



# Full wwPDB X-ray Structure Validation Report ⓘ

Dec 3, 2023 – 03:47 pm GMT

PDB ID : 1E79  
Title : Bovine F1-ATPase inhibited by DCCD (dicyclohexylcarbodiimide)  
Authors : Gibbons, C.; Montgomery, M.G.; Leslie, A.G.W.; Walker, J.E.  
Deposited on : 2000-08-25  
Resolution : 2.40 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.

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 : 1.8.4, 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

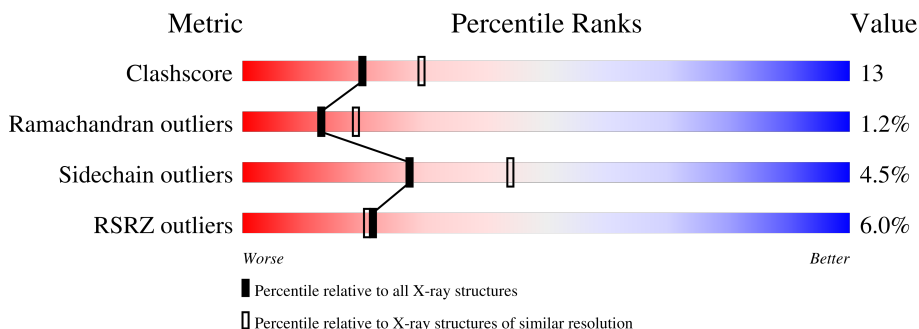
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.40 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.



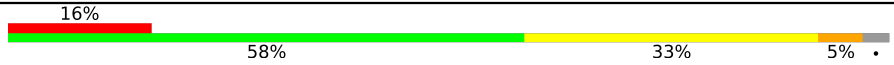


Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
Clashscore	141614	4398 (2.40-2.40)
Ramachandran outliers	138981	4318 (2.40-2.40)
Sidechain outliers	138945	4319 (2.40-2.40)
RSRZ outliers	127900	3811 (2.40-2.40)

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  $\geq 3$ , 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	510	 4% 75% 20% ..
1	B	510	 5% 70% 24% ...
1	C	510	 2% 75% 20% ..
2	D	482	 2% 77% 19% ..
2	E	482	 8% 73% 21% ..
2	F	482	 2% 75% 20% ..

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Length	Quality of chain
3	G	272	
4	H	146	
5	I	50	

## 2 Entry composition

There are 12 unique types of molecules in this entry. The entry contains 26318 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 ATP SYNTHASE ALPHA CHAIN HEART ISOFORM.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	492	3748	2360	661	715	12	0	0	0
1	B	492	3748	2360	661	715	12	0	0	0
1	C	492	3748	2360	661	715	12	0	0	0

There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	481	GLY	SER	cloning artifact	UNP P19483
B	481	GLY	SER	cloning artifact	UNP P19483
C	481	GLY	SER	cloning artifact	UNP P19483

- Molecule 2 is a protein called ATP SYNTHASE BETA CHAIN.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
2	D	467	3538	2243	601	683	11	0	0	0
2	E	466	3530	2238	600	681	11	0	0	0
2	F	466	3530	2238	600	681	11	0	0	0

- Molecule 3 is a protein called ATP SYNTHASE GAMMA CHAIN.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
3	G	263	2051	1291	354	398	8	0	0	0

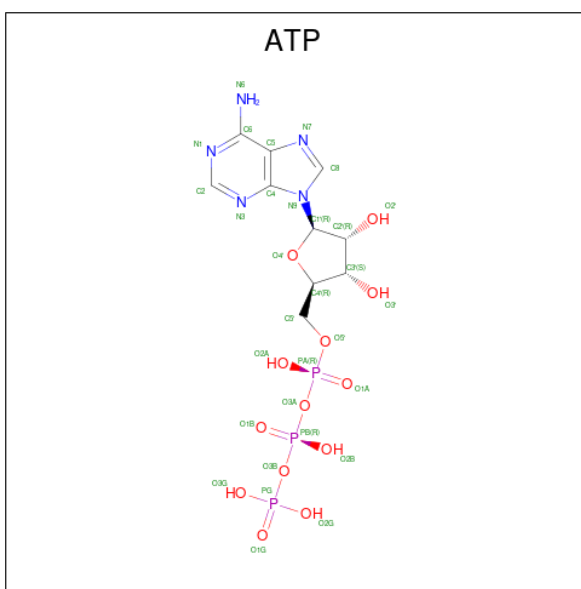
- Molecule 4 is a protein called ATP SYNTHASE DELTA CHAIN.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
4	H	131	970	609	164	195	2	0	0	0

