



# Full wwPDB X-ray Structure Validation Report ⓘ

Jun 15, 2020 – 04:27 am BST

PDB ID : 3SEZ  
Title : Crystal structure of C176A mutant of glutamine-dependent NAD<sup>+</sup> synthetase from *M. tuberculosis* in complex with ATP and NaAD<sup>+</sup>  
Authors : Chuenchor, W.; Gerratana, B.  
Deposited on : 2011-06-11  
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](mailto: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.

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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 : 2.11  
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) : 2.11

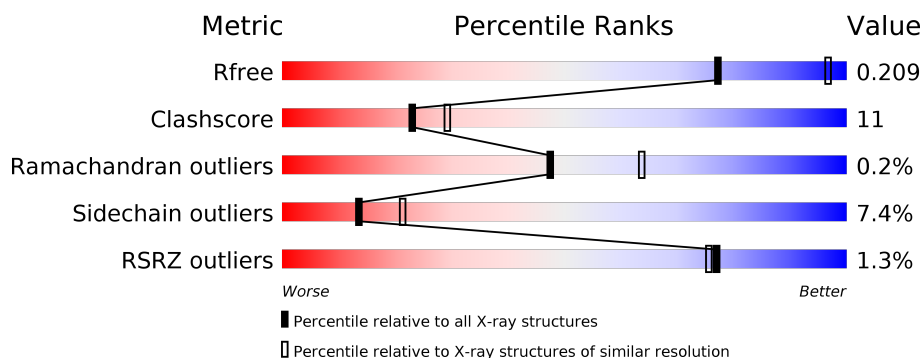
# 1 Overall quality at a glance

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))
$R_{free}$	130704	1332 (2.68-2.64)
Clashscore	141614	1374 (2.68-2.64)
Ramachandran outliers	138981	1349 (2.68-2.64)
Sidechain outliers	138945	1349 (2.68-2.64)
RSRZ outliers	127900	1318 (2.68-2.64)

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  $\geq 3$ , 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	680	<div> <div>%</div> <div> <div></div> <div>74%</div> <div>20%</div> <div>• •</div> </div> </div>
1	B	680	<div> <div>2%</div> <div> <div></div> <div>74%</div> <div>19%</div> <div>• •</div> </div> </div>
1	C	680	<div> <div>%</div> <div> <div></div> <div>73%</div> <div>19%</div> <div>• 5%</div> </div> </div>
1	D	680	<div> <div>%</div> <div> <div></div> <div>71%</div> <div>21%</div> <div>• 5%</div> </div> </div>

## 2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 20820 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 Glutamine-dependent NAD(+) synthetase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	658	Total	C	N	O	S	0	0	0
			5104	3234	909	946	15			
1	B	657	Total	C	N	O	S	0	0	0
			5096	3230	907	944	15			
1	C	648	Total	C	N	O	S	0	0	0
			5014	3175	898	926	15			
1	D	649	Total	C	N	O	S	0	0	0
			5030	3185	898	932	15			

There are 8 discrepancies between the modelled and reference sequences:

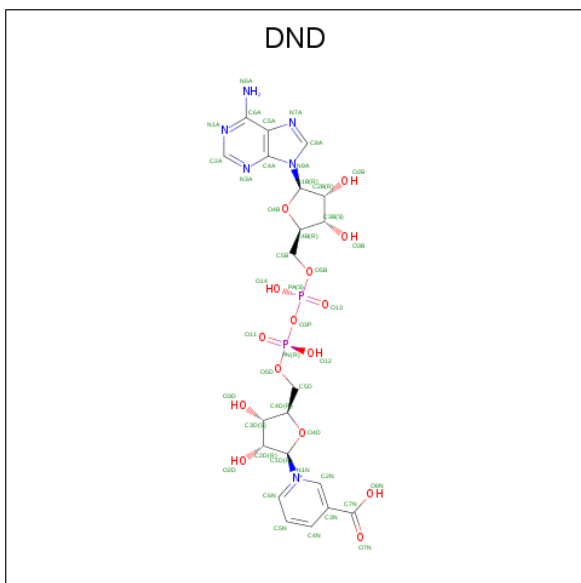
Chain	Residue	Modelled	Actual	Comment	Reference
A	0	SER	-	expression tag	UNP P0A5L6
A	176	ALA	CYS	engineered mutation	UNP P0A5L6
B	0	SER	-	expression tag	UNP P0A5L6
B	176	ALA	CYS	engineered mutation	UNP P0A5L6
C	0	SER	-	expression tag	UNP P0A5L6
C	176	ALA	CYS	engineered mutation	UNP P0A5L6
D	0	SER	-	expression tag	UNP P0A5L6
D	176	ALA	CYS	engineered mutation	UNP P0A5L6

- Molecule 2 is ADENOSINE-5'-TRIPHOSPHATE (three-letter code: ATP) (formula:  $C_{10}H_{16}N_5O_{13}P_3$ ).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total 31	C 10	N 5	O 13	P 3	0	0
2	B	1	Total 31	C 10	N 5	O 13	P 3	0	0
2	C	1	Total 31	C 10	N 5	O 13	P 3	0	0
2	D	1	Total 31	C 10	N 5	O 13	P 3	0	0

- Molecule 3 is NICOTINIC ACID ADENINE DINUCLEOTIDE (three-letter code: DND) (formula:  $C_{21}H_{27}N_6O_{15}P_2$ ).




Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
3	A	1	Total	C	N	O	P	0	0
			44	21	6	15	2		
3	B	1	Total	C	N	O	P	0	0
			44	21	6	15	2		
3	C	1	Total	C	N	O	P	0	0
			44	21	6	15	2		
3	D	1	Total	C	N	O	P	0	0
			44	21	6	15	2		

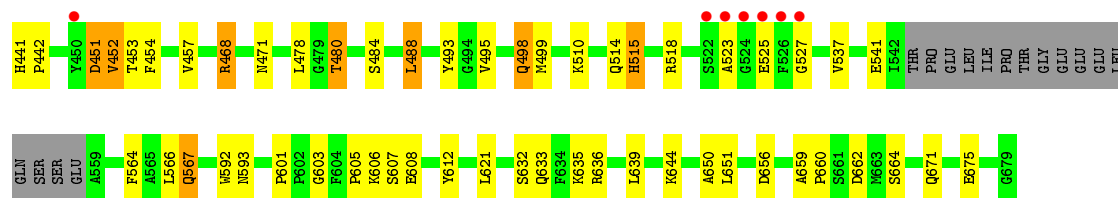
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	79	Total	O	0	0
			79	79		
4	B	67	Total	O	0	0
			67	67		
4	C	51	Total	O	0	0
			51	51		
4	D	79	Total	O	0	0
			79	79		

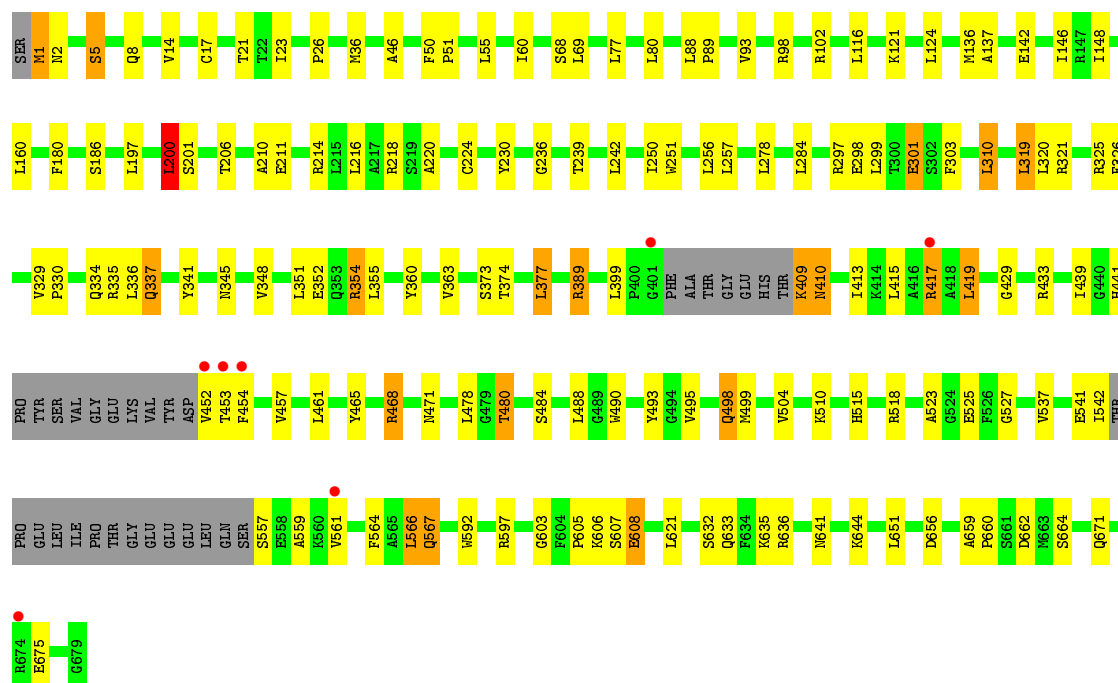
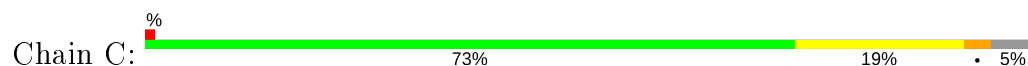
These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are 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 ( $\text{RSRZ} > 2$ ). 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.

- Chain A: 
- LEU  
ILE  
PRO  
THR  
GLY  
GLU  
GLU  
GLU  
LEU  
GLN  
SER  
S557  
E558  
A559  
K560  
F564  
A565  
L566  
Q567  
W592  
M593  
P601  
P602  
G603  
P604  
P605  
K606  
S607  
E608  
Y612  
L621  
Q633  
F634  
K635  
R636  
L639  
K644  
L651  
D656  
A659  
P660  
S664  
Q671  
E675  
F676
- R433  
I439  
G440  
H441  
P442  
V449  
Y450  
D451  
V452  
T453  
F454  
V457  
Y465  
R468  
M471  
L478  
G479  
T480  
S494  
L488  
G499  
S491  
T492  
Y493  
G494  
V495  
Q498  
M499  
K510  
H515  
R518  
A523  
G524  
F526  
G527  
V537  
E541  
I541  
T541  
P541  
G541
- T300  
E301  
L310  
I319  
L320  
R321  
R325  
V329  
P330  
A331  
Q334  
R335  
L336  
E342  
I346  
Q347  
V348  
E352  
Q353  
R354  
L358  
V363  
S373  
L377  
R389  
P400  
G401  
F402  
ALA  
THR  
GLY  
GLU  
HIS  
THR  
K409  
M410  
I413  
R417  
A418  
L419  
I426  
Q430
- R147  
I148  
L160  
L166  
P167  
H172  
V173  
E174  
F180  
S186  
A189  
L197  
L200  
S201  
I205  
T206  
A210  
E211  
R214  
L215  
L216  
A217  
R218  
Y230  
G236  
T239  
L242  
L250  
W251  
L256  
L257  
R262  
L278  
L284  
N292  
R297  
E298  
L299
- SER  
M1  
M2  
S5  
Q8  
V14  
C17  
T18  
H19  
H20  
T21  
T22  
I23  
S32  
M36  
A46  
F50  
P51  
E52  
L53  
I60  
S68  
L69  
L77  
L88  
P89  
V93  
R98  
R102  
V108  
L116  
P125  
T126  
Y127  
R133  
A137  
E142  
T146

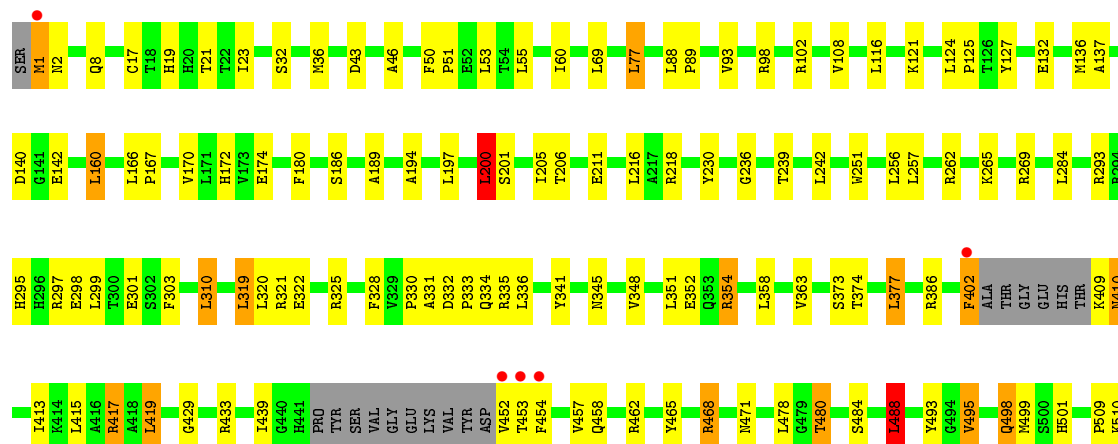
- Chain B:
- 
- 29% 74% 19%
- SER  
M1  
N2  
Q8  
V14  
C17  
T21  
T22  
I23  
M36  
D43  
A46  
F50  
P51  
L55  
I60  
S68  
L69  
L77  
L88  
P89  
V93  
R98  
R102  
V108  
L116  
P125  
R128  
E132  
A137  
D140  
G141  
E142  
I146  
R147  
I148
- L160  
F180  
L200  
S201  
I205  
T206  
A210  
E211  
R214  
L215  
I216  
A217  
R218  
R223  
Y230  
G236  
T239  
L242  
T250  
M251  
L256  
L257  
R262  
K265  
R269  
L284  
R295  
E296  
R297  
E298  
L299  
F300  
R301  
L310  
L319  
L320  
R321  
R325  
R326
- V329  
P330  
A331  
D332  
P333  
R335  
L336  
Q337  
Y341  
N345  
V348  
L351  
E352  
Q353  
L355  
Y360  
V363  
S373  
T374  
L377  
R386  
R389  
F402  
ALA  
THR  
GLY  
GLU  
HIS  
THR  
K409  
N410  
L413  
K414  
L415  
A416  
R417  
A418  
L419  
G429  
R433  
L436  
A439

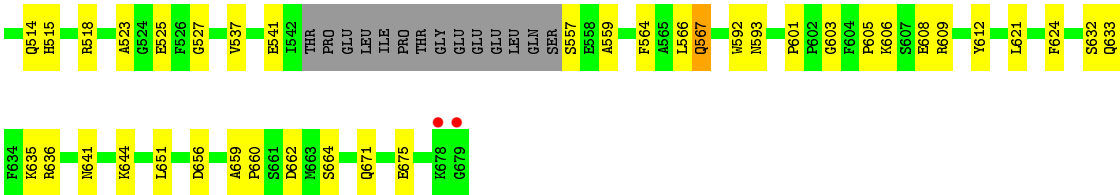


• Molecule 1: Glutamine-dependent NAD(+) synthetase



• Molecule 1: Glutamine-dependent NAD(+) synthetase







## 4 Data and refinement statistics

Property	Value	Source
Space group	P 41 21 2	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	178.41Å 178.41Å 216.30Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	34.33 – 2.65 34.33 – 2.65	Depositor EDS
% Data completeness (in resolution range)	98.0 (34.33-2.65) 90.4 (34.33-2.65)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	0.09	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	4.92 (at 2.65Å)	Xtriage
Refinement program	PHENIX (phenix.refine: 1.7.1_743)	Depositor
R, $R_{free}$	0.172 , 0.214 0.167 , 0.209	Depositor DCC
$R_{free}$ test set	4946 reflections (4.99%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	37.7	Xtriage
Anisotropy	1.210	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.33 , 41.0	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.48$ , $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.96	EDS
Total number of atoms	20820	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	54.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 11.52% of the height of the origin peak. No significant pseudotranslation is detected.*

<sup>1</sup>Intensities estimated from amplitudes.

