Full wwPDB X-ray Structure Validation Report ⓘ

Aug 21, 2020 – 12:30 PM BST

PDB ID	:	4NIF
Title	:	Heterodimeric structure of ERK2 and RSK1
Authors	:	Gogl, G.; Remenyi, A.
Deposited on	:	2013-11-06
Resolution	:	2.15 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:

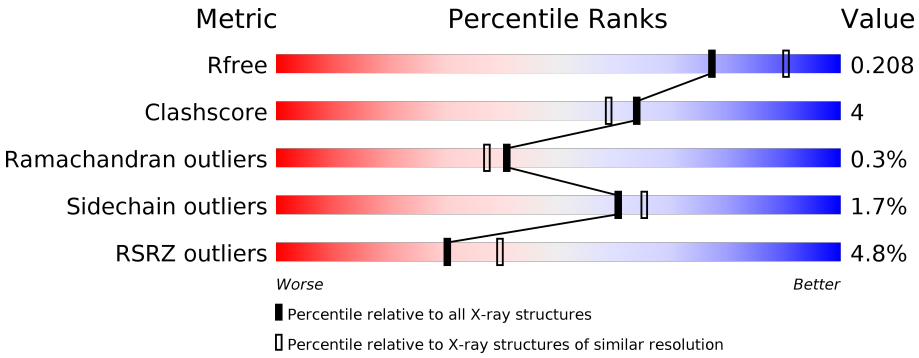
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.13.1
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & 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 2.15 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	1479 (2.16-2.16)
Clashscore	141614	1585 (2.16-2.16)
Ramachandran outliers	138981	1560 (2.16-2.16)
Sidechain outliers	138945	1559 (2.16-2.16)
RSRZ outliers	127900	1456 (2.16-2.16)

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	333	5% 83% 10% • 6%
1	D	333	9% 82% 11% • 6%
2	B	362	3% 87% 9% •
2	E	362	2% 87% 8% • •

2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 11667 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 Ribosomal protein S6 kinase alpha-1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	313	Total	C	N	O	S	0	3	0
			2450	1552	421	464	13			
1	D	313	Total	C	N	O	S	0	2	0
			2455	1558	420	464	13			

There are 16 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	409	GLY	-	EXPRESSION TAG	UNP Q15418
A	410	SER	-	EXPRESSION TAG	UNP Q15418
A	736	HIS	-	EXPRESSION TAG	UNP Q15418
A	737	HIS	-	EXPRESSION TAG	UNP Q15418
A	738	HIS	-	EXPRESSION TAG	UNP Q15418
A	739	HIS	-	EXPRESSION TAG	UNP Q15418
A	740	HIS	-	EXPRESSION TAG	UNP Q15418
A	741	HIS	-	EXPRESSION TAG	UNP Q15418
D	409	GLY	-	EXPRESSION TAG	UNP Q15418
D	410	SER	-	EXPRESSION TAG	UNP Q15418
D	736	HIS	-	EXPRESSION TAG	UNP Q15418
D	737	HIS	-	EXPRESSION TAG	UNP Q15418
D	738	HIS	-	EXPRESSION TAG	UNP Q15418
D	739	HIS	-	EXPRESSION TAG	UNP Q15418
D	740	HIS	-	EXPRESSION TAG	UNP Q15418
D	741	HIS	-	EXPRESSION TAG	UNP Q15418

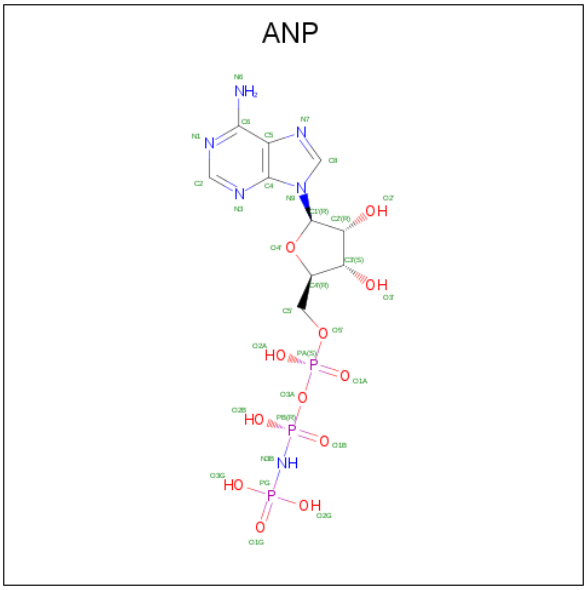
- Molecule 2 is a protein called Mitogen-activated protein kinase 1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	349	Total	C	N	O	S	0	4	0
			2838	1819	484	519	16			
2	E	348	Total	C	N	O	S	0	3	0
			2839	1819	483	521	16			

There are 4 discrepancies between the modelled and reference sequences:

