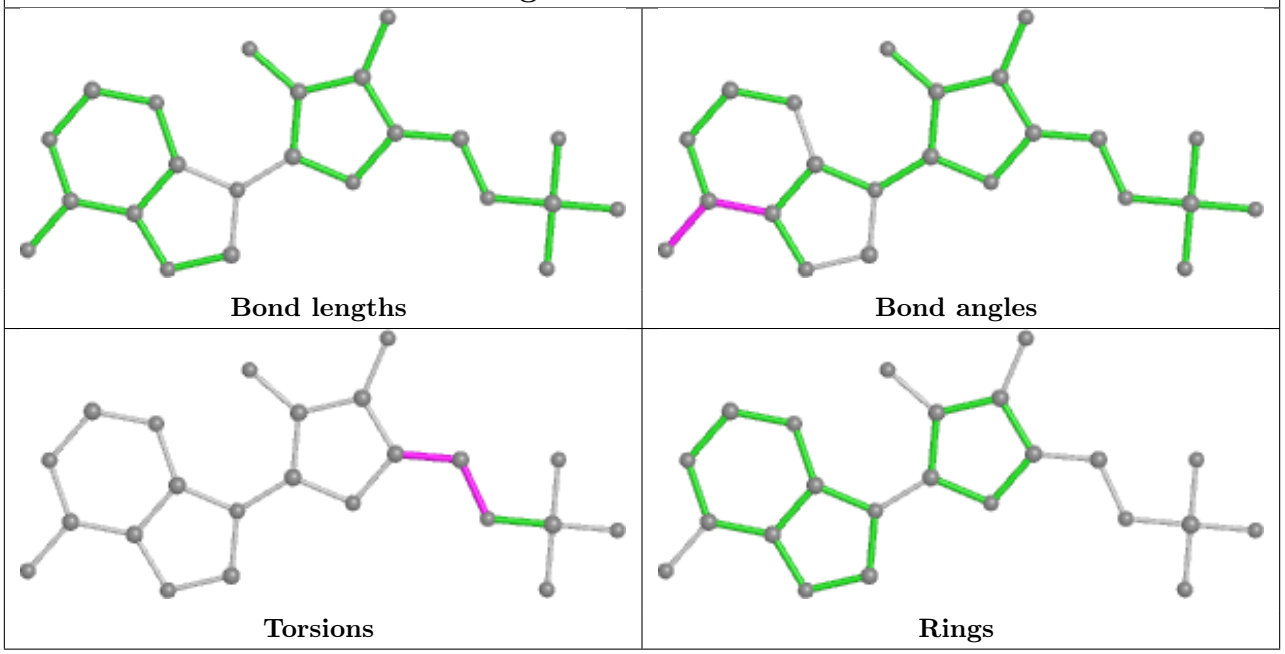
Ligand AMP B 508



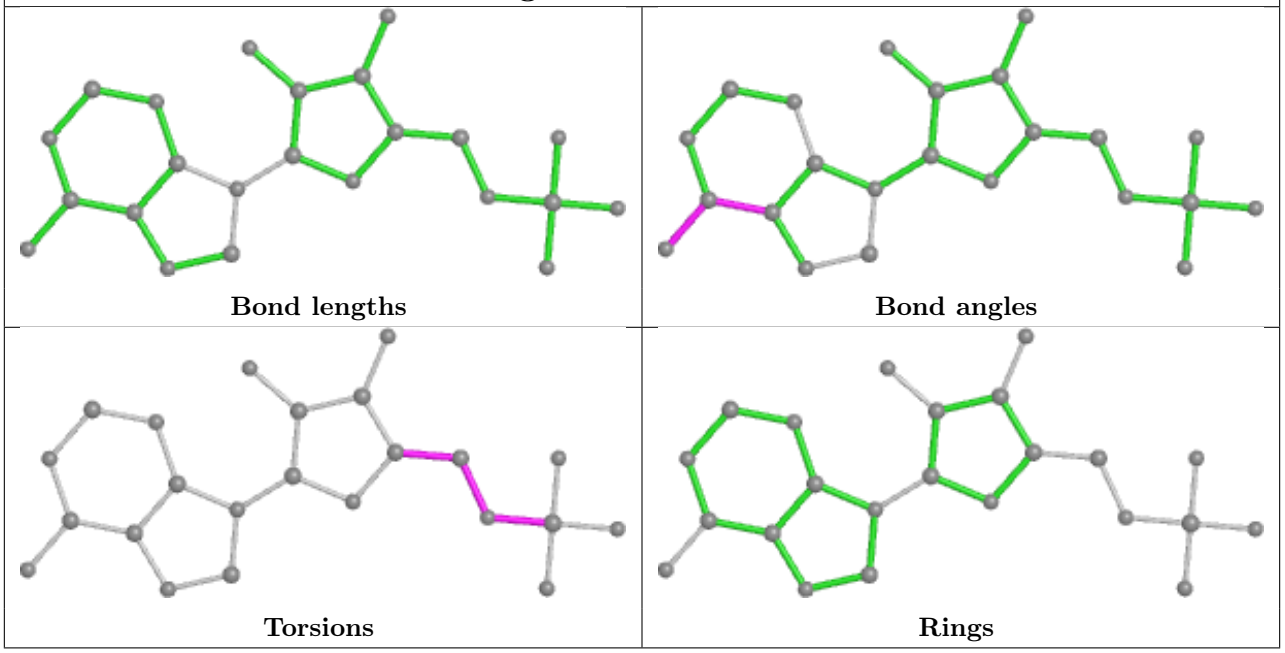
Ligand AMP D 510



Ligand AMP C 509



Ligand AMP A 507



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, 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	334/360 (92%)	0.44	29 (8%) 10 14	21, 41, 85, 100	0
1	B	327/360 (90%)	0.61	36 (11%) 5 7	23, 57, 84, 100	0
1	C	327/360 (90%)	0.53	35 (10%) 6 8	27, 53, 91, 100	0
1	D	334/360 (92%)	0.24	26 (7%) 13 17	21, 36, 82, 90	0
All	All	1322/1440 (91%)	0.45	126 (9%) 8 11	21, 47, 84, 100	0

All (126) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	79	ILE	16.2
1	A	82	PHE	10.2
1	C	412	GLN	10.1
1	A	80	PRO	10.0
1	B	86	THR	8.5
1	A	83	GLY	8.4
1	B	87	GLU	8.1
1	A	295	SER	7.4
1	A	294	SER	7.1
1	C	411	PRO	6.9
1	B	295	SER	6.9
1	C	295	SER	6.3
1	B	88	GLN	6.2
1	A	412	GLN	5.8
1	B	168	VAL	5.6