<sup>2</sup>Theoretical 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

### 5.1 Standard geometry

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

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	0.66	2/5224 (0.0%)	0.76	4/7097 (0.1%)
1	B	0.66	0/5216	0.78	4/7088 (0.1%)
1	C	0.66	0/5129	0.76	3/6967 (0.0%)
1	D	0.66	0/5146	0.78	8/6990 (0.1%)
All	All	0.66	2/20715 (0.0%)	0.77	19/28142 (0.1%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	1
1	B	0	1
All	All	0	2

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	292	ASN	CG-ND2	-8.20	1.12	1.32
1	A	292	ASN	CG-OD1	-7.95	1.06	1.24

All (19) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	417	ARG	NE-CZ-NH1	-7.85	116.37	120.30
1	C	417	ARG	NE-CZ-NH2	7.59	124.09	120.30
1	D	200	LEU	CA-CB-CG	7.42	132.37	115.30
1	D	55	LEU	CB-CG-CD1	-7.35	98.50	111.00
1	B	200	LEU	CA-CB-CG	7.20	131.87	115.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	335	ARG	NE-CZ-NH1	7.02	123.81	120.30
1	D	417	ARG	NE-CZ-NH2	6.93	123.77	120.30
1	C	200	LEU	CA-CB-CG	6.85	131.05	115.30
1	A	417	ARG	NE-CZ-NH2	6.67	123.64	120.30
1	B	417	ARG	NE-CZ-NH2	6.45	123.53	120.30
1	A	200	LEU	CA-CB-CG	6.16	129.46	115.30
1	D	417	ARG	NE-CZ-NH1	-5.97	117.31	120.30
1	A	284	LEU	CA-CB-CG	5.83	128.71	115.30
1	D	293	ARG	NE-CZ-NH1	-5.75	117.42	120.30
1	D	609	ARG	NE-CZ-NH2	-5.63	117.48	120.30
1	A	417	ARG	NE-CZ-NH1	-5.44	117.58	120.30
1	B	284	LEU	CA-CB-CG	5.23	127.34	115.30
1	D	335	ARG	NE-CZ-NH2	-5.05	117.78	120.30
1	D	488	LEU	CA-CB-CG	5.03	126.86	115.30

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	451	ASP	Peptide
1	B	451	ASP	Peptide

## 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	5104	0	4997	117	1
1	B	5096	0	4989	119	1
1	C	5014	0	4916	128	1
1	D	5030	0	4925	117	1
2	A	31	0	12	2	0
2	B	31	0	12	1	0
2	C	31	0	12	2	0
2	D	31	0	12	1	0
3	A	44	0	25	6	0
3	B	44	0	25	0	0
3	C	44	0	25	3	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	D	44	0	25	1	0
4	A	79	0	0	1	0
4	B	67	0	0	4	0
4	C	51	0	0	3	0
4	D	79	0	0	1	0
All	All	20820	0	19975	462	2

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 11.

All (462) 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:D:518:ARG:NH1	1:D:603:GLY:HA3	1.68	1.07
1:B:567:GLN:HE21	1:B:567:GLN:HA	1.17	1.06
1:A:567:GLN:HA	1:A:567:GLN:HE21	1.20	1.02
1:D:567:GLN:HE21	1:D:567:GLN:HA	1.19	1.02
1:C:567:GLN:HA	1:C:567:GLN:HE21	1.21	0.99
1:D:518:ARG:HH12	1:D:603:GLY:HA3	0.83	0.99
1:D:633:GLN:OE1	1:D:636:ARG:NH1	1.97	0.97
1:A:633:GLN:OE1	1:A:636:ARG:NH1	1.98	0.96
1:D:518:ARG:HH12	1:D:603:GLY:CA	1.79	0.95
1:C:633:GLN:OE1	1:C:636:ARG:NH1	1.99	0.94
1:C:46:ALA:HB1	1:C:310:LEU:HD21	1.54	0.89
1:B:633:GLN:OE1	1:B:636:ARG:NH1	2.05	0.89
1:D:46:ALA:HB1	1:D:310:LEU:HD21	1.55	0.88
1:A:46:ALA:HB1	1:A:310:LEU:HD21	1.55	0.87
1:A:172:HIS:CD2	1:A:189:ALA:HB2	2.11	0.86
1:C:518:ARG:HH22	1:C:603:GLY:HA3	1.42	0.85
1:C:329:VAL:HG11	1:C:515:HIS:CD2	2.12	0.84
1:A:329:VAL:HG11	1:A:515:HIS:CD2	2.13	0.83
1:A:671:GLN:NE2	1:A:675:GLU:HG3	1.92	0.83
1:B:493:TYR:CD1	1:B:498:GLN:NE2	2.47	0.83
1:C:518:ARG:HH22	1:C:603:GLY:CA	1.92	0.81
1:A:172:HIS:CD2	1:A:189:ALA:CB	2.64	0.80
1:B:1:MET:HG3	1:B:2:ASN:N	1.94	0.80
1:C:671:GLN:NE2	1:C:675:GLU:HG3	1.95	0.80
1:C:493:TYR:CD1	1:C:498:GLN:NE2	2.51	0.79
1:A:1:MET:HG3	1:A:2:ASN:N	1.98	0.79
1:B:671:GLN:NE2	1:B:675:GLU:HG3	1.97	0.79
1:D:319:LEU:HD13	1:D:321:ARG:HB3	1.65	0.79