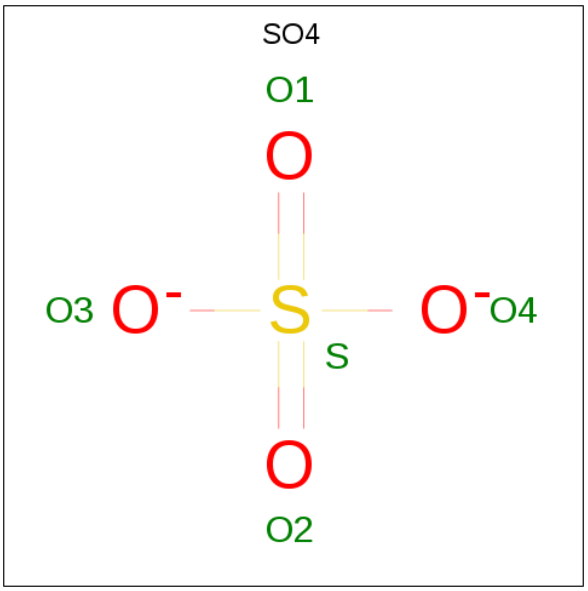
Chain	Residue	Modelled	Actual	Comment	Reference
B	-1	GLY	-	EXPRESSION TAG	UNP P28482
B	0	SER	-	EXPRESSION TAG	UNP P28482
E	-1	GLY	-	EXPRESSION TAG	UNP P28482
E	0	SER	-	EXPRESSION TAG	UNP P28482

- Molecule 3 is PHOSPHOAMINOPHOSPHONIC ACID-ADENYLATE ESTER (three-letter code: ANP) (formula: $C_{10}H_{17}N_6O_{12}P_3$).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
3	B	1	Total	C	N	O	P	0	0
			31	10	6	12	3		
3	E	1	Total	C	N	O	P	0	0
			31	10	6	12	3		

- Molecule 4 is SULFATE ION (three-letter code: SO4) (formula: O_4S).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	B	1	Total O S 5 4 1	0	0
4	B	1	Total O S 5 4 1	0	0
4	E	1	Total O S 5 4 1	0	0

- Molecule 5 is SODIUM ION (three-letter code: NA) (formula: Na).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	B	1	Total Na 1 1	0	0
5	E	1	Total Na 1 1	0	0

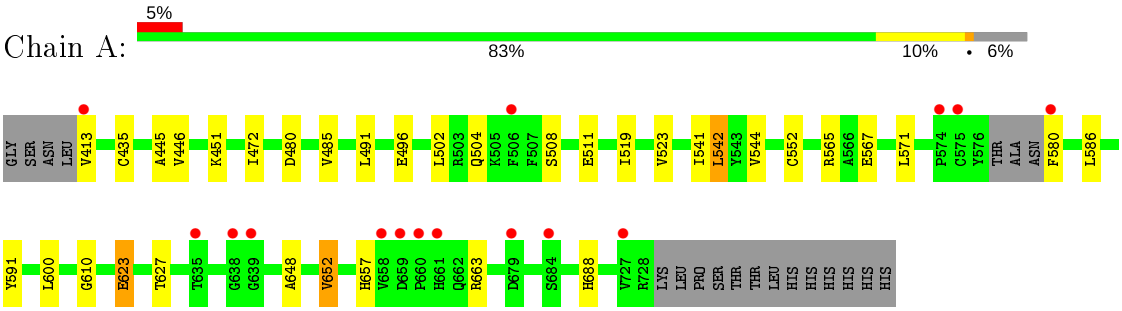
- Molecule 6 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
6	A	165	Total O 165 165	0	0
6	B	344	Total O 344 344	0	0
6	D	174	Total O 174 174	0	0
6	E	323	Total O 323 323	0	0

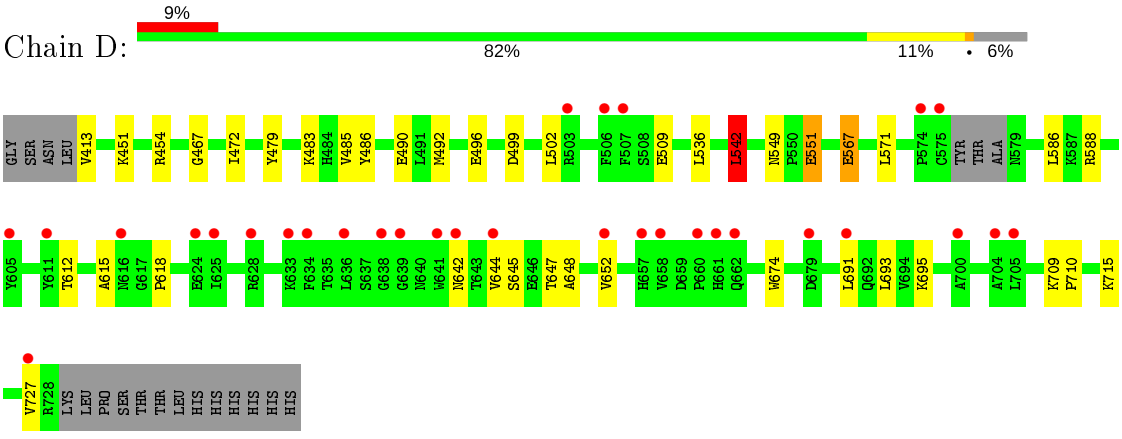
3 Residue-property plots (i)

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.