- Molecule 5 is a protein called ATP SYNTHASE EPSILON CHAIN.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
5	I	47	369	237	66	64	2	0	0	0

- Molecule 6 is ADENOSINE-5'-TRIPHOSPHATE (three-letter code: ATP) (formula:  $C_{10}H_{16}N_5O_{13}P_3$ ).



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

- Molecule 7 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

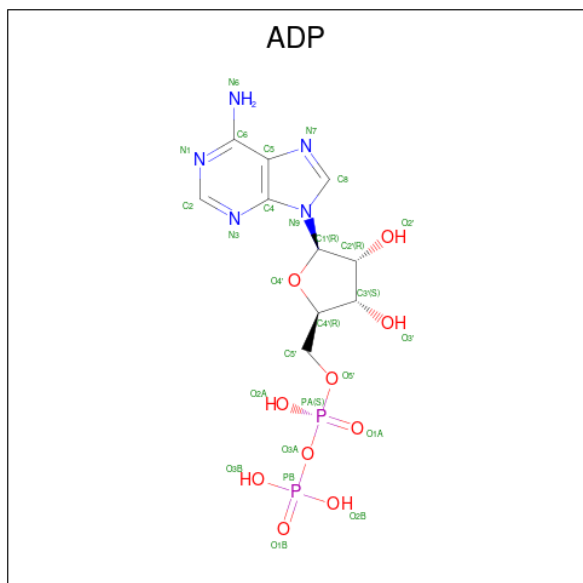
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
7	A	1	Total Mg 1 1	0	0
7	B	1	Total Mg 1 1	0	0
7	C	1	Total Mg 1 1	0	0

Continued on next page...

Continued from previous page...

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
7	D	1	Total Mg 1 1	0	0
7	F	1	Total Mg 1 1	0	0

- Molecule 8 is ADENOSINE-5'-DIPHOSPHATE (three-letter code: ADP) (formula:  $C_{10}H_{15}N_5O_{10}P_2$ ).



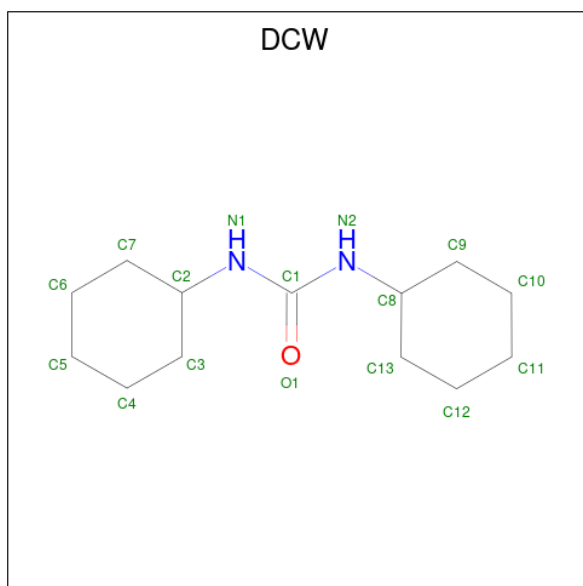
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
8	B	1	Total C N O P 27 10 5 10 2	0	0
8	D	1	Total C N O P 27 10 5 10 2	0	0
8	F	1	Total C N O P 27 10 5 10 2	0	0

- Molecule 9 is GLYCEROL (three-letter code: GOL) (formula:  $C_3H_8O_3$ ).