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:493:TYR:CD1	1:D:498:GLN:NE2	2.51	0.79
1:B:46:ALA:HB1	1:B:310:LEU:HD21	1.64	0.78
1:D:671:GLN:NE2	1:D:675:GLU:HG3	1.97	0.78
1:C:363:VAL:HG13	1:C:478:LEU:HG	1.63	0.78
1:A:493:TYR:CD1	1:A:498:GLN:NE2	2.51	0.78
1:D:363:VAL:HG13	1:D:478:LEU:HG	1.67	0.76
1:C:1:MET:HG3	1:C:2:ASN:N	1.99	0.75
1:C:518:ARG:NH2	1:C:603:GLY:HA3	2.01	0.74
1:A:297:ARG:NH2	1:B:142:GLU:OE2	2.20	0.74
1:B:363:VAL:HG13	1:B:478:LEU:HG	1.70	0.73
1:D:1:MET:HG3	1:D:2:ASN:N	2.01	0.73
1:B:493:TYR:HD1	1:B:498:GLN:HE21	1.34	0.73
1:B:567:GLN:NE2	1:B:567:GLN:HA	1.99	0.73
1:A:671:GLN:HE21	1:A:675:GLU:HG3	1.52	0.72
1:C:329:VAL:CG1	1:C:515:HIS:HD2	2.01	0.72
1:D:336:LEU:HD21	1:D:515:HIS:HD2	1.55	0.72
1:D:567:GLN:CA	1:D:567:GLN:HE21	2.00	0.72
1:A:329:VAL:CG1	1:A:515:HIS:HD2	2.02	0.72
1:A:363:VAL:HG13	1:A:478:LEU:HG	1.71	0.71
1:D:567:GLN:NE2	1:D:567:GLN:HA	2.02	0.71
1:C:329:VAL:CG1	1:C:515:HIS:CD2	2.73	0.71
1:C:297:ARG:NH2	1:D:142:GLU:OE2	2.24	0.70
1:C:671:GLN:HE21	1:C:675:GLU:HG3	1.56	0.70
1:C:377:LEU:HD13	1:C:419:LEU:HD23	1.73	0.70
1:A:329:VAL:CG1	1:A:515:HIS:CD2	2.75	0.69
1:C:98:ARG:HG3	4:C:702:HOH:O	1.90	0.69
1:A:319:LEU:HD13	1:A:321:ARG:HB3	1.75	0.69
1:D:671:GLN:HE21	1:D:675:GLU:HG3	1.58	0.69
1:A:567:GLN:HA	1:A:567:GLN:NE2	2.02	0.68
1:A:567:GLN:CA	1:A:567:GLN:HE21	2.01	0.68
1:C:480:THR:HG21	2:C:680:ATP:O3'	1.94	0.68
1:B:441:HIS:ND1	1:B:442:PRO:CD	2.57	0.68
1:A:480:THR:HG21	2:A:680:ATP:O3'	1.94	0.67
1:C:493:TYR:HD1	1:C:498:GLN:HE21	1.40	0.67
1:C:46:ALA:CB	1:C:310:LEU:HD21	2.23	0.67
1:A:468:ARG:NH2	1:D:495:VAL:HG22	2.10	0.67
1:B:671:GLN:HE21	1:B:675:GLU:HG3	1.60	0.67
1:B:441:HIS:ND1	1:B:442:PRO:HD2	2.10	0.66
1:C:319:LEU:HD13	1:C:321:ARG:HB3	1.77	0.66
1:D:493:TYR:HD1	1:D:498:GLN:HE21	1.43	0.66
1:A:377:LEU:HD13	1:A:419:LEU:HD23	1.78	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:525:GLU:CD	1:C:525:GLU:H	1.98	0.65
1:B:319:LEU:HD13	1:B:321:ARG:HB3	1.78	0.65
1:D:402:PHE:CD2	1:D:402:PHE:N	2.63	0.65
1:D:644:LYS:HE3	1:D:656:ASP:OD1	1.97	0.65
1:C:329:VAL:HG13	1:C:515:HIS:HD2	1.62	0.65
1:D:50:PHE:O	1:D:200:LEU:HB3	1.97	0.65
1:A:441:HIS:ND1	1:A:442:PRO:CD	2.60	0.64
1:A:493:TYR:HD1	1:A:498:GLN:HE21	1.44	0.64
1:D:468:ARG:NH1	1:D:471:ASN:OD1	2.30	0.64
1:D:525:GLU:CD	1:D:525:GLU:H	2.02	0.64
1:B:377:LEU:HD13	1:B:419:LEU:HD23	1.79	0.64
1:C:567:GLN:HA	1:C:567:GLN:NE2	2.05	0.63
1:A:525:GLU:CD	1:A:525:GLU:H	2.01	0.63
1:C:468:ARG:NH1	1:C:471:ASN:OD1	2.31	0.63
1:A:493:TYR:HB2	1:A:635:LYS:HG2	1.80	0.63
1:A:297:ARG:O	1:A:301:GLU:HG2	1.99	0.63
1:D:46:ALA:CB	1:D:310:LEU:HD21	2.29	0.62
1:A:495:VAL:HG22	1:D:468:ARG:NH2	2.14	0.62
1:D:480:THR:HG21	2:D:680:ATP:O3'	1.99	0.62
1:C:490:TRP:NE1	3:C:681:DND:H13	2.15	0.62
1:B:525:GLU:H	1:B:525:GLU:CD	2.02	0.62
1:B:413:ILE:HD13	1:B:417:ARG:HH21	1.65	0.62
1:A:441:HIS:CE1	1:A:442:PRO:HG2	2.35	0.62
1:D:297:ARG:O	1:D:301:GLU:HG2	1.99	0.61
1:D:336:LEU:HD21	1:D:515:HIS:CD2	2.36	0.61
1:C:644:LYS:HE3	1:C:656:ASP:OD1	2.01	0.61
1:D:493:TYR:HB2	1:D:635:LYS:HG2	1.83	0.61
1:D:402:PHE:HD2	1:D:402:PHE:N	1.97	0.61
1:D:514:GLN:HG3	1:D:515:HIS:ND1	2.17	0.60
1:C:493:TYR:HB2	1:C:635:LYS:HG2	1.83	0.60
1:B:413:ILE:CD1	1:B:417:ARG:HH21	2.14	0.60
1:D:377:LEU:HD13	1:D:419:LEU:HD23	1.82	0.60
1:A:402:PHE:CD2	1:A:402:PHE:N	2.70	0.59
1:C:567:GLN:HE21	1:C:567:GLN:CA	2.01	0.59
1:A:441:HIS:ND1	1:A:442:PRO:HD2	2.17	0.59
1:B:567:GLN:CA	1:B:567:GLN:HE21	1.99	0.59
1:A:329:VAL:HG13	1:A:515:HIS:HD2	1.66	0.59
1:B:441:HIS:CE1	1:B:442:PRO:HG2	2.36	0.59
1:B:2:ASN:HB3	1:B:8:GLN:NE2	2.18	0.59
1:B:514:GLN:HG3	1:B:515:HIS:ND1	2.18	0.59
1:B:644:LYS:HE3	1:B:656:ASP:OD1	2.02	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:17:CYS:HB3	1:D:36:MET:HE2	1.85	0.59
1:A:330:PRO:HG2	1:A:336:LEU:HA	1.85	0.58
1:A:468:ARG:NH1	1:A:471:ASN:OD1	2.35	0.58
1:B:310:LEU:HD12	1:B:310:LEU:C	2.24	0.58
1:A:495:VAL:HG22	1:D:468:ARG:HH21	1.68	0.58
1:A:98:ARG:HD2	4:A:712:HOH:O	2.03	0.58
1:B:452:VAL:HG12	1:B:453:THR:N	2.19	0.58
1:C:50:PHE:O	1:C:200:LEU:HB3	2.04	0.57
1:B:50:PHE:O	1:B:200:LEU:HB3	2.05	0.57
1:A:146:ILE:HG23	1:A:148:ILE:HD13	1.85	0.57
1:A:17:CYS:HB3	1:A:36:MET:HE2	1.85	0.57
1:B:330:PRO:HG2	1:B:336:LEU:HA	1.85	0.57
1:B:468:ARG:NH2	1:C:495:VAL:HG22	2.20	0.57
1:B:46:ALA:CB	1:B:310:LEU:HD21	2.32	0.57
1:A:50:PHE:O	1:A:200:LEU:HB3	2.04	0.56
1:A:510:LYS:HD2	1:A:564:PHE:CD2	2.40	0.56
1:A:468:ARG:HH21	1:D:495:VAL:HG22	1.69	0.56
1:C:490:TRP:CD1	3:C:681:DND:H13	2.40	0.56
1:A:17:CYS:HB3	1:A:36:MET:CE	2.36	0.56
1:C:632:SER:OG	1:C:636:ARG:NH2	2.38	0.56
1:C:413:ILE:HD11	1:C:417:ARG:HH21	1.70	0.56
1:B:468:ARG:NH1	1:B:471:ASN:OD1	2.38	0.56
1:A:46:ALA:CB	1:A:310:LEU:HD21	2.30	0.56
1:D:69:LEU:HD13	1:D:69:LEU:C	2.26	0.56
1:D:98:ARG:HD2	4:D:696:HOH:O	2.05	0.56
1:B:336:LEU:HD21	1:B:515:HIS:CD2	2.40	0.55
1:D:17:CYS:HB3	1:D:36:MET:CE	2.36	0.55
1:A:363:VAL:CG1	1:A:478:LEU:HG	2.36	0.55
1:D:325:ARG:HB3	1:D:592:TRP:CZ2	2.42	0.55
1:A:492:THR:OG1	3:A:681:DND:H11	2.07	0.55
1:D:330:PRO:HG2	1:D:336:LEU:HA	1.89	0.55
1:B:325:ARG:HB3	1:B:592:TRP:CZ2	2.42	0.55
1:C:46:ALA:HB1	1:C:310:LEU:CD2	2.33	0.55
1:B:495:VAL:HG22	1:C:468:ARG:NH2	2.22	0.55
1:C:341:TYR:CE1	1:C:345:ASN:ND2	2.75	0.55
1:B:223:ARG:HD3	4:B:710:HOH:O	2.06	0.55
1:C:330:PRO:HG2	1:C:336:LEU:HA	1.89	0.55
1:C:452:VAL:HG12	1:C:453:THR:N	2.22	0.55
1:B:363:VAL:CG1	1:B:478:LEU:HG	2.36	0.55
1:C:557:SER:O	1:C:561:VAL:HG22	2.07	0.54
1:C:98:ARG:HD2	4:C:718:HOH:O	2.07	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:363:VAL:CG1	1:C:478:LEU:HG	2.35	0.54
1:B:386:ARG:HH21	1:D:265:LYS:HG2	1.72	0.54
1:B:480:THR:HG21	2:B:680:ATP:O3'	2.08	0.54
1:A:77:LEU:HD11	1:A:108:VAL:HG21	1.90	0.54
1:B:98:ARG:HD2	4:B:708:HOH:O	2.08	0.54
1:B:441:HIS:HE2	1:B:451:ASP:HB2	1.73	0.53
1:A:659:ALA:HB1	1:A:660:PRO:CD	2.38	0.53
1:D:439:ILE:O	1:D:439:ILE:CG2	2.57	0.53
1:A:413:ILE:HD11	1:A:417:ARG:HH21	1.72	0.53
1:C:510:LYS:HD2	1:C:564:PHE:CD2	2.44	0.53
1:B:140:ASP:HB2	1:D:295:HIS:CD2	2.43	0.53
1:C:325:ARG:HB3	1:C:592:TRP:CZ2	2.44	0.53
1:B:14:VAL:HG23	1:B:250:ILE:HD13	1.91	0.52
1:B:297:ARG:O	1:B:301:GLU:HG2	2.09	0.52
1:B:146:ILE:HG23	1:B:148:ILE:HD13	1.91	0.52
1:B:21:THR:O	1:B:236:GLY:HA3	2.10	0.52
1:B:510:LYS:HD2	1:B:564:PHE:CD2	2.45	0.52
1:C:351:LEU:HD22	1:C:355:LEU:HD11	1.92	0.52
1:D:632:SER:OG	1:D:636:ARG:NH2	2.43	0.52
1:A:510:LYS:HE3	1:A:564:PHE:CE2	2.45	0.52
1:A:453:THR:O	1:A:457:VAL:HG23	2.10	0.51
1:A:23:ILE:HB	1:A:60:ILE:HG22	1.91	0.51
1:A:441:HIS:HE2	1:A:451:ASP:HB2	1.75	0.51
1:B:495:VAL:HG22	1:C:468:ARG:HH21	1.76	0.51
1:D:429:GLY:O	1:D:433:ARG:HG3	2.10	0.51
1:B:493:TYR:HB2	1:B:635:LYS:HG2	1.92	0.51
1:C:2:ASN:HB3	1:C:8:GLN:NE2	2.26	0.51
1:D:410:ASN:N	1:D:410:ASN:OD1	2.41	0.51
3:A:681:DND:H24	1:D:501:HIS:HB3	1.91	0.51
1:B:265:LYS:HG2	1:D:386:ARG:HH21	1.76	0.51
1:B:336:LEU:HD21	1:B:515:HIS:HD2	1.75	0.51
1:B:632:SER:OG	1:B:636:ARG:NH2	2.44	0.51
1:C:329:VAL:HG11	1:C:515:HIS:NE2	2.26	0.51
1:B:429:GLY:O	1:B:433:ARG:HG3	2.11	0.51
1:D:23:ILE:HB	1:D:60:ILE:HG22	1.93	0.51
1:B:484:SER:O	1:B:488:LEU:HD22	2.10	0.51
1:A:14:VAL:HG23	1:A:250:ILE:HD13	1.93	0.50
1:D:510:LYS:HD2	1:D:564:PHE:CD2	2.46	0.50
1:C:218:ARG:HD2	1:C:251:TRP:CZ3	2.46	0.50
1:D:2:ASN:HB3	1:D:8:GLN:NE2	2.26	0.50
1:C:518:ARG:HH12	1:C:603:GLY:HA3	1.76	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:180:PHE:CD2	1:B:216:LEU:CD1	2.95	0.50
1:B:2:ASN:HB3	1:B:8:GLN:HE22	1.76	0.50
1:B:636:ARG:HD3	1:B:651:LEU:HB3	1.93	0.50
1:C:102:ARG:HD3	1:C:137:ALA:HB2	1.94	0.50
1:D:239:THR:HA	1:D:242:LEU:O	2.12	0.50
1:A:413:ILE:CD1	1:A:417:ARG:HH21	2.25	0.50
1:B:659:ALA:HB1	1:B:660:PRO:CD	2.41	0.50
1:D:21:THR:O	1:D:236:GLY:HA3	2.12	0.50
1:C:146:ILE:HG23	1:C:148:ILE:HD13	1.92	0.50
1:C:439:ILE:CG2	1:C:439:ILE:O	2.59	0.50
1:A:172:HIS:HD2	1:A:189:ALA:HB2	1.72	0.50
1:B:348:VAL:O	1:B:352:GLU:HG3	2.12	0.50
1:B:537:VAL:O	1:B:541:GLU:HG2	2.12	0.50
1:C:297:ARG:O	1:C:301:GLU:HG2	2.12	0.50
1:C:659:ALA:HB1	1:C:660:PRO:CD	2.42	0.49
1:B:452:VAL:CG1	1:B:453:THR:N	2.76	0.49
1:C:17:CYS:HB3	1:C:36:MET:CE	2.42	0.49
1:B:523:ALA:HB1	1:B:525:GLU:OE1	2.11	0.49
1:D:523:ALA:HB1	1:D:525:GLU:OE1	2.12	0.49
1:D:230:TYR:C	1:D:230:TYR:CD1	2.85	0.49
1:D:453:THR:O	1:D:457:VAL:HG23	2.12	0.49
1:A:441:HIS:ND1	1:A:442:PRO:N	2.60	0.49
1:A:358:LEU:HD21	3:D:681:DND:N6A	2.27	0.49
1:B:88:LEU:N	1:B:89:PRO:HD2	2.28	0.49
1:C:510:LYS:HE3	1:C:564:PHE:CE2	2.48	0.49
1:A:523:ALA:HB1	1:A:525:GLU:OE1	2.13	0.49
1:A:329:VAL:HG11	1:A:515:HIS:NE2	2.28	0.49
1:B:523:ALA:HB3	1:B:525:GLU:OE2	2.13	0.49
1:C:21:THR:O	1:C:236:GLY:HA3	2.12	0.49
1:D:484:SER:O	1:D:488:LEU:HD22	2.13	0.49
1:A:88:LEU:N	1:A:89:PRO:HD2	2.28	0.48
1:B:659:ALA:HB1	1:B:660:PRO:HD2	1.94	0.48
1:D:348:VAL:O	1:D:352:GLU:HG3	2.13	0.48
1:B:510:LYS:HE3	1:B:564:PHE:CE2	2.48	0.48
1:B:329:VAL:HG11	1:B:515:HIS:CD2	2.48	0.48
1:C:518:ARG:NH1	1:C:603:GLY:HA3	2.27	0.48
1:D:557:SER:C	1:D:559:ALA:N	2.64	0.48
1:A:490:TRP:NE1	3:A:681:DND:H13	2.29	0.48
1:C:23:ILE:HB	1:C:60:ILE:HG22	1.95	0.48
1:A:484:SER:O	1:A:488:LEU:HD22	2.13	0.48
1:C:186:SER:HB2	1:C:197:LEU:HD13	1.94	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:523:ALA:HB1	1:C:525:GLU:OE1	2.14	0.48
3:A:681:DND:C2A	1:D:501:HIS:HB3	2.43	0.48
1:A:644:LYS:HE3	1:A:656:ASP:OD1	2.14	0.48
1:B:468:ARG:NH2	1:C:495:VAL:O	2.47	0.48
1:C:14:VAL:HG23	1:C:250:ILE:HD13	1.95	0.48
1:A:125:PRO:HB3	1:A:127:TYR:CE2	2.49	0.48
1:A:2:ASN:HB3	1:A:8:GLN:NE2	2.29	0.48
1:B:441:HIS:ND1	1:B:442:PRO:N	2.62	0.48
1:C:518:ARG:CZ	1:C:603:GLY:HA3	2.43	0.48
1:D:659:ALA:HB1	1:D:660:PRO:CD	2.44	0.48
1:B:230:TYR:C	1:B:230:TYR:CD1	2.88	0.47
1:B:518:ARG:NH1	1:B:603:GLY:HA3	2.29	0.47
1:C:180:PHE:CD2	1:C:216:LEU:CD1	2.96	0.47
1:C:518:ARG:NH2	1:C:603:GLY:CA	2.65	0.47
1:D:523:ALA:CB	1:D:525:GLU:OE1	2.62	0.47
1:A:537:VAL:O	1:A:541:GLU:HG2	2.14	0.47
1:B:146:ILE:HG23	1:B:148:ILE:CD1	2.43	0.47
1:B:23:ILE:HB	1:B:60:ILE:HG22	1.95	0.47
1:B:69:LEU:HD13	1:B:69:LEU:C	2.34	0.47
1:C:605:PRO:HD2	1:C:608:GLU:HG3	1.97	0.47
1:C:337:GLN:C	1:C:337:GLN:OE1	2.53	0.47
1:A:200:LEU:H	1:A:200:LEU:HD23	1.80	0.47
1:B:360:TYR:HB3	1:B:389:ARG:HD2	1.97	0.47
1:C:537:VAL:O	1:C:541:GLU:HG2	2.14	0.47
1:A:439:ILE:HD11	1:D:465:TYR:CD1	2.50	0.47
1:B:210:ALA:O	1:B:214:ARG:HG3	2.15	0.47
1:C:88:LEU:HD11	1:C:310:LEU:HD11	1.96	0.47
1:D:605:PRO:HD2	1:D:608:GLU:HG3	1.97	0.47
1:B:498:GLN:OE1	1:B:499:MET:HE2	2.15	0.47
1:C:413:ILE:CD1	1:C:417:ARG:HH21	2.27	0.47
1:C:2:ASN:HB3	1:C:8:GLN:HE22	1.80	0.47
1:A:566:LEU:HA	1:A:566:LEU:HD12	1.76	0.47
1:A:348:VAL:O	1:A:352:GLU:HG3	2.15	0.47
1:B:17:CYS:HB3	1:B:36:MET:CE	2.45	0.47
1:C:452:VAL:CG1	1:C:453:THR:N	2.78	0.47
1:D:2:ASN:HB3	1:D:8:GLN:HE22	1.79	0.47
1:D:510:LYS:HE3	1:D:564:PHE:CE2	2.50	0.47
1:B:77:LEU:HD11	1:B:108:VAL:HG21	1.97	0.46
1:C:410:ASN:OD1	1:C:410:ASN:N	2.40	0.46
1:A:310:LEU:C	1:A:310:LEU:HD12	2.35	0.46
1:B:218:ARG:HD2	1:B:251:TRP:CZ3	2.50	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:523:ALA:HB3	1:D:525:GLU:OE2	2.15	0.46
1:A:605:PRO:HD2	1:A:608:GLU:HG3	1.98	0.46
1:C:210:ALA:O	1:C:214:ARG:HG3	2.16	0.46
1:B:295:HIS:CD2	1:D:140:ASP:HB2	2.51	0.46
1:D:363:VAL:CG1	1:D:478:LEU:HG	2.40	0.46
1:D:557:SER:C	1:D:559:ALA:H	2.18	0.46
1:C:453:THR:O	1:C:457:VAL:HG23	2.16	0.46
1:D:331:ALA:HA	1:D:601:PRO:HA	1.97	0.46
1:A:468:ARG:NH2	1:D:495:VAL:O	2.49	0.46
1:A:146:ILE:HG23	1:A:148:ILE:CD1	2.45	0.46
1:A:636:ARG:HD3	1:A:651:LEU:HB3	1.98	0.46
1:B:125:PRO:HD2	1:B:132:GLU:CD	2.36	0.46
1:B:341:TYR:CE1	1:B:345:ASN:ND2	2.84	0.46
1:C:1:MET:CG	1:C:2:ASN:N	2.73	0.46
1:D:218:ARG:HD2	1:D:251:TRP:CZ3	2.51	0.46
1:A:21:THR:O	1:A:236:GLY:HA3	2.16	0.46
1:A:298:GLU:HG3	1:A:299:LEU:N	2.31	0.45
1:B:523:ALA:CB	1:B:525:GLU:OE1	2.64	0.45
1:B:1:MET:CG	1:B:2:ASN:N	2.71	0.45
1:B:351:LEU:HD22	1:B:355:LEU:HD11	1.96	0.45
1:A:523:ALA:CB	1:A:525:GLU:OE1	2.64	0.45
1:B:310:LEU:HD12	1:B:310:LEU:O	2.17	0.45
1:B:98:ARG:HG3	4:B:744:HOH:O	2.16	0.45
3:A:681:DND:H24	1:D:501:HIS:O	2.16	0.45
1:A:180:PHE:CD2	1:A:216:LEU:CD1	3.00	0.45
1:A:518:ARG:CZ	1:A:603:GLY:HA3	2.46	0.45
1:C:429:GLY:O	1:C:433:ARG:HG3	2.17	0.45
1:B:310:LEU:C	1:B:310:LEU:CD1	2.85	0.45
1:B:495:VAL:O	1:C:468:ARG:NH2	2.50	0.45
1:D:310:LEU:C	1:D:310:LEU:HD12	2.36	0.45
1:D:19:HIS:HB2	1:D:32:SER:OG	2.17	0.45
1:C:484:SER:O	1:C:488:LEU:HD22	2.16	0.45
1:B:468:ARG:HH21	1:C:495:VAL:HG22	1.80	0.45
1:C:662:ASP:N	1:C:662:ASP:OD1	2.50	0.45
1:C:160:LEU:HD13	1:C:303:PHE:CD2	2.51	0.45
1:D:186:SER:HB2	1:D:197:LEU:HD13	1.99	0.45
1:A:172:HIS:HD2	1:A:189:ALA:CB	2.24	0.44
1:A:200:LEU:N	1:A:200:LEU:HD23	2.32	0.44
1:A:239:THR:HA	1:A:242:LEU:O	2.17	0.44
1:B:650:ALA:O	1:B:656:ASP:HB2	2.17	0.44
1:B:662:ASP:N	1:B:662:ASP:OD1	2.50	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:88:LEU:N	1:D:89:PRO:HD2	2.33	0.44
1:C:17:CYS:HB3	1:C:36:MET:HE2	1.99	0.44
1:A:126:THR:OG1	1:A:133:ARG:HB2	2.17	0.44
1:A:278:LEU:C	1:A:278:LEU:HD23	2.38	0.44
1:B:514:GLN:O	1:B:518:ARG:HG3	2.17	0.44
1:C:523:ALA:HB3	1:C:525:GLU:OE2	2.18	0.44
1:C:566:LEU:HD12	1:C:566:LEU:HA	1.81	0.44
1:C:636:ARG:HD3	1:C:651:LEU:HB3	1.99	0.44
1:D:166:LEU:N	1:D:167:PRO:HD3	2.32	0.44
1:A:218:ARG:HD2	1:A:251:TRP:CZ3	2.52	0.44
1:A:523:ALA:HB3	1:A:525:GLU:OE2	2.17	0.44
1:A:557:SER:C	1:A:559:ALA:N	2.71	0.44
1:C:310:LEU:CD1	1:C:310:LEU:C	2.86	0.44
1:C:523:ALA:CB	1:C:525:GLU:OE1	2.66	0.44
1:D:205:ILE:HD11	1:D:262:ARG:NH2	2.32	0.44
1:C:230:TYR:C	1:C:230:TYR:CD1	2.90	0.44
1:C:88:LEU:HD11	1:C:310:LEU:CD1	2.48	0.44
1:A:23:ILE:HB	1:A:60:ILE:CG2	2.48	0.44
1:A:468:ARG:HA	1:A:468:ARG:HD3	1.42	0.44
1:D:174:GLU:CD	1:D:186:SER:HB3	2.38	0.44
1:D:659:ALA:HB1	1:D:660:PRO:HD2	2.00	0.44
1:A:325:ARG:HB3	1:A:592:TRP:CZ2	2.53	0.44
1:C:121:LYS:HG2	1:C:124:LEU:HD12	2.00	0.44
1:B:205:ILE:HD11	1:B:262:ARG:NH2	2.33	0.43
1:B:453:THR:O	1:B:457:VAL:HG23	2.18	0.43
1:B:50:PHE:HB3	1:B:51:PRO:CD	2.48	0.43
1:B:593:ASN:HA	1:B:612:TYR:O	2.18	0.43
1:C:239:THR:HA	1:C:242:LEU:O	2.18	0.43
1:B:298:GLU:HG3	1:B:299:LEU:N	2.33	0.43
1:C:351:LEU:HD12	1:C:504:VAL:HG11	2.00	0.43
1:D:537:VAL:O	1:D:541:GLU:HG2	2.17	0.43
1:A:19:HIS:HB2	1:A:32:SER:OG	2.18	0.43
1:A:498:GLN:OE1	1:A:499:MET:HE2	2.18	0.43
1:B:332:ASP:HA	1:B:333:PRO:HD3	1.90	0.43
1:C:88:LEU:N	1:C:89:PRO:HD2	2.33	0.43
1:A:210:ALA:O	1:A:214:ARG:HG3	2.19	0.43
1:C:200:LEU:HD23	1:C:200:LEU:N	2.34	0.43
1:C:278:LEU:HD23	1:C:278:LEU:C	2.38	0.43
1:C:298:GLU:HG3	1:C:299:LEU:N	2.34	0.43
1:C:498:GLN:OE1	1:C:499:MET:HE2	2.18	0.43
1:A:147:ARG:C	1:A:148:ILE:HD12	2.39	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:88:LEU:N	1:B:89:PRO:CD	2.81	0.43
1:D:102:ARG:HD3	1:D:137:ALA:HB2	2.01	0.43
1:D:498:GLN:OE1	1:D:499:MET:HE2	2.19	0.43
1:D:53:LEU:HA	1:D:53:LEU:HD23	1.80	0.43
1:D:77:LEU:HD11	1:D:108:VAL:HG21	2.01	0.43
1:A:2:ASN:HB3	1:A:8:GLN:HE22	1.84	0.43
1:C:310:LEU:HD12	1:C:310:LEU:C	2.38	0.43
1:D:567:GLN:HE22	1:D:624:PHE:HB2	1.84	0.43
1:D:662:ASP:OD1	1:D:662:ASP:N	2.52	0.43
1:C:360:TYR:HB3	1:C:389:ARG:HD2	2.01	0.43
1:A:186:SER:HB2	1:A:197:LEU:HD13	2.02	0.42
1:A:230:TYR:C	1:A:230:TYR:CD1	2.91	0.42
1:C:220:ALA:O	1:C:224:CYS:HB2	2.19	0.42
1:C:468:ARG:HD3	1:C:468:ARG:HA	1.50	0.42
1:D:125:PRO:HD2	1:D:132:GLU:CD	2.38	0.42
1:B:439:ILE:CG2	1:B:439:ILE:O	2.67	0.42
1:C:326:PHE:HB3	1:C:329:VAL:HB	2.01	0.42
1:B:239:THR:HA	1:B:242:LEU:O	2.20	0.42
1:B:331:ALA:HA	1:B:601:PRO:HA	2.01	0.42
1:C:297:ARG:HG2	1:C:301:GLU:OE2	2.19	0.42
1:C:337:GLN:O	1:C:337:GLN:OE1	2.36	0.42
1:D:170:VAL:HG12	1:D:194:ALA:HA	2.01	0.42
1:D:468:ARG:HA	1:D:468:ARG:HD3	1.52	0.42
1:D:636:ARG:HD3	1:D:651:LEU:HB3	2.01	0.42
1:A:659:ALA:HB1	1:A:660:PRO:HD2	2.01	0.42
1:B:636:ARG:O	1:B:639:LEU:HB2	2.19	0.42
1:A:377:LEU:HD13	1:A:419:LEU:CD2	2.47	0.42
1:D:172:HIS:CD2	1:D:189:ALA:HB2	2.54	0.42
1:D:180:PHE:CD2	1:D:216:LEU:CD1	3.03	0.42
1:A:205:ILE:HD11	1:A:262:ARG:NH2	2.35	0.42
1:A:50:PHE:HB3	1:A:51:PRO:CD	2.49	0.42
1:B:68:SER:HB2	4:B:698:HOH:O	2.20	0.42
1:C:557:SER:C	1:C:559:ALA:H	2.20	0.42
1:B:102:ARG:HD3	1:B:137:ALA:HB2	2.01	0.42
1:A:174:GLU:CD	1:A:186:SER:HB3	2.40	0.42
1:A:402:PHE:HD2	1:A:402:PHE:N	2.14	0.42
1:B:330:PRO:HG3	1:B:335:ARG:HG3	2.01	0.42
1:C:180:PHE:CD2	1:C:216:LEU:HD13	2.55	0.42
1:A:439:ILE:O	1:A:439:ILE:CG2	2.68	0.42
2:A:680:ATP:O2A	3:A:681:DND:O8N	2.38	0.42
1:C:557:SER:C	1:C:559:ALA:N	2.72	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:80:LEU:HA	1:C:80:LEU:HD23	1.92	0.42
1:D:413:ILE:HD11	1:D:417:ARG:HH21	1.84	0.42
1:A:331:ALA:HA	1:A:601:PRO:HA	2.01	0.41
1:D:354:ARG:HH22	1:D:641:ASN:CG	2.22	0.41
1:A:557:SER:C	1:A:559:ALA:H	2.24	0.41
1:C:461:LEU:HA	1:C:461:LEU:HD23	1.94	0.41
1:A:166:LEU:N	1:A:167:PRO:HD3	2.35	0.41
1:C:50:PHE:HB3	1:C:51:PRO:CD	2.51	0.41
1:C:567:GLN:NE2	4:C:687:HOH:O	2.47	0.41
1:D:121:LYS:HG2	1:D:124:LEU:HD12	2.02	0.41
1:D:332:ASP:OD1	1:D:333:PRO:HD2	2.20	0.41
1:D:374:THR:HG23	1:D:415:LEU:CD2	2.50	0.41
1:A:342:GLU:O	1:A:346:ILE:HG13	2.20	0.41
1:A:429:GLY:O	1:A:433:ARG:HG3	2.20	0.41
1:B:605:PRO:HD2	1:B:608:GLU:HG3	2.02	0.41
1:C:348:VAL:O	1:C:352:GLU:HG3	2.19	0.41
1:C:377:LEU:HD13	1:C:419:LEU:CD2	2.45	0.41
1:D:593:ASN:HA	1:D:612:TYR:O	2.20	0.41
1:B:88:LEU:HD11	1:B:310:LEU:HD11	2.02	0.41
1:B:337:GLN:OE1	1:B:337:GLN:C	2.58	0.41
1:C:69:LEU:C	1:C:69:LEU:HD13	2.40	0.41
1:A:102:ARG:HD3	1:A:137:ALA:HB2	2.03	0.41
1:B:409:LYS:CG	1:B:410:ASN:H	2.33	0.41
1:C:441:HIS:C	1:C:441:HIS:ND1	2.73	0.41
1:C:542:ILE:N	1:C:542:ILE:HD12	2.36	0.41
1:D:310:LEU:O	1:D:310:LEU:HD12	2.21	0.41
1:B:43:ASP:OD2	1:B:269:ARG:NH2	2.54	0.41
1:C:5:SER:OG	1:C:8:GLN:HG3	2.21	0.41
1:D:160:LEU:HD13	1:D:303:PHE:CD2	2.56	0.41
1:D:358:LEU:HA	1:D:358:LEU:HD23	1.79	0.41
1:D:567:GLN:NE2	1:D:624:PHE:HB2	2.35	0.41
1:C:399:LEU:N	2:C:680:ATP:C2	2.89	0.41
1:D:50:PHE:HB3	1:D:51:PRO:CD	2.51	0.41
1:A:69:LEU:C	1:A:69:LEU:HD13	2.40	0.41
1:B:374:THR:HG23	1:B:415:LEU:CD2	2.51	0.41
1:B:468:ARG:HD3	1:B:468:ARG:HA	1.44	0.41
1:C:354:ARG:HH22	1:C:641:ASN:CG	2.23	0.41
1:A:593:ASN:HA	1:A:612:TYR:O	2.20	0.41
1:C:374:THR:HG23	1:C:415:LEU:CD2	2.51	0.41
1:C:659:ALA:HB1	1:C:660:PRO:HD2	2.01	0.41
1:D:341:TYR:CE1	1:D:345:ASN:ND2	2.88	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:5:SER:OG	1:A:8:GLN:HG3	2.21	0.41
1:B:297:ARG:HG2	1:B:301:GLU:OE2	2.21	0.41
1:B:326:PHE:HB3	1:B:329:VAL:HB	2.03	0.41
1:B:55:LEU:HD12	1:B:55:LEU:HA	1.82	0.41
1:D:298:GLU:HG3	1:D:299:LEU:N	2.35	0.41
1:B:439:ILE:HD11	1:C:465:TYR:CD1	2.57	0.40
1:C:490:TRP:CE2	3:C:681:DND:H13	2.56	0.40
1:D:125:PRO:HB3	1:D:127:TYR:CE2	2.55	0.40
1:D:374:THR:HG23	1:D:415:LEU:HD22	2.03	0.40
1:D:458:GLN:O	1:D:462:ARG:HG3	2.21	0.40
1:D:23:ILE:HB	1:D:60:ILE:CG2	2.51	0.40
1:A:297:ARG:HG2	1:A:301:GLU:OE2	2.21	0.40
1:A:53:LEU:HD23	1:A:53:LEU:HA	1.89	0.40
1:B:128:ARG:HH11	1:B:128:ARG:HD2	1.71	0.40
1:B:265:LYS:HA	1:B:265:LYS:HD3	1.87	0.40
1:D:478:LEU:HD23	1:D:478:LEU:HA	1.84	0.40
1:A:400:PRO:HD2	1:A:426:ILE:O	2.21	0.40
1:A:465:TYR:CD1	1:D:439:ILE:HD11	2.57	0.40
1:C:409:LYS:CG	1:C:410:ASN:H	2.33	0.40
1:A:636:ARG:O	1:A:639:LEU:HB2	2.21	0.40
1:C:26:PRO:HA	1:C:55:LEU:O	2.22	0.40
1:D:43:ASP:OD2	1:D:269:ARG:NH2	2.53	0.40
1:D:328:PHE:CG	1:D:509:PRO:HG3	2.57	0.40
1:D:514:GLN:O	1:D:518:ARG:HG3	2.22	0.40