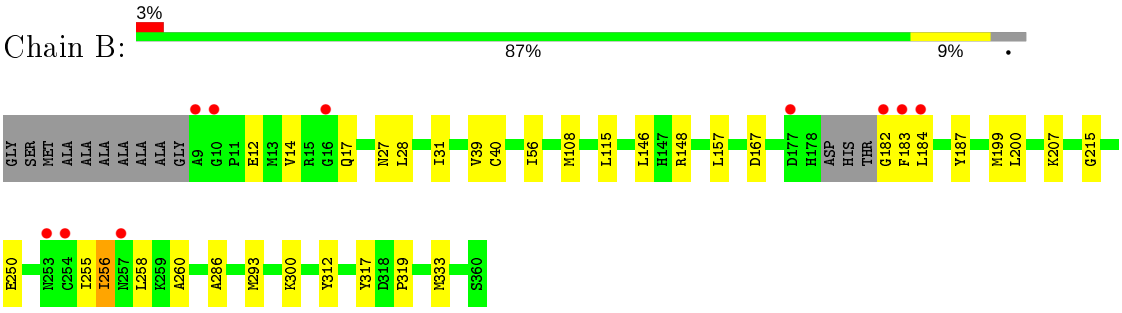
- Molecule 1: Ribosomal protein S6 kinase alpha-1



- Molecule 1: Ribosomal protein S6 kinase alpha-1

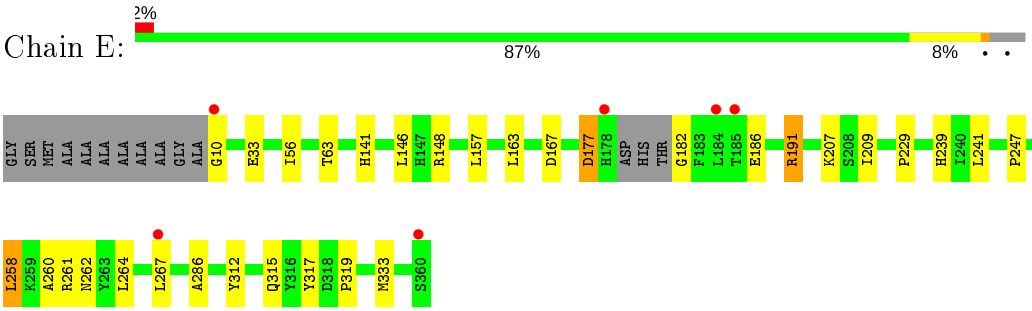


- Molecule 2: Mitogen-activated protein kinase 1



- Molecule 2: Mitogen-activated protein kinase 1

Chain E:


2%
87%
8%
GLY SER MET ALA ALA ALA ALA ALA GLY ALA G10 E33 I56 T63 H141 L146 H147 R148 L157 L163 D167 D177 H178 ASP HIS THR G182 F183 L184 T185 E186 R191 K207 S208 I209 P229 H239 I240 L241 P247 C254 I255 I256 N257
L258 K259 A260 R261 N262 Y263 L264 L267 A286 Y312 Q315 Y316 Y317 D318 P319 M333 S360

4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α, β, γ	93.49Å 87.85Å 116.54Å 90.00° 108.22° 90.00°	Depositor
Resolution (Å)	60.63 – 2.15 68.81 – 2.15	Depositor EDS
% Data completeness (in resolution range)	99.8 (60.63-2.15) 94.8 (68.81-2.15)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	3.03 (at 2.14Å)	Xtriage
Refinement program	PHENIX (phenix.refine: dev_1439)	Depositor
R, R_{free}	0.158 , 0.208 0.162 , 0.208	Depositor DCC
R_{free} test set	4860 reflections (4.99%)	wwPDB-VP
Wilson B-factor (Å^2)	30.8	Xtriage
Anisotropy	0.385	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.36 , 60.4	EDS
L-test for twinning[2]	$< \|L\| > = 0.48$, $< L^2 > = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.96	EDS
Total number of atoms	11667	wwPDB-VP
Average B, all atoms (Å^2)	46.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.70% 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: NA, ANP, 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	0.35	0/2499	0.49	0/3387
1	D	0.33	0/2504	0.50	1/3390 (0.0%)
2	B	0.40	0/2908	0.51	0/3942
2	E	0.37	0/2906	0.51	1/3938 (0.0%)
All	All	0.37	0/10817	0.50	2/14657 (0.0%)

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	D	542	LEU	CA-CB-CG	5.95	128.97	115.30
2	E	191	ARG	NE-CZ-NH2	-5.53	117.54	120.30

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	2450	0	2418	21	0
1	D	2455	0	2442	25	0
2	B	2838	0	2790	20	0
2	E	2839	0	2799	23	0
3	B	31	0	13	2	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	E	31	0	13	1	0
4	B	10	0	0	0	0
4	E	5	0	0	1	0
5	B	1	0	0	0	0
5	E	1	0	0	0	0
6	A	165	0	0	5	0
6	B	344	0	0	3	0
6	D	174	0	0	5	0
6	E	323	0	0	5	0
All	All	11667	0	10475	88	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 4.