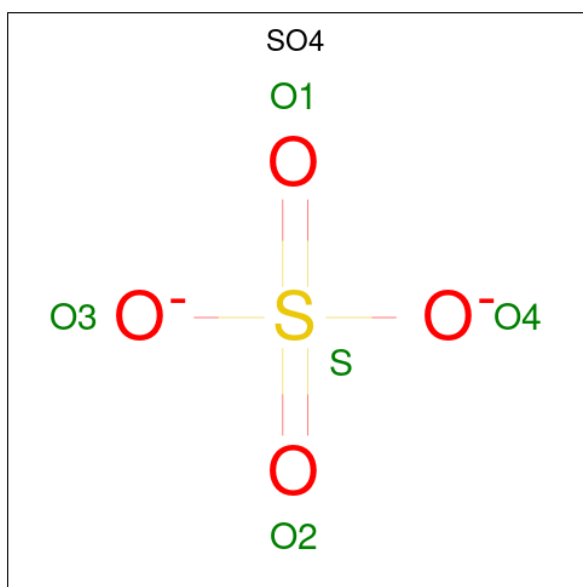
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
9	B	1	Total	C	O	0	0
			6	3	3		

- Molecule 10 is DICYCLOHEXYLUREA (three-letter code: DCW) (formula:  $C_{13}H_{24}N_2O$ ).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
10	D	1	Total	C	N	O	0	0
			16	13	2	1		

- Molecule 11 is SULFATE ION (three-letter code: SO4) (formula:  $O_4S$ ).



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

- Molecule 12 is water.

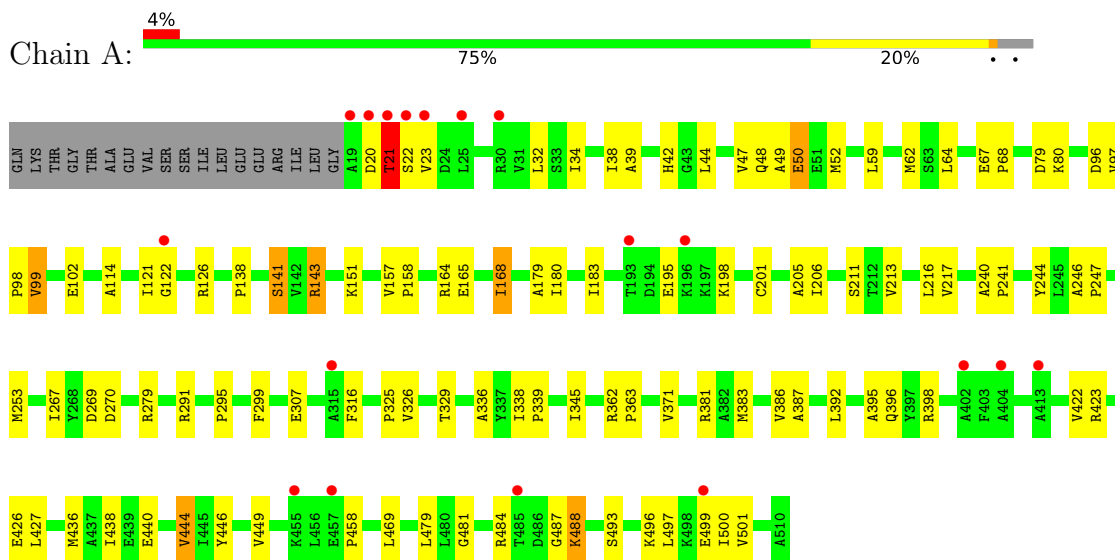
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
12	A	163	Total	O	0	0
			163	163		
12	B	140	Total	O	0	0
			140	140		
12	C	167	Total	O	0	0
			167	167		
12	D	148	Total	O	0	0
			148	148		
12	E	95	Total	O	0	0
			95	95		
12	F	164	Total	O	0	0
			164	164		
12	G	25	Total	O	0	0
			25	25		
12	H	5	Total	O	0	0
			5	5		
12	I	4	Total	O	0	0
			4	4		