All (2) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:297:ARG:NH2	1:C:142:GLU:OE2[8_555]	2.18	0.02
1:A:142:GLU:OE2	1:D:297:ARG:NH2[8_555]	2.19	0.01

## 5.3 Torsion angles

### 5.3.1 Protein backbone

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	652/680 (96%)	624 (96%)	27 (4%)	1 (0%)	47	64
1	B	651/680 (96%)	626 (96%)	24 (4%)	1 (0%)	47	64
1	C	640/680 (94%)	614 (96%)	25 (4%)	1 (0%)	47	64
1	D	641/680 (94%)	616 (96%)	24 (4%)	1 (0%)	47	64
All	All	2584/2720 (95%)	2480 (96%)	100 (4%)	4 (0%)	47	64

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	527	GLY
1	B	527	GLY
1	C	527	GLY
1	D	527	GLY

### 5.3.2 Protein sidechains ⓘ

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	527/548 (96%)	487 (92%)	40 (8%)	13	21
1	B	525/548 (96%)	487 (93%)	38 (7%)	14	22
1	C	515/548 (94%)	476 (92%)	39 (8%)	13	21
1	D	518/548 (94%)	480 (93%)	38 (7%)	14	21
All	All	2085/2192 (95%)	1930 (93%)	155 (7%)	13	21