All (88) 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)
2:E:260:ALA:O	6:E:786:HOH:O	1.96	0.80
2:E:177:ASP:OD1	2:E:177:ASP:N	2.18	0.76
2:E:255:ILE:O	2:E:261:ARG:NH2	2.18	0.68
2:B:17:GLN:NE2	6:B:703:HOH:O	2.29	0.64
2:E:10:GLY:N	6:E:705:HOH:O	2.30	0.64
2:E:264:LEU:HA	2:E:267:LEU:HD12	1.83	0.60
1:A:519:ILE:HD13	1:A:541:ILE:HD13	1.82	0.59
1:D:647:THR:HG23	1:D:674:TRP:HD1	1.69	0.58
1:D:642:ASN:N	6:D:951:HOH:O	2.17	0.57
1:D:472:ILE:O	6:D:801:HOH:O	2.17	0.56
1:D:549:ASN:OD1	1:D:551:GLU:HG2	2.06	0.56
2:B:317:TYR:CZ	2:B:319:PRO:HG3	2.42	0.55
2:B:215:GLY:HA2	2:B:293:MET:HE3	1.89	0.54
2:E:229:PRO:O	2:E:239:HIS:ND1	2.37	0.53
2:B:148:ARG:HB3	2:B:183:PHE:HZ	1.72	0.53
2:B:250:GLU:OE1	2:B:300:LYS:NZ	2.42	0.53
1:A:504:GLN:NE2	1:A:511:GLU:OE1	2.41	0.53
2:E:157:LEU:HD21	2:E:163:LEU:HD12	1.90	0.53
1:A:502:LEU:O	1:A:688:HIS:NE2	2.42	0.52
2:B:255:ILE:HG22	2:B:256:ILE:O	2.09	0.52
1:A:435[B]:CYS:SG	1:A:446:VAL:HG23	2.50	0.52
1:D:612:THR:HG22	1:D:615:ALA:H	1.74	0.51
2:E:10:GLY:N	6:E:793:HOH:O	2.44	0.51
2:E:317:TYR:CZ	2:E:319:PRO:HG3	2.45	0.51

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:E:191:ARG:NH2	4:E:402:SO4:O2	2.34	0.50
1:A:472:ILE:O	6:A:872:HOH:O	2.19	0.50
1:D:467:GLY:O	6:D:801:HOH:O	2.19	0.50
1:D:567:GLU:HG3	6:D:922:HOH:O	2.12	0.50
2:B:148:ARG:HB3	2:B:183:PHE:CZ	2.47	0.49
1:D:588:ARG:NE	6:D:901:HOH:O	2.45	0.48
1:A:413:VAL:N	6:A:905:HOH:O	2.46	0.48
1:A:657:HIS:O	1:A:663:ARG:NH2	2.44	0.48
1:D:499:ASP:OD2	1:D:695:LYS:HD2	2.14	0.48
1:A:544:VAL:HG12	1:A:552:CYS:HB3	1.96	0.47
2:B:12:GLU:HB2	2:B:28:LEU:HD22	1.97	0.47
1:A:565:ARG:NH2	6:A:885:HOH:O	2.45	0.47
1:D:451:LYS:HG3	1:D:483:LYS:O	2.15	0.47
1:A:591:TYR:OH	6:A:891:HOH:O	2.21	0.46
2:E:33:GLU:OE2	6:E:741:HOH:O	2.20	0.46
1:A:610:GLY:HA3	1:A:688:HIS:HA	1.98	0.46
1:A:508:SER:OG	6:A:958:HOH:O	2.20	0.46
2:E:286:ALA:HB2	2:E:312:TYR:CE1	2.51	0.46
2:E:258:LEU:O	2:E:262:ASN:N	2.38	0.45
2:E:146:LEU:HD22	2:E:207:LYS:HA	1.99	0.45
1:A:445:ALA:HB2	1:A:491:LEU:HD23	1.99	0.45
1:D:648:ALA:HB2	1:D:674:TRP:NE1	2.31	0.45
1:A:623:GLU:O	1:A:627:THR:HG23	2.17	0.45
1:D:648:ALA:O	1:D:652:VAL:HG23	2.16	0.45
2:E:255:ILE:HG22	2:E:256:ILE:O	2.17	0.45
1:D:645:SER:HB3	1:D:647:THR:HG22	1.99	0.45
1:D:647:THR:HG23	1:D:674:TRP:CD1	2.51	0.44
2:B:286:ALA:HB2	2:B:312:TYR:CE1	2.52	0.44
1:A:567:GLU:HB2	2:B:187:TYR:HA	2.00	0.44
2:B:115:LEU:HD22	2:B:157:LEU:HD13	1.99	0.44
2:B:199:MET:HE1	6:B:523:HOH:O	2.18	0.43
2:B:167:ASP:OD2	3:B:401:ANP:O1G	2.36	0.43
1:A:451:LYS:HD3	1:A:485:VAL:HG23	2.00	0.43
1:A:523:VAL:HG21	1:A:600:LEU:HD11	2.01	0.43
2:B:200:LEU:HD22	2:B:260:ALA:HB1	2.00	0.43
2:E:264:LEU:N	6:E:786:HOH:O	2.11	0.43
1:A:451:LYS:NZ	1:A:480:ASP:OD2	2.40	0.43
1:D:618:PRO:HD2	1:D:693:LEU:HD12	2.02	0.42
2:B:14:VAL:HG21	2:B:40[A]:CYS:SG	2.59	0.42
2:E:63:THR:HB	2:E:186:GLU:OE2	2.18	0.42
1:D:509:GLU:OE2	1:D:644:VAL:HA	2.19	0.42