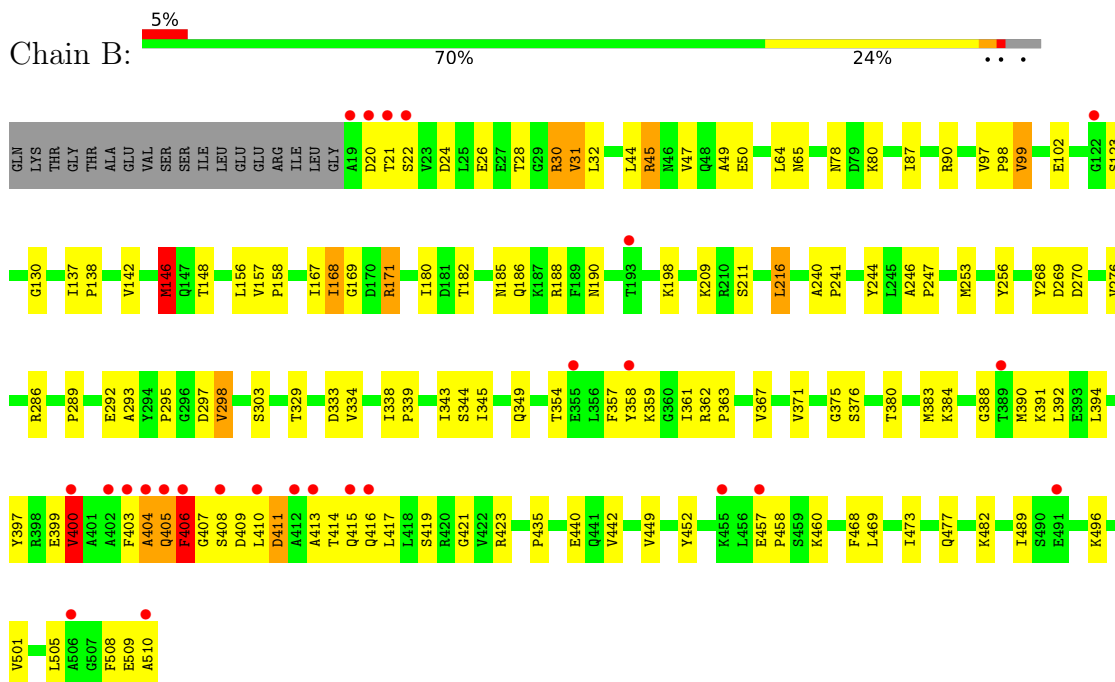
### 3 Residue-property plots i

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.

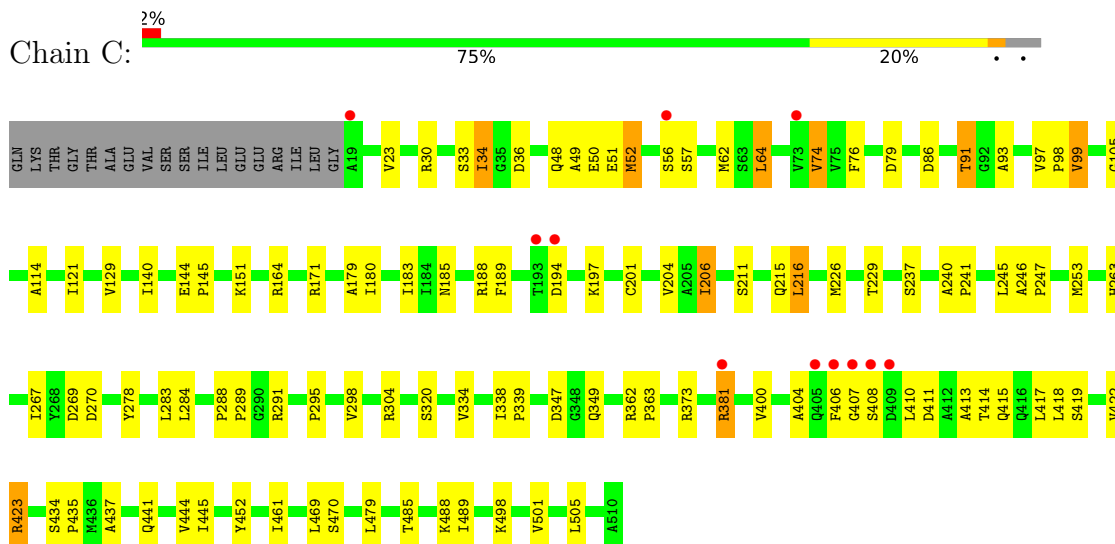
- Molecule 1: ATP SYNTHASE ALPHA CHAIN HEART ISOFORM