1	C	299	LEU	4.8
1	D	412	GLN	4.8
1	C	297	VAL	4.8
1	C	292	VAL	4.6
1	A	81	ARG	4.5
1	A	411	PRO	4.4

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Mol	Chain	Res	Type	RSRZ
1	C	294	SER	4.3
1	C	296	GLY	4.1
1	B	133	LYS	4.1
1	D	84	VAL	4.0
1	C	362	ASN	3.9
1	A	84	VAL	3.9
1	B	197	SER	3.9
1	A	410	ILE	3.8
1	C	287	VAL	3.8
1	A	353	GLU	3.8
1	D	362	ASN	3.8
1	D	354	ILE	3.8
1	B	92	LEU	3.7
1	C	363	ALA	3.6
1	D	87	GLU	3.5
1	D	198	ALA	3.5
1	C	301	ASP	3.5
1	B	172	THR	3.5
1	A	317	ALA	3.5
1	B	294	SER	3.5
1	A	375	TYR	3.4
1	B	193	ALA	3.4
1	A	168	VAL	3.4
1	D	342	ARG	3.4
1	B	169	VAL	3.3
1	B	196	ALA	3.3
1	A	354	ILE	3.3
1	C	356	PRO	3.3
1	B	296	GLY	3.2
1	A	352	MET	3.2
1	C	87	GLU	3.2
1	D	86	THR	3.2
1	B	90	ASP	3.2
1	C	168	VAL	3.2
1	A	363	ALA	3.1
1	B	301	ASP	3.0
1	C	293	THR	3.0
1	B	175	LEU	2.9
1	D	196	ALA	2.9
1	B	112	LEU	2.9
1	C	410	ILE	2.9
1	A	319	LEU	2.9