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:146:LEU:HD22	2:B:207:LYS:HA	2.00	0.42
1:D:451:LYS:HE3	1:D:485:VAL:HG23	2.01	0.42
1:A:496:GLU:HA	1:A:542:LEU:HD13	2.02	0.42
2:B:148:ARG:HH22	2:B:182:GLY:HA3	1.85	0.42
2:E:141:HIS:CE1	2:E:207:LYS:HB3	2.55	0.41
2:E:167:ASP:OD2	3:E:401:ANP:O3G	2.38	0.41
1:D:479:TYR:HB2	1:D:486:TYR:HB2	2.02	0.41
2:E:241:LEU:HD11	2:E:264:LEU:HD22	2.03	0.41
1:D:502:LEU:HB2	1:D:691:LEU:HD13	2.03	0.41
1:D:709:LYS:HA	1:D:710:PRO:HD2	1.92	0.41
2:B:27:ASN:HB2	6:B:811:HOH:O	2.21	0.41
2:B:31:ILE:HD11	2:B:39:VAL:HG12	2.01	0.41
1:D:451:LYS:HA	1:D:454:ARG:O	2.20	0.41
2:E:182:GLY:O	2:E:186:GLU:HG3	2.21	0.41
1:D:490:GLU:HB2	1:D:492:MET:CE	2.50	0.41
1:A:648:ALA:O	1:A:652:VAL:HG22	2.21	0.41
1:D:496:GLU:HA	1:D:542:LEU:HD13	2.02	0.41
2:B:108:MET:O	3:B:401:ANP:H2	2.21	0.40
1:D:586:LEU:HD23	1:D:586:LEU:HA	1.90	0.40
2:E:241:LEU:HD22	2:E:247:PRO:HD3	2.02	0.40
2:E:148:ARG:HG2	2:E:209:ILE:HD11	2.04	0.40
1:A:586:LEU:HA	1:A:586:LEU:HD23	1.92	0.40
1:D:536:LEU:HA	1:D:536:LEU:HD12	1.93	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	312/333 (94%)	303 (97%)	9 (3%)	0	100	100
1	D	311/333 (93%)	304 (98%)	7 (2%)	0	100	100

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
2	B	349/362 (96%)	334 (96%)	12 (3%)	3 (1%)	17 11
2	E	347/362 (96%)	332 (96%)	14 (4%)	1 (0%)	41 37
All	All	1319/1390 (95%)	1273 (96%)	42 (3%)	4 (0%)	41 37

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	B	258	LEU
2	B	184	LEU
2	E	256	ILE
2	B	256	ILE

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	268/294 (91%)	263 (98%)	5 (2%)	57 61
1	D	270/294 (92%)	263 (97%)	7 (3%)	46 47
2	B	307/319 (96%)	305 (99%)	2 (1%)	84 89
2	E	310/319 (97%)	305 (98%)	5 (2%)	62 67
All	All	1155/1226 (94%)	1136 (98%)	19 (2%)	60 67

All (19) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	542	LEU
1	A	571	LEU
1	A	580	PHE
1	A	623	GLU
1	A	652	VAL
2	B	56	ILE
2	B	333	MET
1	D	413	VAL

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	D	542	LEU
1	D	551	GLU
1	D	567	GLU
1	D	571	LEU
1	D	715	LYS
1	D	727	VAL
2	E	56	ILE
2	E	177	ASP
2	E	258	LEU
2	E	315	GLN
2	E	333	MET

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (1) such sidechains are listed below:

Mol	Chain	Res	Type
2	B	249	GLN

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 7 ligands modelled in this entry, 2 are monoatomic - leaving 5 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	$\#\|Z\|>2$
4	SO4	B	403	-	4,4,4	0.20	0	6,6,6	0.11	0
3	ANP	B	401	-	29,33,33	2.87	6 (20%)	31,52,52	2.37	6 (19%)
3	ANP	E	401	-	29,33,33	2.44	7 (24%)	31,52,52	1.46	5 (16%)
4	SO4	B	402	-	4,4,4	0.17	0	6,6,6	0.34	0
4	SO4	E	402	-	4,4,4	0.16	0	6,6,6	0.31	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
3	ANP	B	401	-	-	1/14/38/38	0/3/3/3
3	ANP	E	401	-	-	1/14/38/38	0/3/3/3

All (13) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	B	401	ANP	PG-O1G	9.42	1.61	1.46
3	E	401	ANP	PB-O1B	7.88	1.58	1.46
3	B	401	ANP	PB-O1B	7.48	1.58	1.46
3	B	401	ANP	PB-N3B	4.71	1.75	1.63
3	B	401	ANP	C2'-C1'	-4.70	1.46	1.53
3	E	401	ANP	C2'-C1'	-4.69	1.46	1.53
3	E	401	ANP	PB-N3B	4.65	1.75	1.63
3	E	401	ANP	C2'-C3'	-3.90	1.42	1.53
3	E	401	ANP	PG-O1G	3.67	1.52	1.46
3	B	401	ANP	C2'-C3'	-3.60	1.43	1.53
3	E	401	ANP	C6-N6	3.11	1.45	1.34
3	B	401	ANP	C6-N6	2.83	1.44	1.34
3	E	401	ANP	O4'-C4'	-2.28	1.39	1.45