All (155) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	1	MET
1	A	68	SER
1	A	77	LEU
1	A	93	VAL

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Mol	Chain	Res	Type
1	A	116	LEU
1	A	160	LEU
1	A	200	LEU
1	A	201	SER
1	A	206	THR
1	A	211	GLU
1	A	256	LEU
1	A	257	LEU
1	A	284	LEU
1	A	301	GLU
1	A	310	LEU
1	A	319	LEU
1	A	320	LEU
1	A	334	GLN
1	A	354	ARG
1	A	373	SER
1	A	377	LEU
1	A	389	ARG
1	A	402	PHE
1	A	409	LYS
1	A	410	ASN
1	A	419	LEU
1	A	452	VAL
1	A	454	PHE
1	A	468	ARG
1	A	480	THR
1	A	488	LEU
1	A	495	VAL
1	A	498	GLN
1	A	558	GLU
1	A	560	LYS
1	A	566	LEU
1	A	567	GLN
1	A	606	LYS
1	A	621	LEU
1	A	664	SER
1	B	1	MET
1	B	68	SER
1	B	77	LEU
1	B	93	VAL
1	B	116	LEU
1	B	160	LEU

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Mol	Chain	Res	Type
1	B	200	LEU
1	B	201	SER
1	B	206	THR
1	B	211	GLU
1	B	256	LEU
1	B	257	LEU
1	B	284	LEU
1	B	301	GLU
1	B	310	LEU
1	B	319	LEU
1	B	320	LEU
1	B	334	GLN
1	B	354	ARG
1	B	373	SER
1	B	377	LEU
1	B	389	ARG
1	B	409	LYS
1	B	410	ASN
1	B	419	LEU
1	B	452	VAL
1	B	454	PHE
1	B	468	ARG
1	B	480	THR
1	B	488	LEU
1	B	498	GLN
1	B	515	HIS
1	B	566	LEU
1	B	567	GLN
1	B	606	LYS
1	B	607	SER
1	B	621	LEU
1	B	664	SER
1	C	1	MET
1	C	5	SER
1	C	68	SER
1	C	77	LEU
1	C	93	VAL
1	C	116	LEU
1	C	136	MET
1	C	200	LEU
1	C	201	SER
1	C	206	THR

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Mol	Chain	Res	Type
1	C	211	GLU
1	C	256	LEU
1	C	257	LEU
1	C	284	LEU
1	C	301	GLU
1	C	310	LEU
1	C	319	LEU
1	C	320	LEU
1	C	334	GLN
1	C	337	GLN
1	C	354	ARG
1	C	373	SER
1	C	377	LEU
1	C	389	ARG
1	C	409	LYS
1	C	410	ASN
1	C	419	LEU
1	C	454	PHE
1	C	468	ARG
1	C	480	THR
1	C	498	GLN
1	C	566	LEU
1	C	567	GLN
1	C	597	ARG
1	C	606	LYS
1	C	607	SER
1	C	608	GLU
1	C	621	LEU
1	C	664	SER
1	D	1	MET
1	D	77	LEU
1	D	93	VAL
1	D	116	LEU
1	D	136	MET
1	D	160	LEU
1	D	200	LEU
1	D	201	SER
1	D	206	THR
1	D	211	GLU
1	D	256	LEU
1	D	257	LEU
1	D	284	LEU

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Mol	Chain	Res	Type
1	D	310	LEU
1	D	319	LEU
1	D	320	LEU
1	D	322	GLU
1	D	334	GLN
1	D	351	LEU
1	D	354	ARG
1	D	373	SER
1	D	377	LEU
1	D	402	PHE
1	D	409	LYS
1	D	410	ASN
1	D	419	LEU
1	D	452	VAL
1	D	454	PHE
1	D	468	ARG
1	D	480	THR
1	D	488	LEU
1	D	495	VAL
1	D	498	GLN
1	D	566	LEU
1	D	567	GLN
1	D	606	LYS
1	D	621	LEU
1	D	664	SER

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (17) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	172	HIS
1	A	345	ASN
1	A	515	HIS
1	A	567	GLN
1	B	8	GLN
1	B	172	HIS
1	B	295	HIS
1	B	345	ASN
1	B	567	GLN
1	C	172	HIS
1	C	345	ASN
1	C	515	HIS
1	C	567	GLN

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Mol	Chain	Res	Type
1	D	8	GLN
1	D	295	HIS
1	D	345	ASN
1	D	567	GLN

### 5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

### 5.5 Carbohydrates [i](#)

There are no carbohydrates in this entry.

### 5.6 Ligand geometry [i](#)

8 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	ATP	B	680	-	26,33,33	0.85	1 (3%)	31,52,52	1.27	1 (3%)
2	ATP	D	680	-	26,33,33	0.94	2 (7%)	31,52,52	1.25	2 (6%)
3	DND	B	681	-	40,48,48	1.18	2 (5%)	47,73,73	1.20	3 (6%)
2	ATP	C	680	-	26,33,33	0.79	1 (3%)	31,52,52	1.37	4 (12%)
3	DND	C	681	-	40,48,48	0.97	2 (5%)	47,73,73	1.21	2 (4%)
3	DND	D	681	-	40,48,48	1.05	3 (7%)	47,73,73	1.25	4 (8%)
3	DND	A	681	-	40,48,48	0.94	3 (7%)	47,73,73	1.39	4 (8%)
2	ATP	A	680	-	26,33,33	0.84	1 (3%)	31,52,52	1.46	5 (16%)

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	ATP	B	680	-	-	11/18/38/38	0/3/3/3
2	ATP	D	680	-	-	2/18/38/38	0/3/3/3
3	DND	B	681	-	-	9/22/62/62	0/5/5/5
2	ATP	C	680	-	-	4/18/38/38	0/3/3/3
3	DND	C	681	-	-	4/22/62/62	0/5/5/5
3	DND	D	681	-	-	8/22/62/62	0/5/5/5
3	DND	A	681	-	-	5/22/62/62	0/5/5/5
2	ATP	A	680	-	-	0/18/38/38	0/3/3/3

All (15) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	B	681	DND	C3N-C7N	5.12	1.52	1.47
3	D	681	DND	C3N-C7N	4.48	1.51	1.47
3	C	681	DND	C3N-C7N	3.77	1.51	1.47
2	D	680	ATP	O4'-C1'	2.89	1.45	1.41
3	A	681	DND	O4B-C1B	2.88	1.45	1.41
3	B	681	DND	O4B-C1B	2.88	1.45	1.41
3	A	681	DND	C3N-C7N	2.78	1.50	1.47
2	A	680	ATP	O4'-C1'	2.47	1.44	1.41
2	B	680	ATP	O4'-C1'	2.45	1.44	1.41
3	C	681	DND	O4D-C1D	2.20	1.44	1.41
3	D	681	DND	O4D-C1D	2.13	1.44	1.41
2	C	680	ATP	O4'-C1'	2.09	1.44	1.41
3	A	681	DND	C2A-N3A	2.07	1.35	1.32
2	D	680	ATP	C2-N3	2.02	1.35	1.32
3	D	681	DND	O4B-C1B	2.02	1.43	1.41

All (25) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	D	681	DND	N3A-C2A-N1A	-5.31	120.38	128.68
3	C	681	DND	N3A-C2A-N1A	-5.01	120.85	128.68
3	A	681	DND	N3A-C2A-N1A	-4.92	120.99	128.68
2	A	680	ATP	N3-C2-N1	-4.76	121.23	128.68
2	D	680	ATP	N3-C2-N1	-4.56	121.55	128.68
2	B	680	ATP	N3-C2-N1	-4.55	121.57	128.68

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	C	680	ATP	N3-C2-N1	-4.41	121.78	128.68
3	B	681	DND	N3A-C2A-N1A	-4.22	122.08	128.68
3	A	681	DND	C3D-C2D-C1D	3.50	106.24	100.98
3	D	681	DND	C3D-C2D-C1D	3.27	105.91	100.98
3	C	681	DND	C3D-C2D-C1D	3.08	105.62	100.98
2	C	680	ATP	PB-O3B-PG	-3.04	122.41	132.83
3	B	681	DND	C3D-C2D-C1D	3.01	105.51	100.98
3	A	681	DND	N6A-C6A-N1A	2.85	124.50	118.57
3	D	681	DND	O4D-C4D-C3D	2.55	110.16	105.11
2	D	680	ATP	C4-C5-N7	-2.46	106.84	109.40
3	B	681	DND	C3B-C2B-C1B	2.44	104.64	100.98
3	A	681	DND	C5A-C6A-N6A	-2.43	116.65	120.35
2	A	680	ATP	PB-O3B-PG	-2.32	124.86	132.83
2	A	680	ATP	C2-N1-C6	2.22	122.56	118.75
3	D	681	DND	C4A-C5A-N7A	-2.11	107.20	109.40
2	C	680	ATP	O3G-PG-O2G	2.07	115.53	107.64
2	A	680	ATP	PA-O3A-PB	-2.06	125.74	132.83
2	A	680	ATP	O2B-PB-O1B	2.06	122.44	112.24
2	C	680	ATP	C2-N1-C6	2.02	122.21	118.75

There are no chirality outliers.

All (43) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	B	680	ATP	PB-O3B-PG-O2G
3	B	681	DND	O4D-C1D-N1N-C6N
3	B	681	DND	O4D-C1D-N1N-C2N
3	B	681	DND	C2D-C1D-N1N-C6N
3	B	681	DND	C2D-C1D-N1N-C2N
3	C	681	DND	O4D-C4D-C5D-O5D
3	D	681	DND	O4D-C1D-N1N-C6N
3	D	681	DND	O4D-C1D-N1N-C2N
3	D	681	DND	C2D-C1D-N1N-C6N
3	D	681	DND	C2D-C1D-N1N-C2N
3	A	681	DND	O4D-C1D-N1N-C6N
3	B	681	DND	O4D-C4D-C5D-O5D
3	C	681	DND	C3D-C4D-C5D-O5D
3	D	681	DND	O4D-C4D-C5D-O5D
2	B	680	ATP	O4'-C4'-C5'-O5'
3	B	681	DND	C3D-C4D-C5D-O5D
2	B	680	ATP	PA-O3A-PB-O1B
3	B	681	DND	PN-O3P-PA-O13

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Mol	Chain	Res	Type	Atoms
2	C	680	ATP	PG-O3B-PB-O1B
3	A	681	DND	PN-O3P-PA-O13
3	D	681	DND	C4B-C5B-O5B-PA
3	A	681	DND	C4B-C5B-O5B-PA
3	B	681	DND	C4B-C5B-O5B-PA
3	B	681	DND	PN-O3P-PA-O5B
3	D	681	DND	PN-O3P-PA-O5B
3	A	681	DND	PN-O3P-PA-O5B
2	B	680	ATP	C3'-C4'-C5'-O5'
2	B	680	ATP	PB-O3B-PG-O3G
2	B	680	ATP	C5'-O5'-PA-O3A
3	A	681	DND	O4D-C4D-C5D-O5D
2	C	680	ATP	PB-O3A-PA-O1A
3	C	681	DND	C4B-C5B-O5B-PA
2	B	680	ATP	PA-O3A-PB-O2B
2	C	680	ATP	PG-O3B-PB-O2B
3	D	681	DND	C3D-C4D-C5D-O5D
2	D	680	ATP	PG-O3B-PB-O1B
2	B	680	ATP	PB-O3B-PG-O1G
2	B	680	ATP	PG-O3B-PB-O2B
2	D	680	ATP	PG-O3B-PB-O2B
2	C	680	ATP	PB-O3A-PA-O2A
2	B	680	ATP	C5'-O5'-PA-O1A
2	B	680	ATP	C5'-O5'-PA-O2A
3	C	681	DND	C5B-O5B-PA-O13

There are no ring outliers.

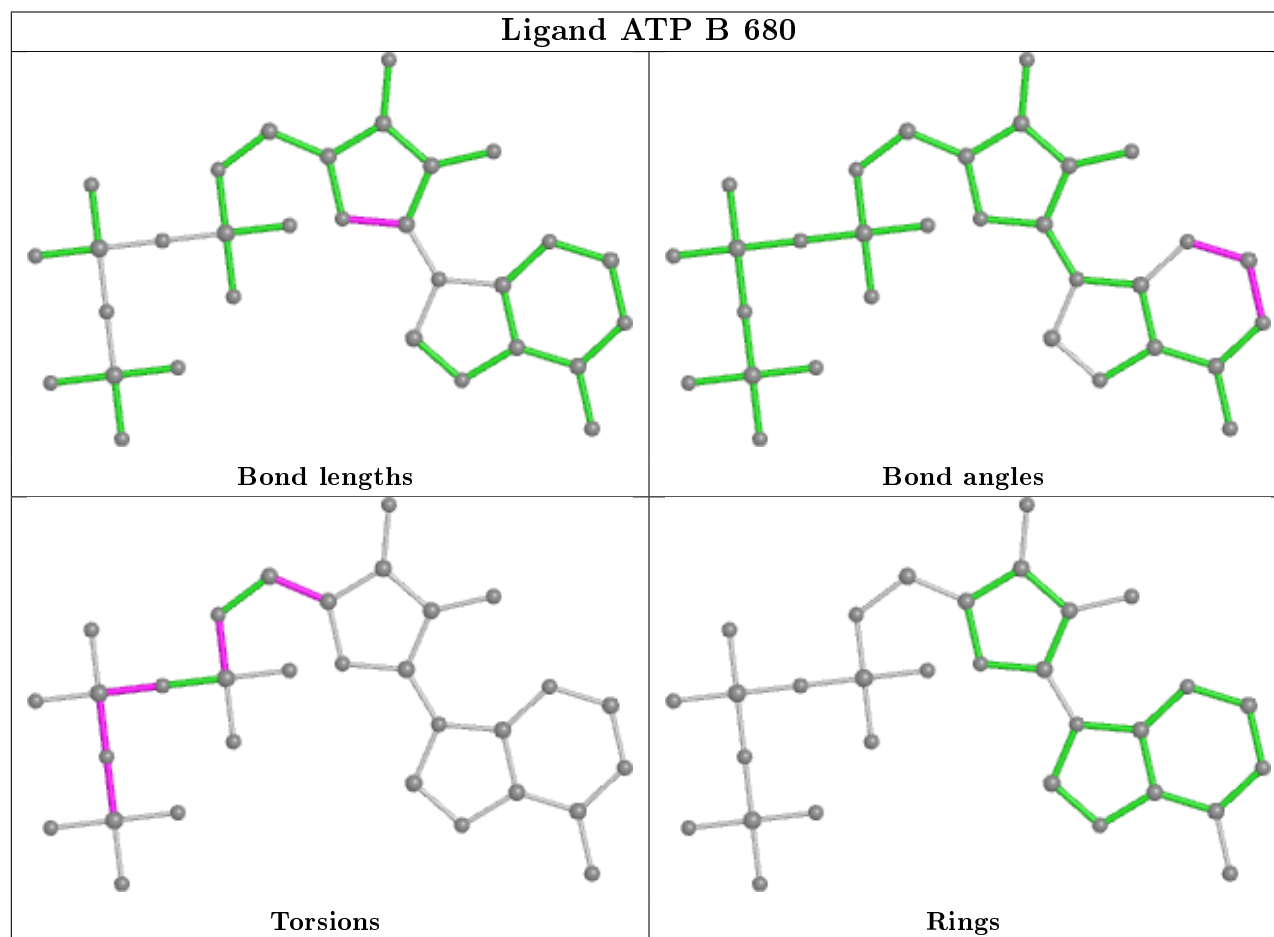
7 monomers are involved in 15 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	B	680	ATP	1	0
2	D	680	ATP	1	0
2	C	680	ATP	2	0
3	C	681	DND	3	0
3	D	681	DND	1	0
3	A	681	DND	6	0
2	A	680	ATP	2	0