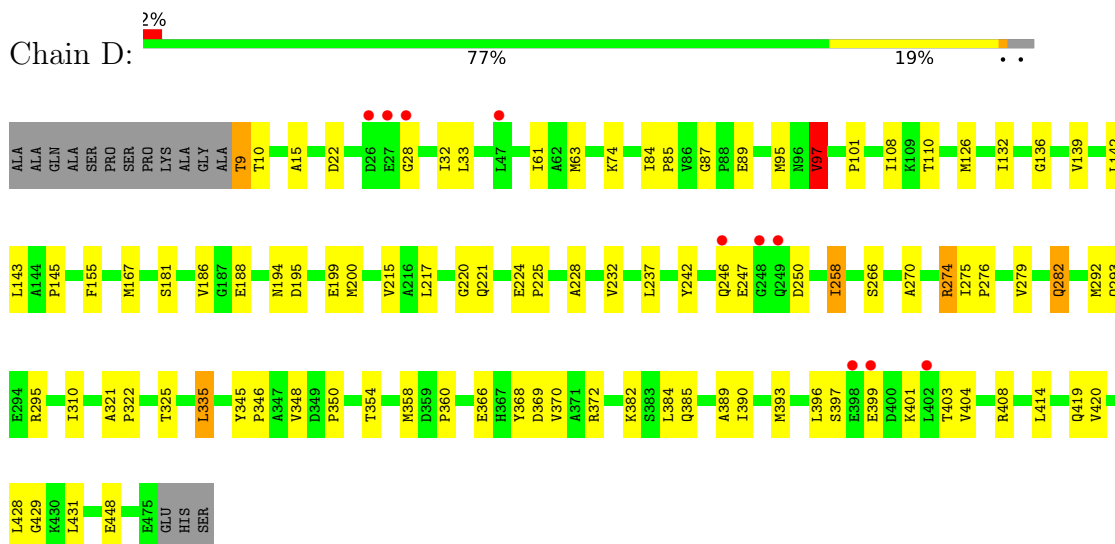
- Molecule 1: ATP SYNTHASE ALPHA CHAIN HEART ISOFORM



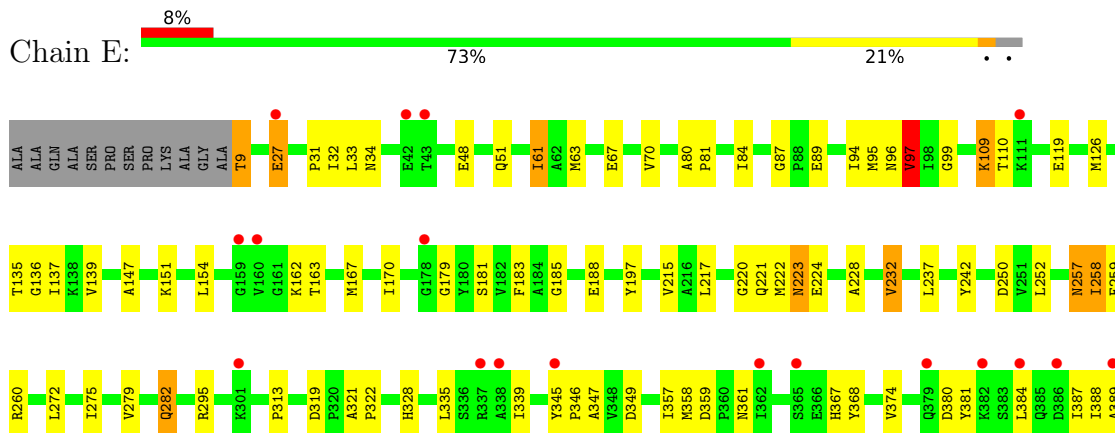
- Molecule 1: ATP SYNTHASE ALPHA CHAIN HEART ISOFORM