All (11) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
3	B	401	ANP	O1G-PG-N3B	-8.41	99.39	111.77
3	B	401	ANP	O1B-PB-N3B	-5.86	103.13	111.77
3	E	401	ANP	N3-C2-N1	-4.46	121.70	128.68
3	B	401	ANP	N3-C2-N1	-4.08	122.31	128.68
3	B	401	ANP	O2B-PB-O1B	3.75	117.78	109.92
3	E	401	ANP	O2B-PB-O1B	3.25	116.74	109.92
3	B	401	ANP	O2B-PB-O3A	2.80	114.00	104.64

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
3	B	401	ANP	O5'-C5'-C4'	2.52	117.65	108.99
3	E	401	ANP	O2B-PB-O3A	-2.43	96.52	104.64
3	E	401	ANP	C4-C5-N7	-2.07	107.24	109.40
3	E	401	ANP	O5'-C5'-C4'	2.06	116.09	108.99

There are no chirality outliers.

All (2) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	B	401	ANP	PG-N3B-PB-O1B
3	E	401	ANP	PB-N3B-PG-O1G

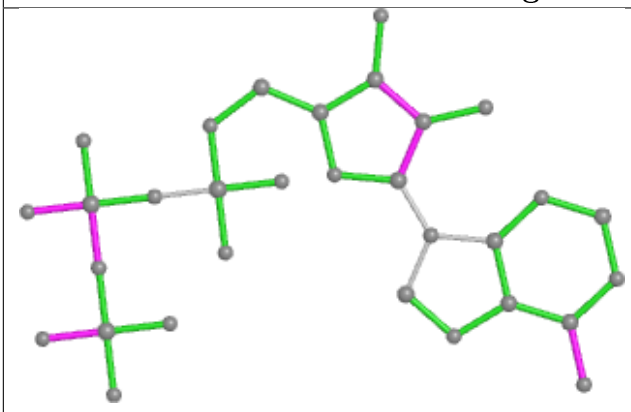
There are no ring outliers.

3 monomers are involved in 4 short contacts:

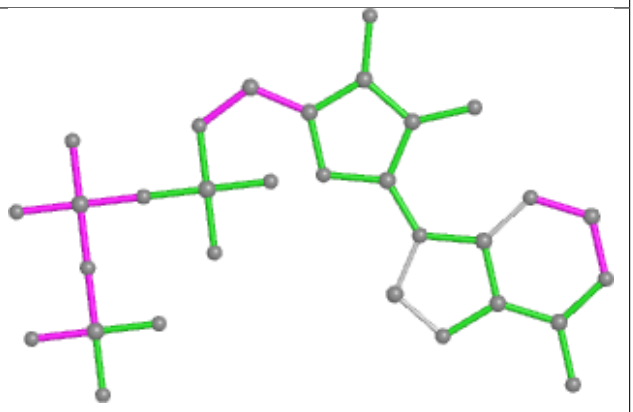
Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	B	401	ANP	2	0
3	E	401	ANP	1	0
4	E	402	SO4	1	0

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.