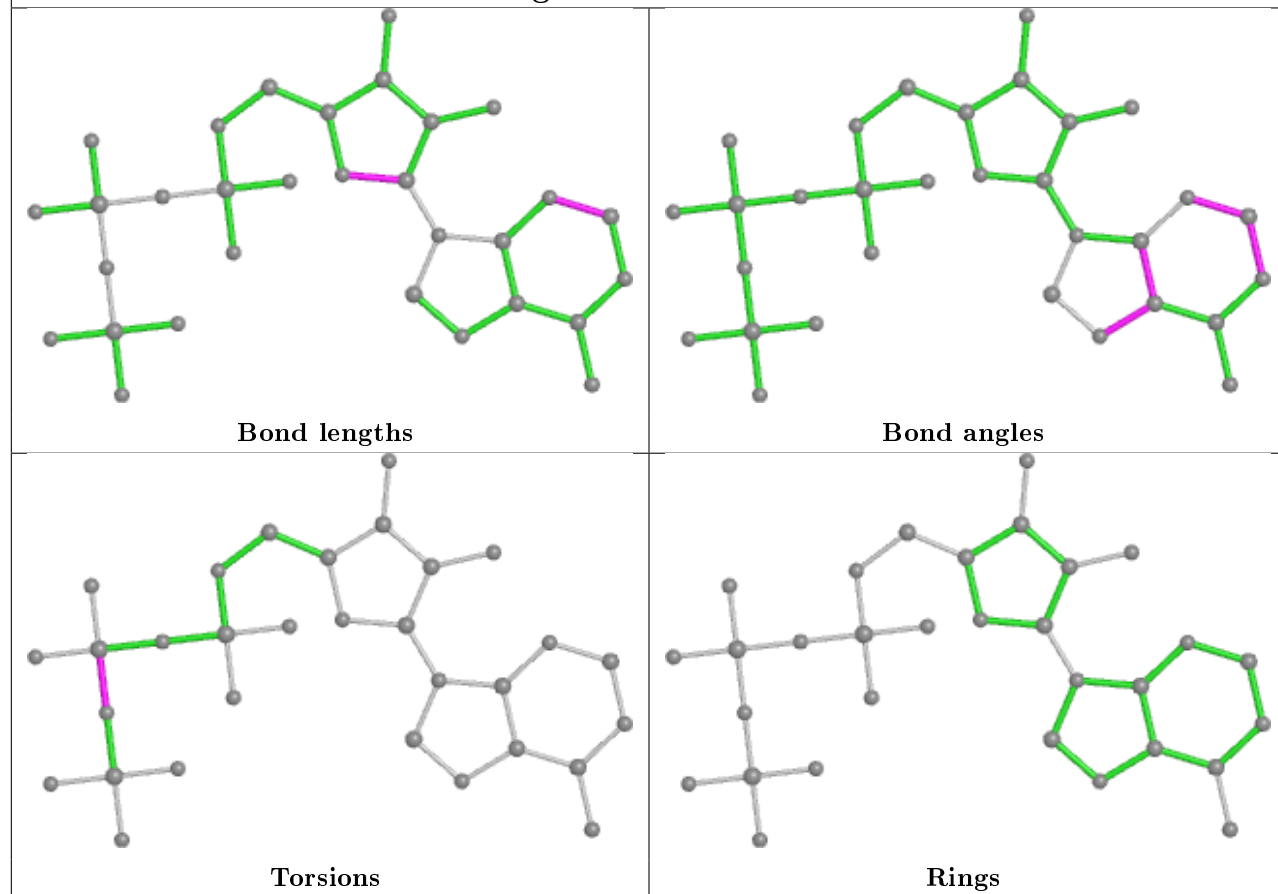
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is



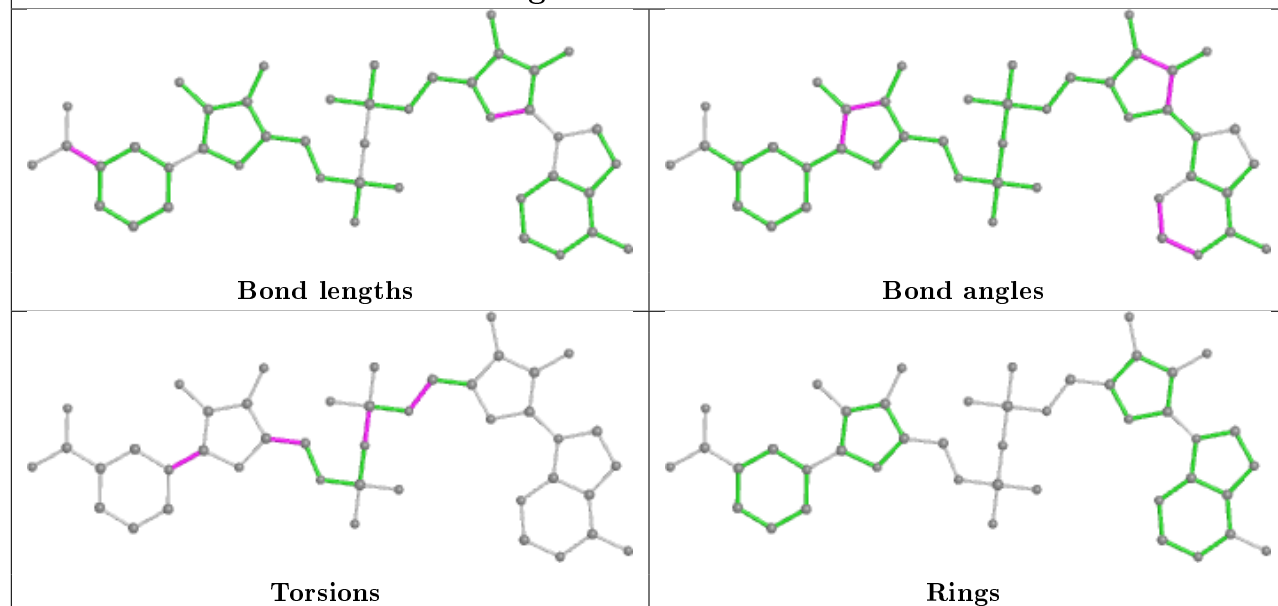
within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question 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.