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Mol	Chain	Res	Type	RSRZ
1	C	285	THR	2.8
1	D	361	HIS	2.8
1	C	360	LYS	2.8
1	D	363	ALA	2.8
1	B	108	ARG	2.8
1	B	319	LEU	2.7
1	C	298	LEU	2.7
1	B	121	ILE	2.7
1	D	301	ASP	2.7
1	A	198	ALA	2.7
1	B	314	VAL	2.7
1	C	320	SER	2.7
1	B	127	GLN	2.6
1	C	166	ALA	2.6
1	A	289	THR	2.6
1	B	122	MET	2.6
1	B	136	LYS	2.6
1	B	91	VAL	2.6
1	D	314	VAL	2.6
1	B	132	LEU	2.5
1	C	198	ALA	2.5
1	A	359	ASP	2.5
1	A	298	LEU	2.5
1	B	171	SER	2.5
1	B	327	GLN	2.5
1	C	319	LEU	2.5
1	D	195	PHE	2.4
1	B	198	ALA	2.4
1	C	353	GLU	2.4
1	D	80	PRO	2.4
1	D	199	ILE	2.4
1	D	357	MET	2.4
1	D	197	SER	2.3
1	B	255	LYS	2.3
1	D	169	VAL	2.3
1	D	168	VAL	2.3
1	B	118	LEU	2.2
1	A	85	LYS	2.2
1	B	194	ILE	2.2
1	C	300	LEU	2.2
1	A	314	VAL	2.2
1	D	367	LYS	2.2

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Mol	Chain	Res	Type	RSRZ
1	C	133	LYS	2.2
1	B	298	LEU	2.2
1	C	290	LYS	2.2
1	D	194	ILE	2.2
1	C	169	VAL	2.1
1	A	299	LEU	2.1
1	A	197	SER	2.1
1	D	216	ASN	2.1
1	A	362	ASN	2.1
1	B	253	THR	2.1
1	D	353	GLU	2.1
1	C	381	TRP	2.1
1	C	165	ALA	2.1
1	B	251	ASN	2.1
1	C	317	ALA	2.1
1	C	316	CYS	2.1
1	C	387	LEU	2.0
1	D	348	ARG	2.0
1	C	291	LYS	2.0
1	A	194	ILE	2.0
1	D	193	ALA	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	ZN	A	502	1/1	0.90	0.06	63,63,63,63	0
3	AMP	B	508	23/23	0.93	0.15	49,56,66,66	0

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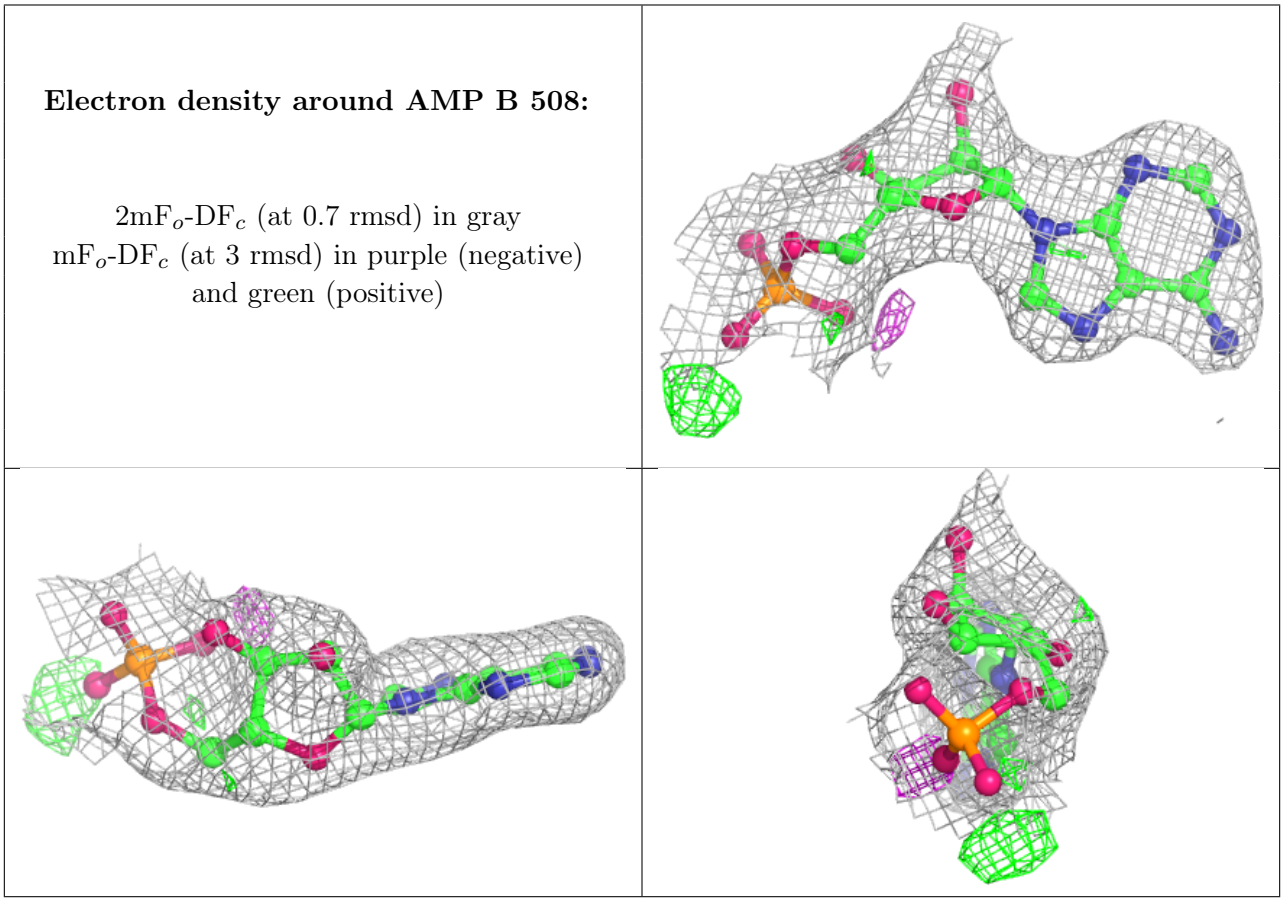
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
3	AMP	C	509	23/23	0.94	0.16	57,58,60,61	0
3	AMP	A	507	23/23	0.95	0.17	48,53,57,58	0
3	AMP	D	510	23/23	0.95	0.11	49,54,62,63	0
2	ZN	C	502	1/1	0.96	0.08	67,67,67,67	0
2	ZN	D	501	1/1	0.98	0.13	38,38,38,38	0
2	ZN	D	502	1/1	0.98	0.02	63,63,63,63	0
2	ZN	B	502	1/1	0.98	0.05	68,68,68,68	0
2	ZN	A	501	1/1	0.99	0.13	37,37,37,37	0
2	ZN	C	501	1/1	0.99	0.10	44,44,44,44	0
2	ZN	B	501	1/1	0.99	0.13	47,47,47,47	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.