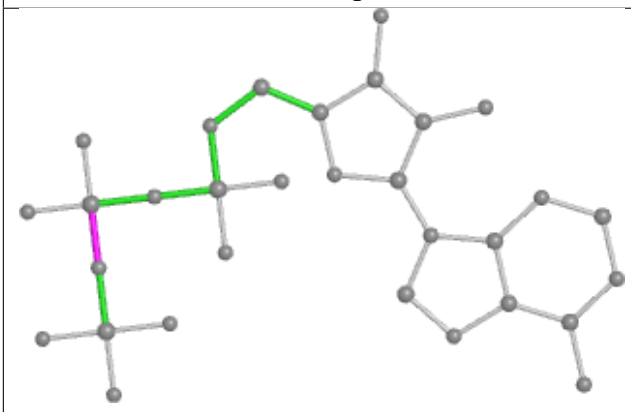
Ligand ANP B 401



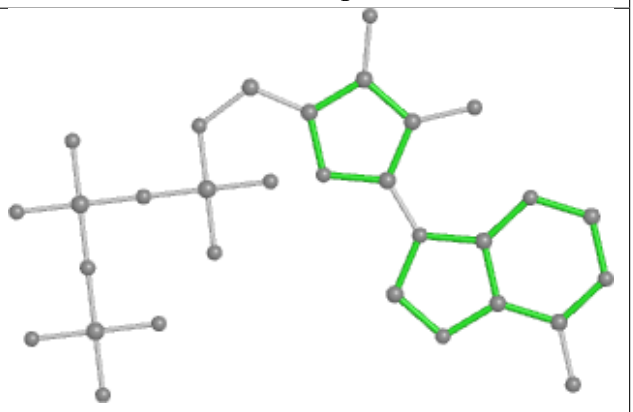
Bond lengths



Bond angles

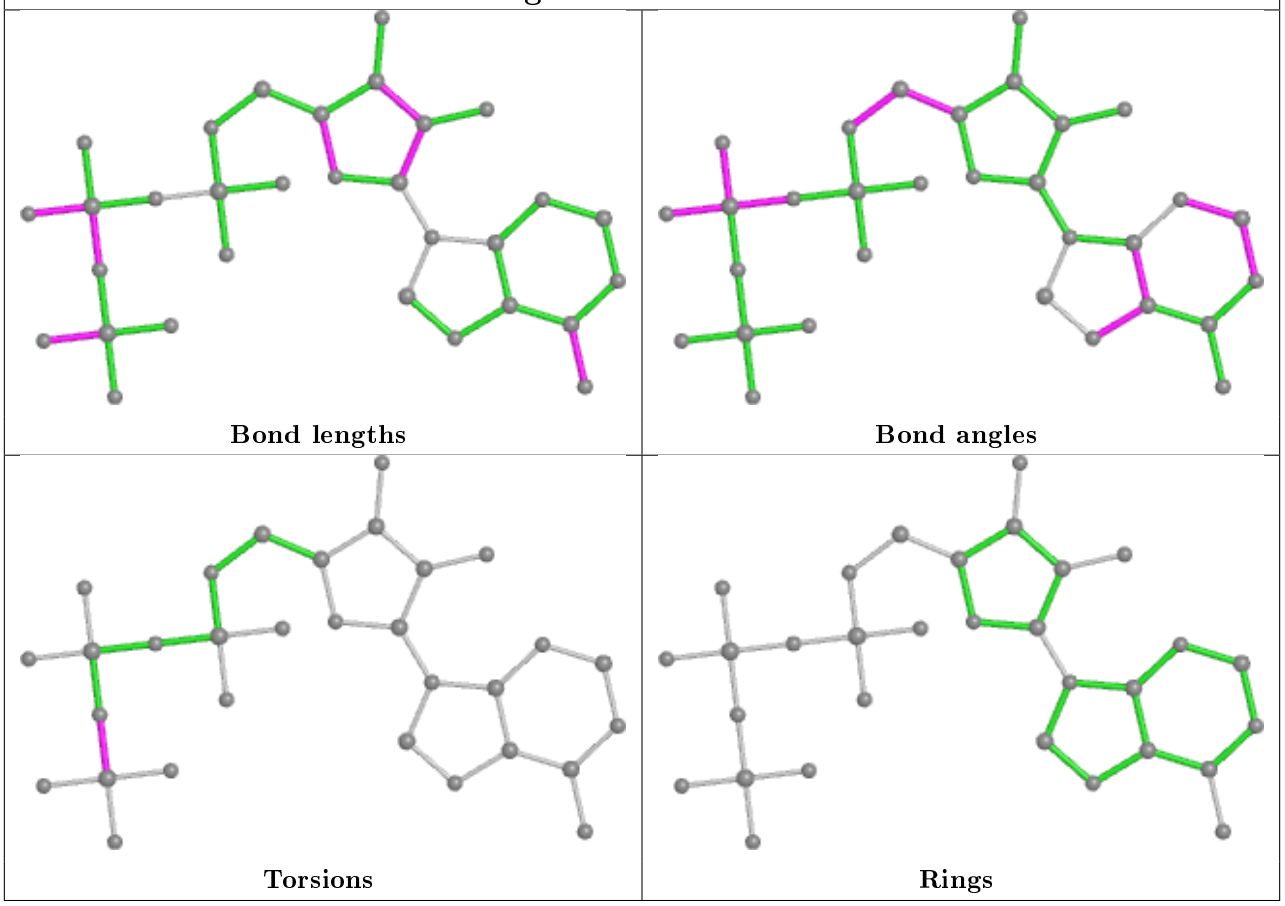


Torsions



Rings

Ligand ANP E 401



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	313/333 (93%)	0.28	15 (4%) 30 39	23, 48, 80, 109	1 (0%)
1	D	313/333 (93%)	0.47	31 (9%) 7 11	23, 49, 87, 122	0
2	B	349/362 (96%)	0.14	10 (2%) 51 61	21, 36, 79, 117	0
2	E	348/362 (96%)	0.15	8 (2%) 60 68	23, 37, 84, 124	0
All	All	1323/1390 (95%)	0.26	64 (4%) 30 39	21, 41, 85, 124	1 (0%)

All (64) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	B	10	GLY	7.5
2	B	9	ALA	7.4
2	E	10	GLY	4.7
1	D	661	HIS	4.7
1	A	575	CYS	4.1
1	D	658	VAL	3.9
1	A	661	HIS	3.8
1	D	641	TRP	3.8
1	D	638	GLY	3.6
1	A	658	VAL	3.5
1	D	625	ILE	3.4
1	A	506	PHE	3.4
2	E	184	LEU	3.4
2	B	182	GLY	3.4
1	D	660	PRO	3.3
2	B	253	ASN	3.3
2	B	16	GLY	3.2
1	D	507	PHE	3.2
1	A	639	GLY	3.1
2	E	178	HIS	3.1
1	A	638	GLY	3.0