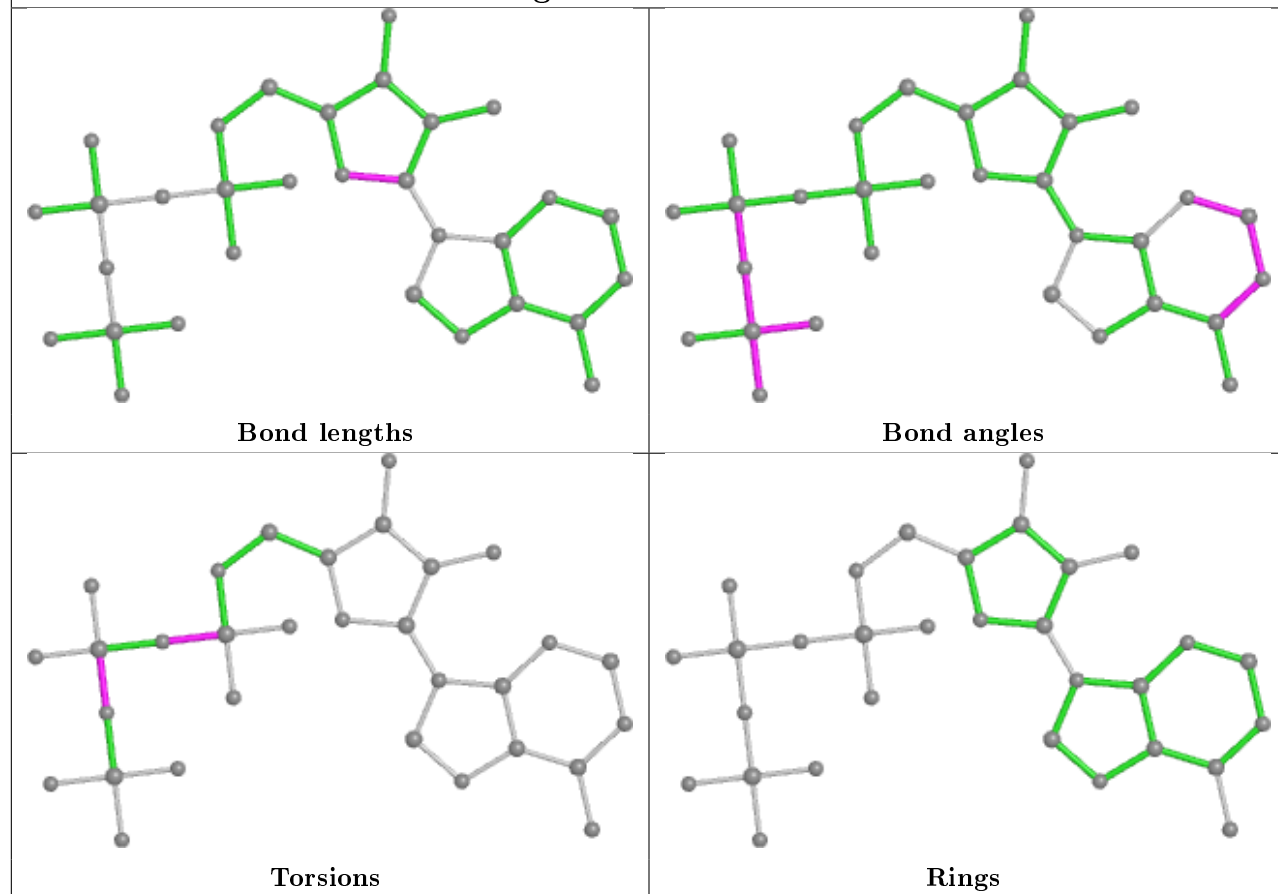
## Ligand ATP D 680



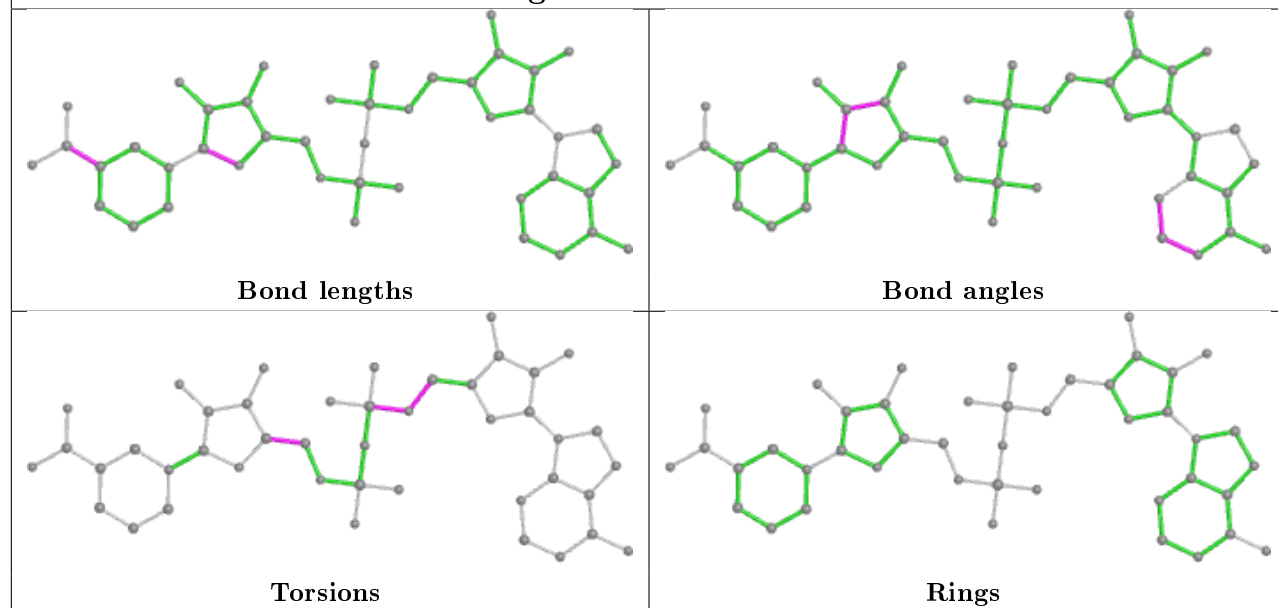
## Ligand DND B 681

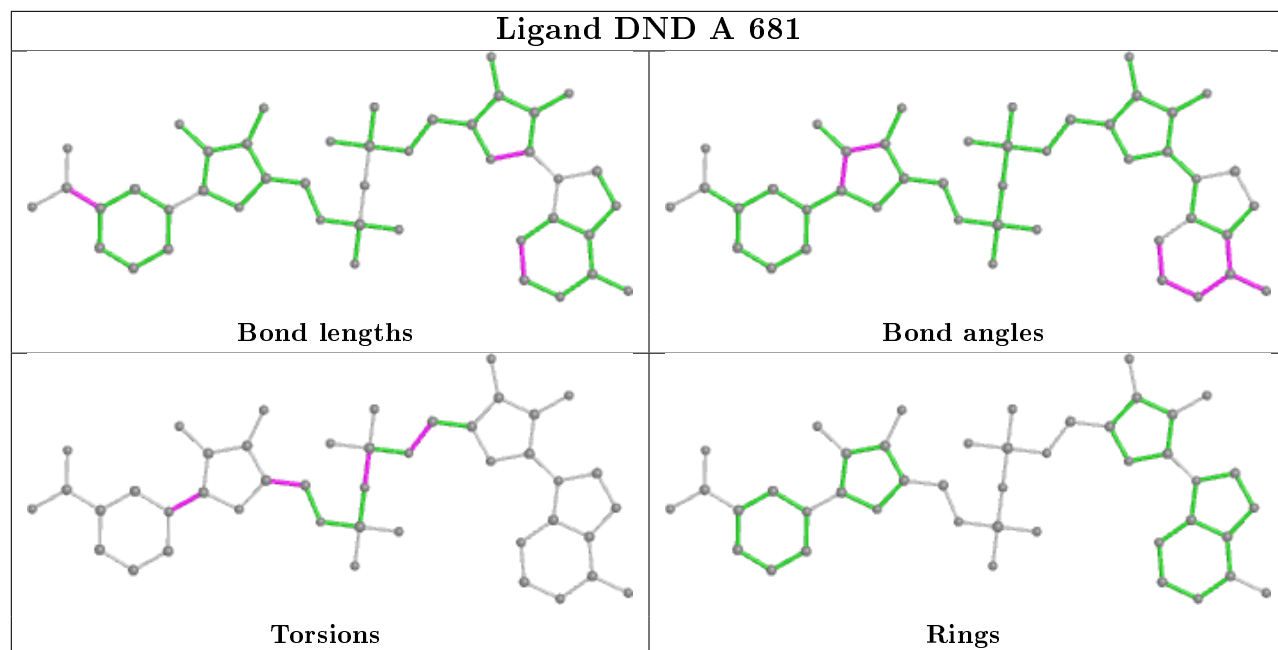
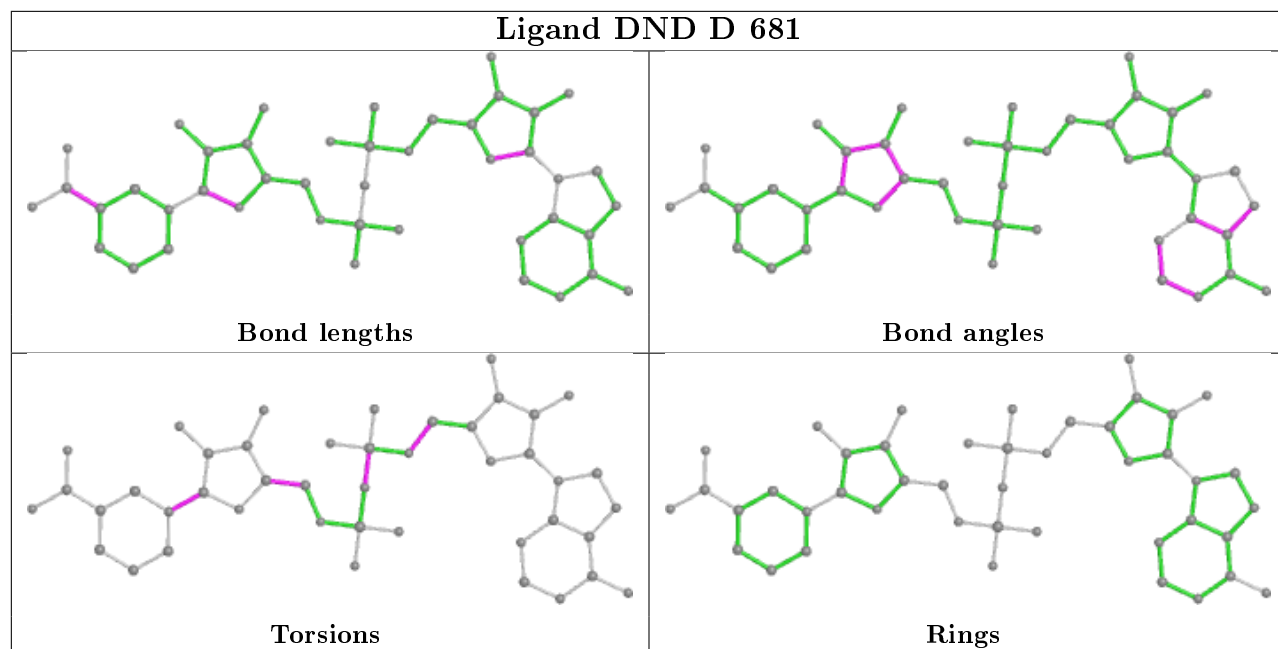


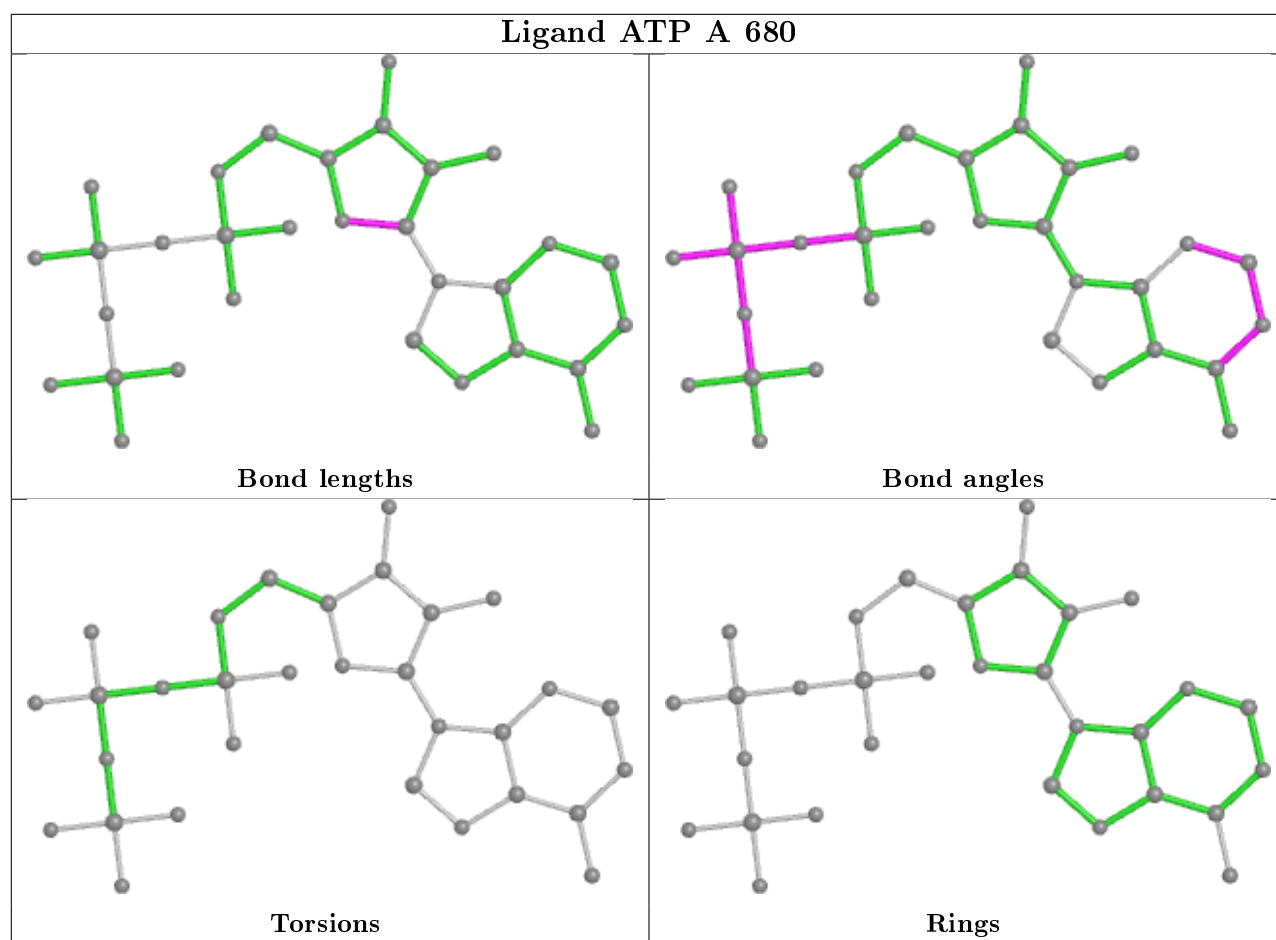
## Ligand ATP C 680



## Ligand DND C 681







## 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<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
1	A	658/680 (96%)	-0.45	7 (1%) 80 79	30, 49, 85, 147	0
1	B	657/680 (96%)	-0.42	13 (1%) 65 60	30, 50, 85, 147	0
1	C	648/680 (95%)	-0.44	7 (1%) 80 79	33, 52, 85, 148	0
1	D	649/680 (95%)	-0.45	7 (1%) 80 79	33, 49, 86, 146	0
All	All	2612/2720 (96%)	-0.44	34 (1%) 77 75	30, 50, 86, 148	0

All (34) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	453	THR	4.0
1	C	453	THR	4.0
1	C	454	PHE	3.6
1	C	452	VAL	3.3
1	B	523	ALA	3.2
1	A	524	GLY	3.1
1	D	452	VAL	3.1
1	B	450	TYR	3.1
1	A	450	TYR	3.1
1	B	524	GLY	2.9
1	A	449	VAL	2.9
1	A	678	LYS	2.8
1	B	417	ARG	2.8
1	D	402	PHE	2.8
1	B	298	GLU	2.7
1	C	417	ARG	2.7
1	D	678	LYS	2.6
1	A	523	ALA	2.5
1	A	418	ALA	2.4
1	C	561	VAL	2.4
1	D	454	PHE	2.4

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Mol	Chain	Res	Type	RSRZ
1	B	525	GLU	2.4
1	D	679	GLY	2.3
1	C	401	GLY	2.3
1	D	1	MET	2.3
1	B	333	PRO	2.2
1	B	526	PHE	2.2
1	B	522	SER	2.2
1	C	674	ARG	2.1
1	B	334	GLN	2.1
1	A	526	PHE	2.1
1	B	410	ASN	2.1
1	B	527	GLY	2.1
1	B	1	MET	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 carbohydrates in this entry.

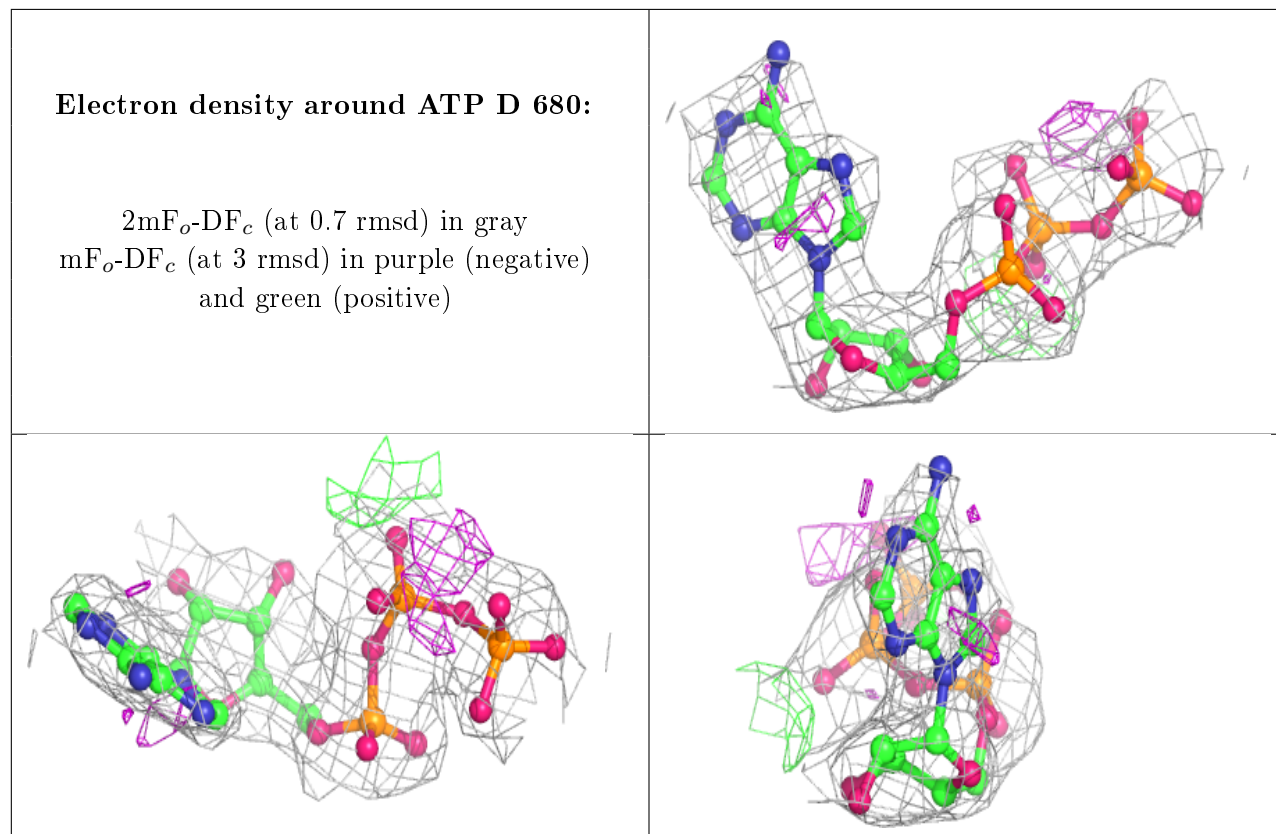
## 6.4 Ligands [i](#)

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<sup>th</sup> 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
2	ATP	D	680	31/31	0.88	0.18	61,85,130,136	0
2	ATP	A	680	31/31	0.88	0.24	59,98,151,255	0
3	DND	C	681	44/44	0.91	0.26	61,90,139,166	0
3	DND	D	681	44/44	0.91	0.23	57,86,153,164	0
2	ATP	B	680	31/31	0.91	0.21	55,81,185,260	0
2	ATP	C	680	31/31	0.92	0.14	53,90,153,230	0
3	DND	A	681	44/44	0.94	0.16	43,77,118,140	0
3	DND	B	681	44/44	0.94	0.19	48,78,161,169	0

The following is a graphical depiction of the model fit to experimental electron density of all

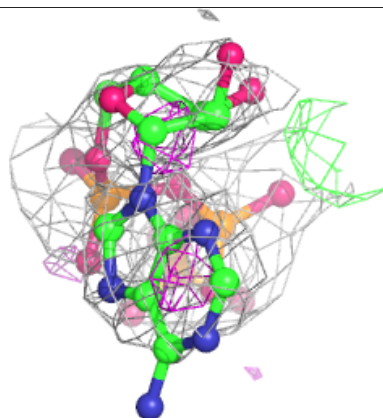
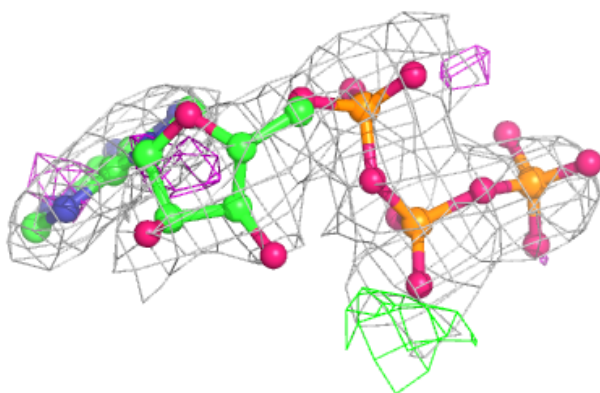
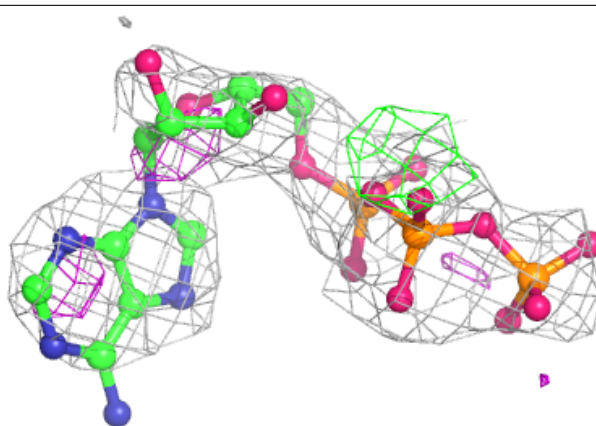
instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation to approximate a three-dimensional view.