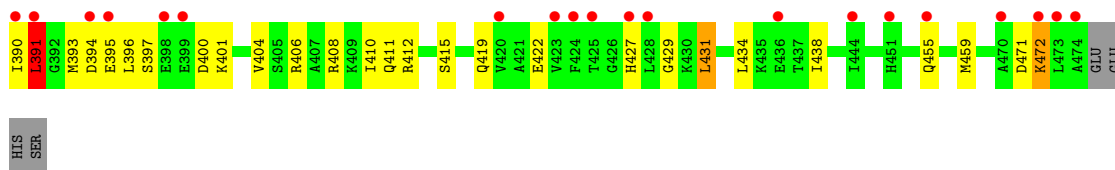


- Molecule 2: ATP SYNTHASE BETA CHAIN

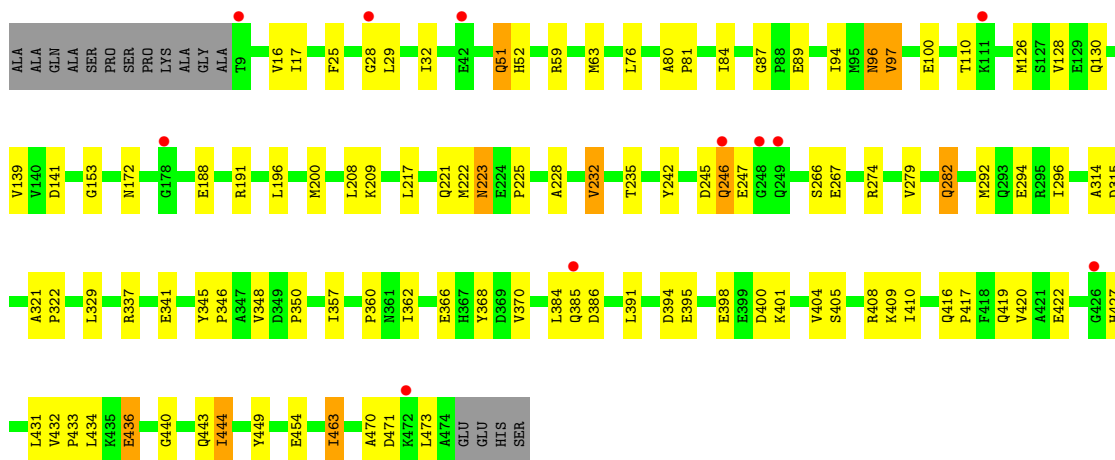
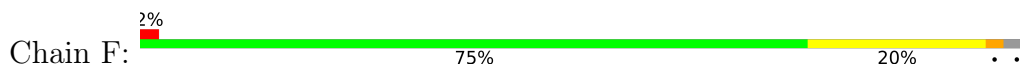