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
2	E	185	THR	3.0
1	D	624	GLU	3.0
2	B	254	CYS	3.0
1	A	660	PRO	2.8
1	D	652	VAL	2.8
1	A	580	PHE	2.8
1	D	657	HIS	2.8
1	D	700	ALA	2.7
2	B	257	ASN	2.7
2	B	183	PHE	2.6
2	E	267	LEU	2.6
1	D	575	CYS	2.6
1	A	574	PRO	2.5
1	D	639	GLY	2.5
2	B	184	LEU	2.4
1	D	704	ALA	2.4
1	A	679	ASP	2.4
1	D	636	LEU	2.4
1	D	727	VAL	2.4
1	D	506	PHE	2.4
1	A	413	VAL	2.4
1	A	727	VAL	2.4
1	D	634	PHE	2.3
2	E	360	SER	2.3
1	A	635	THR	2.3
1	D	628	ARG	2.3
1	D	616	ASN	2.3
1	D	642	ASN	2.3
1	D	679	ASP	2.2
1	D	633	LYS	2.2
1	A	659	ASP	2.2
1	D	503	ARG	2.2
1	D	705	LEU	2.2
1	D	605	TYR	2.2
2	B	177	ASP	2.2
1	D	574	PRO	2.2
1	D	662	GLN	2.2
1	D	691	LEU	2.1
1	D	644	VAL	2.1
1	D	611	TYR	2.1
2	E	254	CYS	2.1
1	A	684	SER	2.1

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
2	E	257	ASN	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)

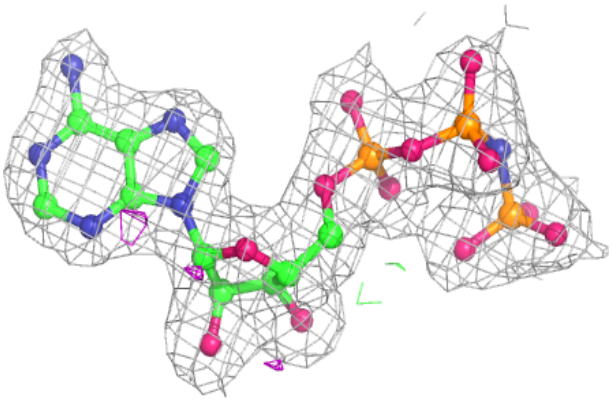
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95^{th} percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9'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

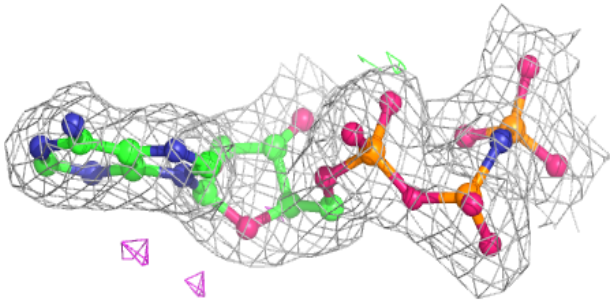
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
4	SO4	B	403	5/5	0.88	0.16	70,71,77,84	0
4	SO4	B	402	5/5	0.99	0.14	30,31,34,34	0
3	ANP	E	401	31/31	0.99	0.13	21,27,32,36	0
3	ANP	B	401	31/31	0.99	0.13	19,25,29,29	0
4	SO4	E	402	5/5	0.99	0.14	31,31,34,35	0
5	NA	E	403	1/1	1.00	0.25	20,20,20,20	0
5	NA	B	404	1/1	1.00	0.26	18,18,18,18	0

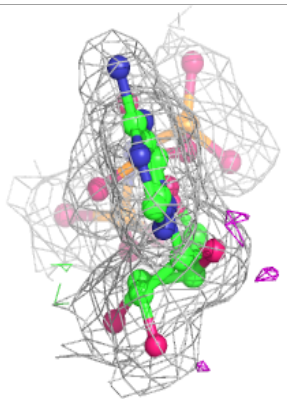
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation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

Electron density around ANP E 401:

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

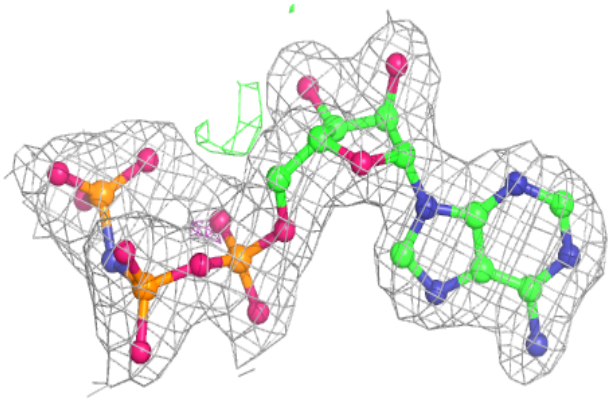


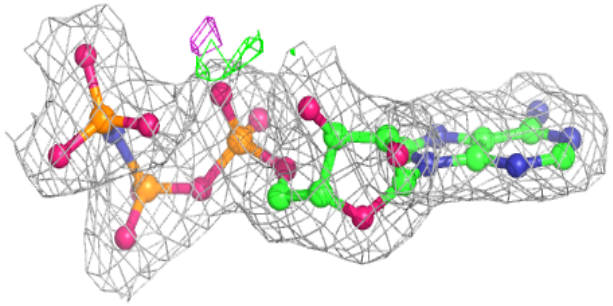


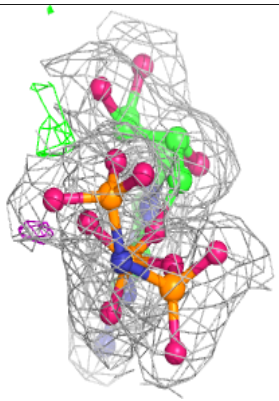


Electron density around ANP B 401:

$2mF_o$-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.