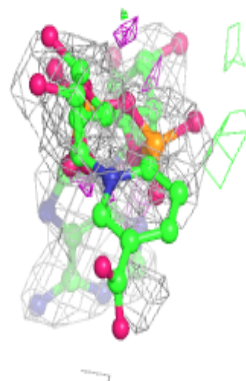
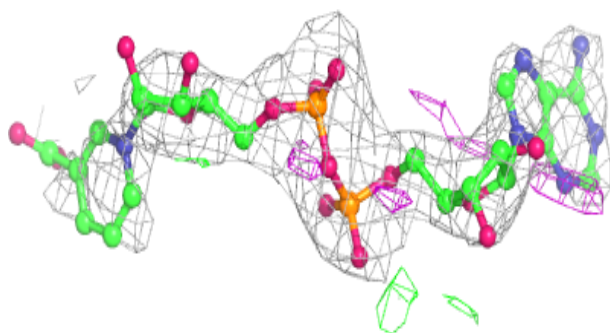
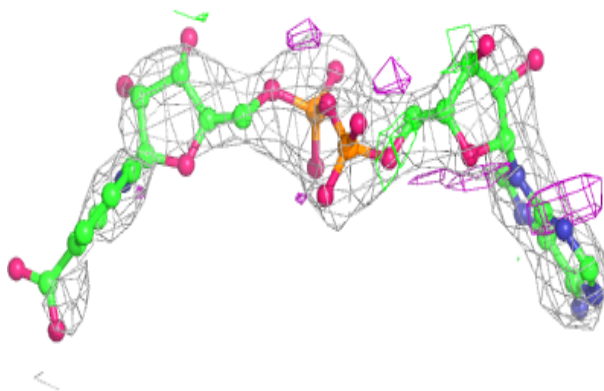


**Electron density around ATP A 680:**

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

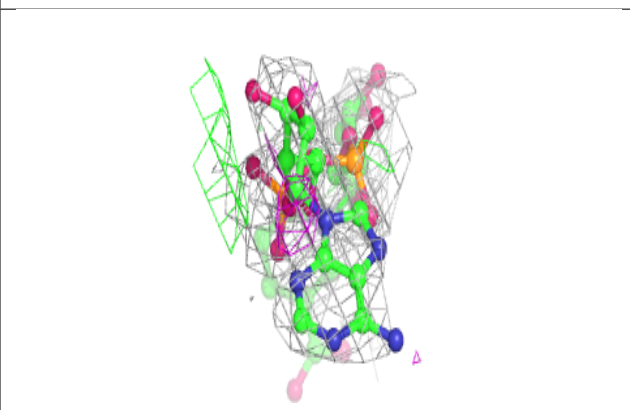
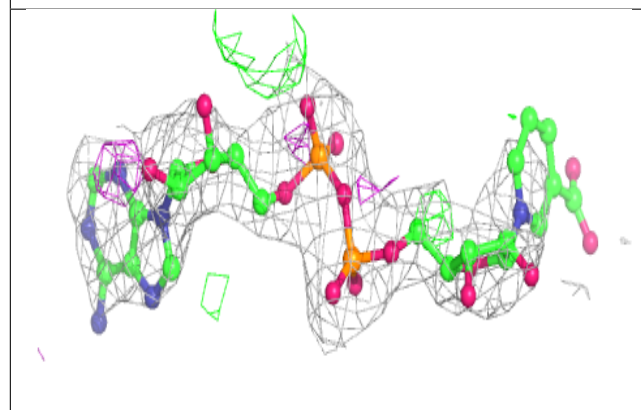
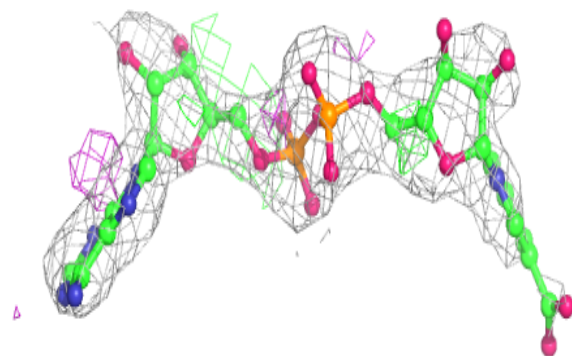
**Electron density around DND C 681:**

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

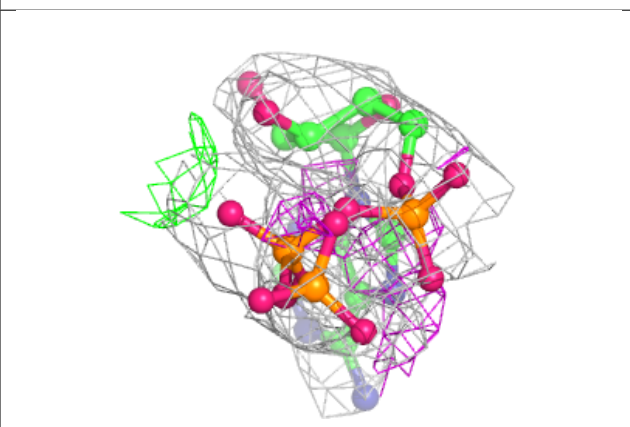
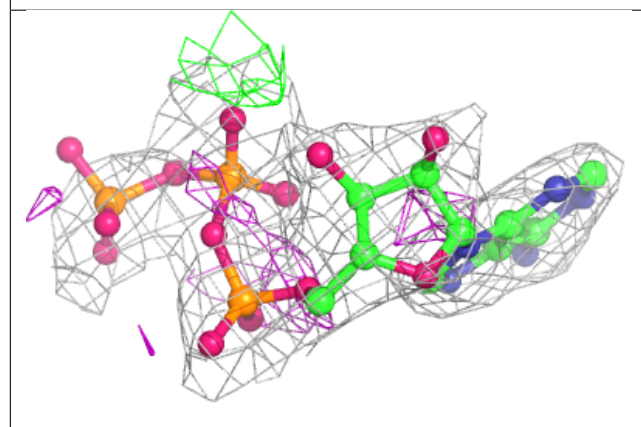
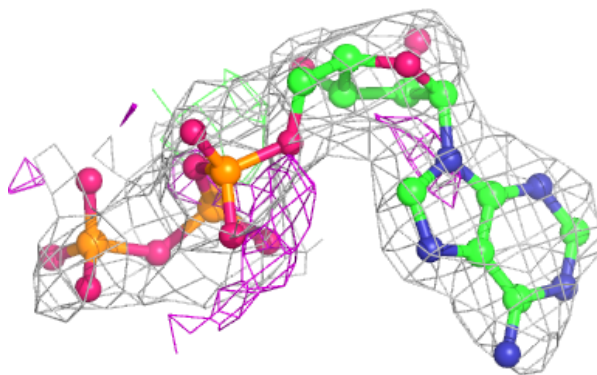


**Electron density around DND D 681:**

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

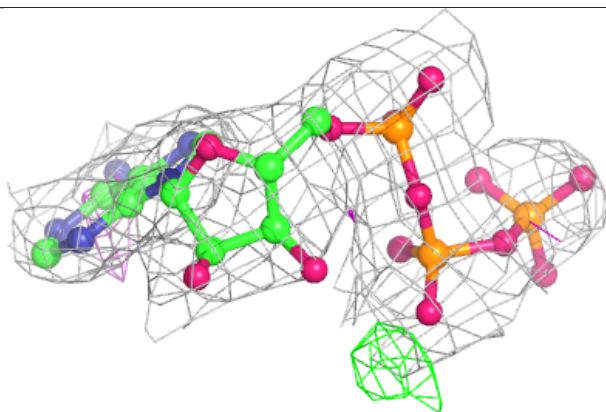
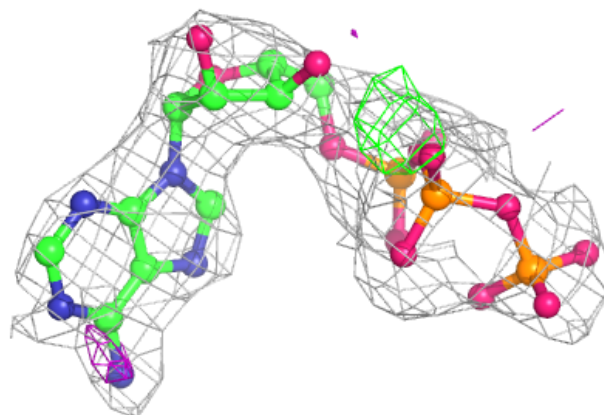
**Electron density around ATP B 680:**

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

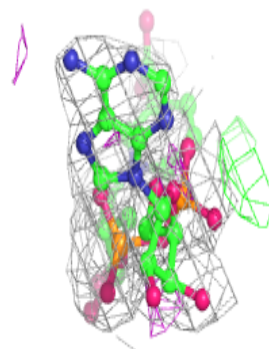
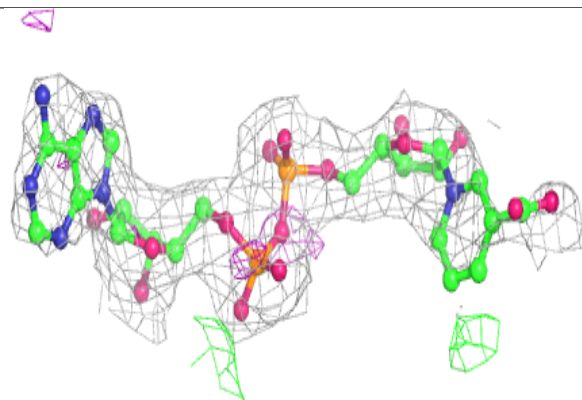
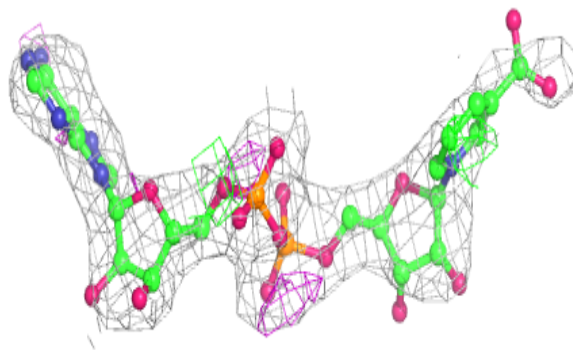


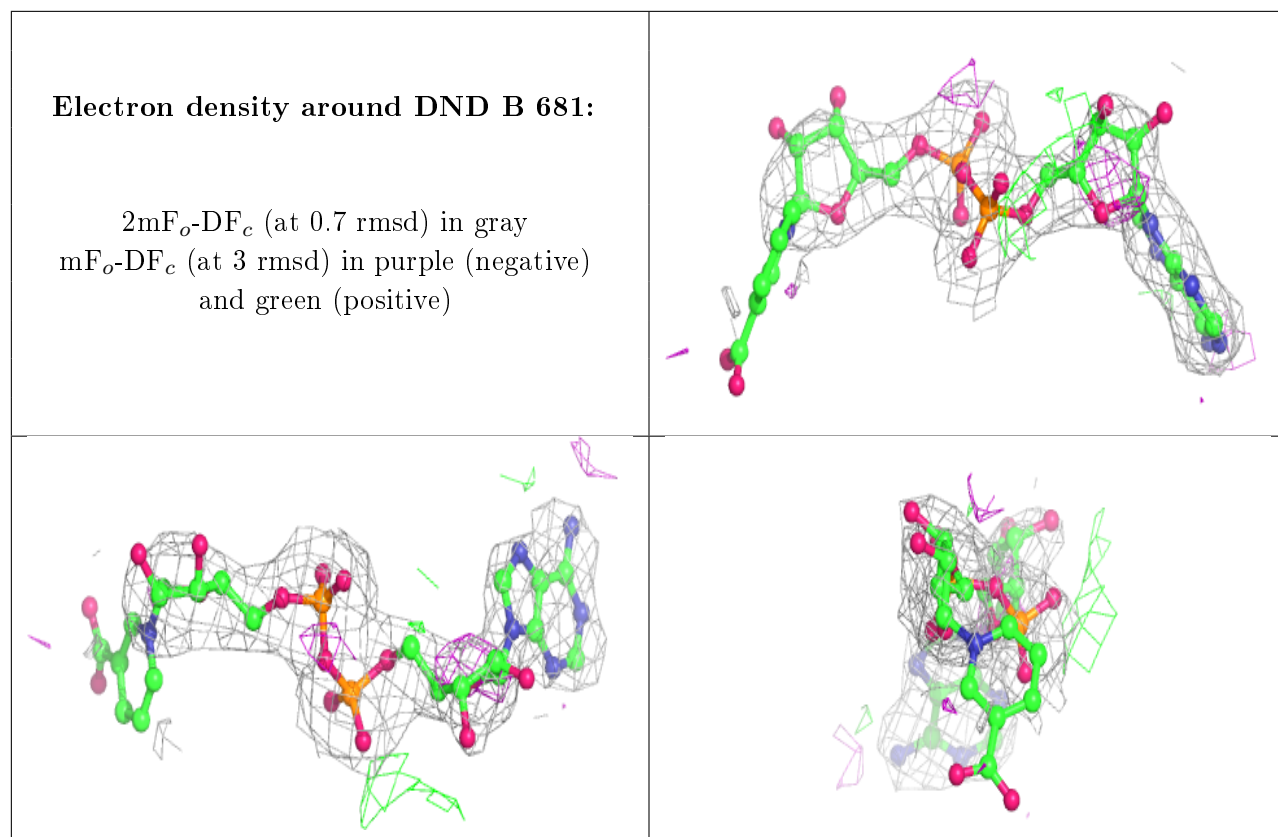
**Electron density around ATP C 680:**

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

**Electron density around DND A 681:**

$2mF_o-DF_c$  (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.