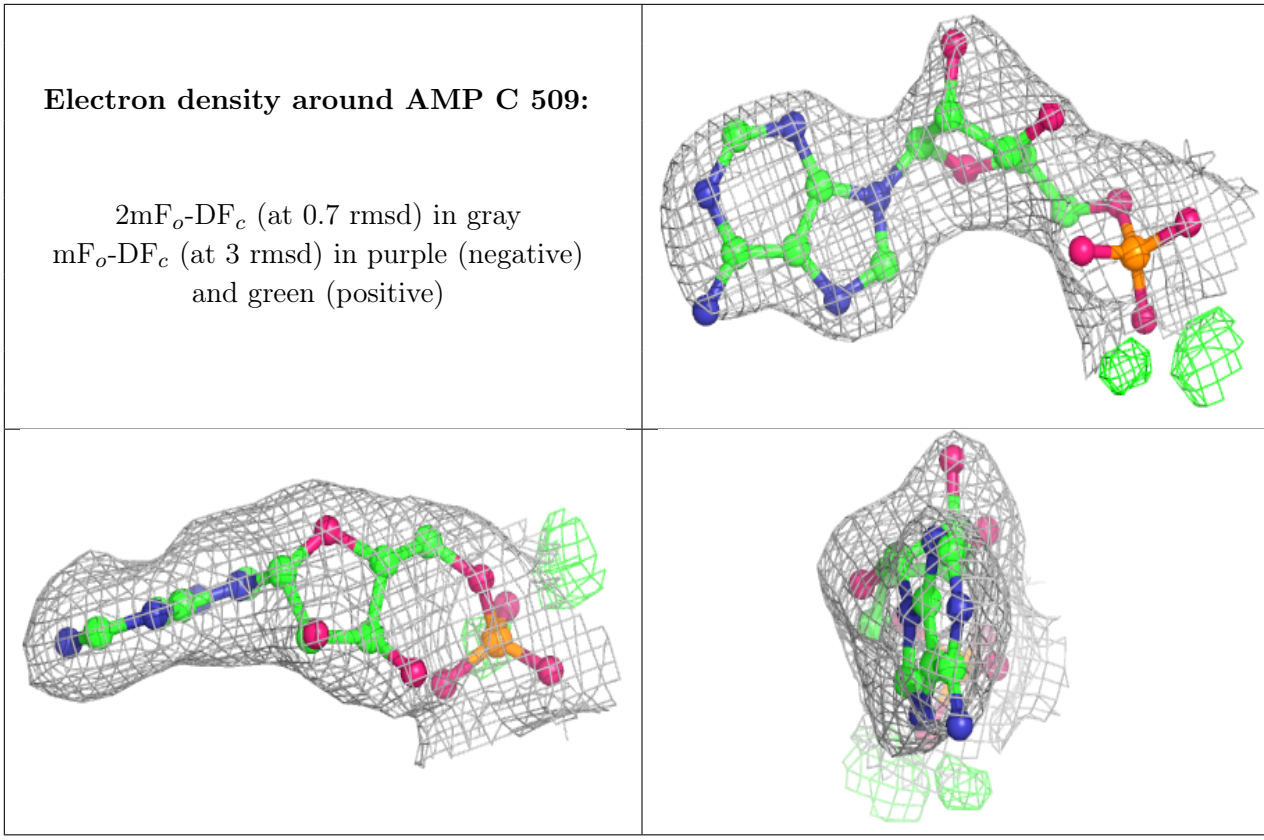
Electron density around AMP B 508:

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



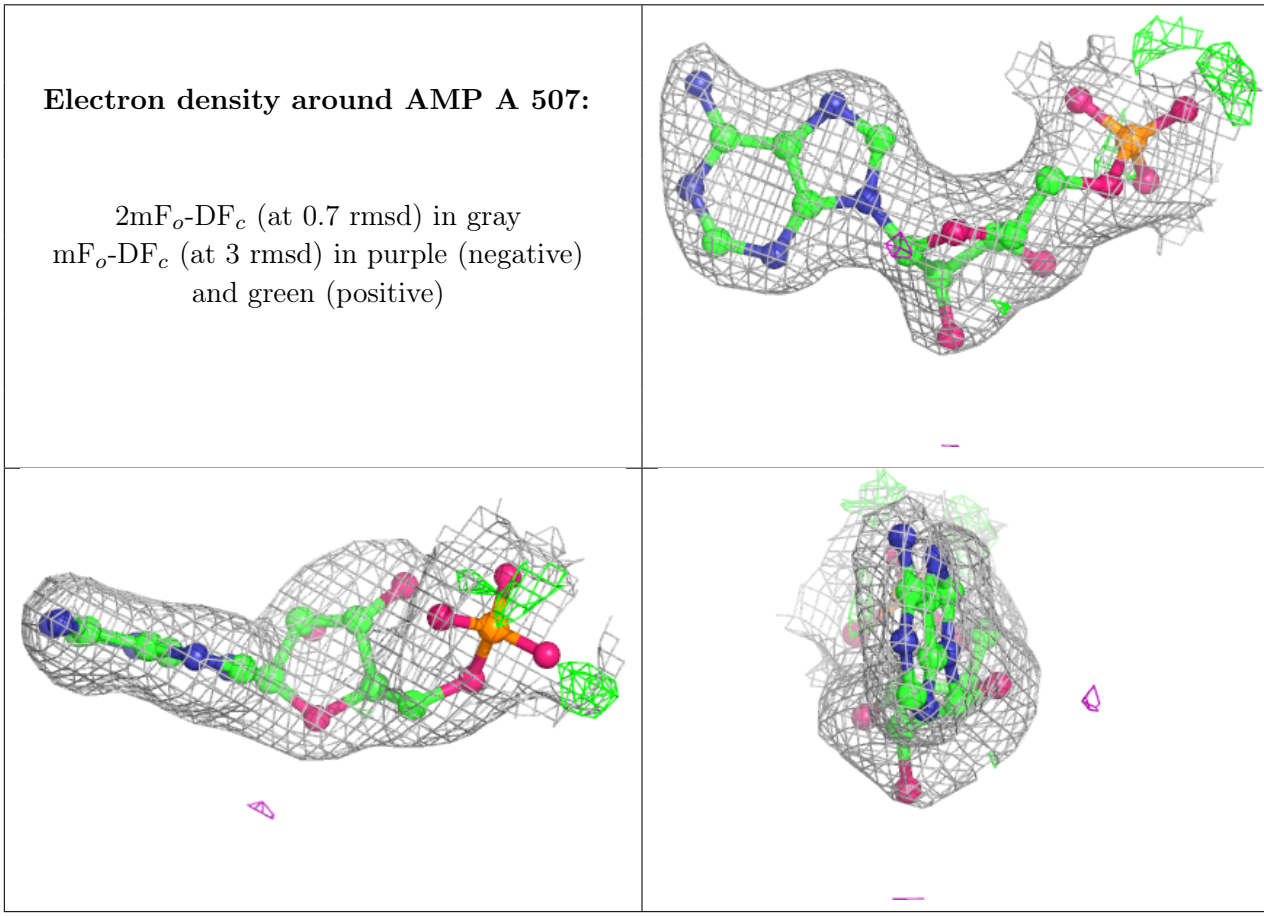
Electron density around AMP C 509:

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



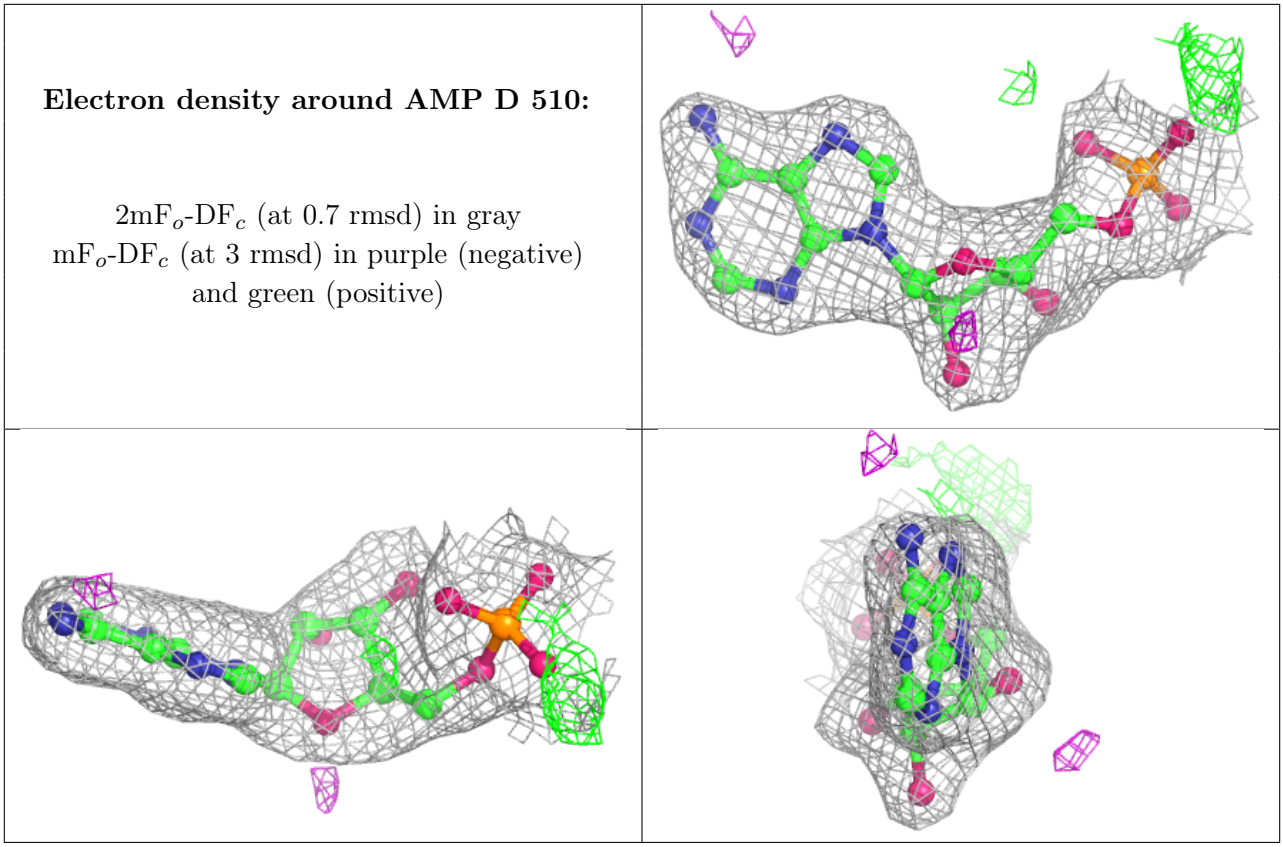
Electron density around AMP A 507:

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



Electron density around AMP D 510:

$2mF_o$-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.