- Molecule 2: ATP SYNTHASE BETA CHAIN

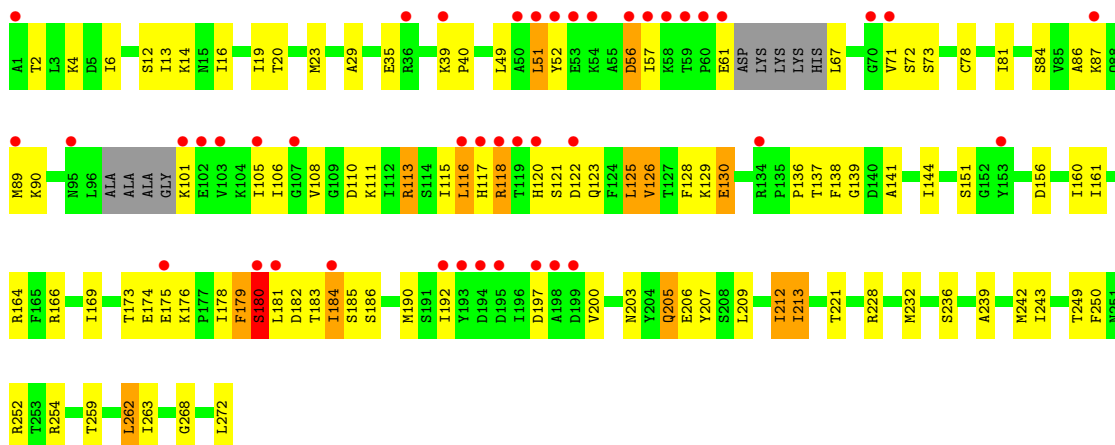




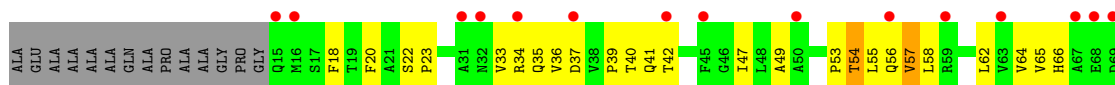
- Molecule 2: ATP SYNTHASE BETA CHAIN

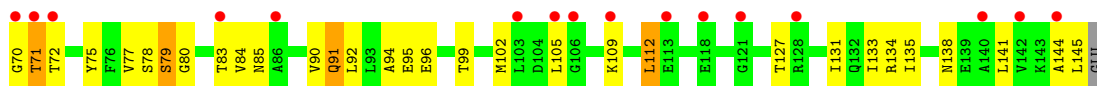


- Molecule 3: ATP SYNTHASE GAMMA CHAIN



- Molecule 4: ATP SYNTHASE DELTA CHAIN





- Molecule 5: ATP SYNTHASE EPSILON CHAIN



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	267.20Å 107.20Å 135.90Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	20.00 – 2.40 19.98 – 2.40	Depositor EDS
% Data completeness (in resolution range)	92.2 (20.00-2.40) 91.9 (19.98-2.40)	Depositor EDS
$R_{merge}$	0.09	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.93 (at 2.41Å)	Xtrriage
Refinement program	REFMAC	Depositor
R, $R_{free}$	0.225 , 0.281 0.204 , (Not available)	Depositor DCC
$R_{free}$ test set	No test flags present.	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	36.9	Xtrriage
Anisotropy	0.222	Xtrriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.34 , 57.0	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.49$ , $\langle L^2 \rangle = 0.32$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
$F_o, F_c$ correlation	0.94	EDS
Total number of atoms	26318	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	55.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.07% 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 [i](#)

### 5.1 Standard geometry [i](#)

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

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with  $|Z| > 5$  is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z  >5	RMSZ	# Z  >5
1	A	0.39	0/3799	0.78	0/5126
1	B	0.39	0/3799	0.81	2/5126 (0.0%)
1	C	0.40	0/3799	0.81	2/5126 (0.0%)
2	D	0.40	0/3595	0.81	2/4877 (0.0%)
2	E	0.38	0/3587	0.76	1/4867 (0.0%)
2	F	0.39	0/3587	0.79	1/4867 (0.0%)
3	G	0.35	0/2074	0.72	2/2785 (0.1%)
4	H	0.33	0/982	0.67	0/1337
5	I	0.34	0/374	0.71	0/501
All	All	0.38	0/25596	0.78	10/34612 (0.0%)

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
2	D	0	1

There are no bond length outliers.

All (10) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	D	195	ASP	N-CA-CB	8.67	126.21	110.60
1	B	45	ARG	NE-CZ-NH2	-7.26	116.67	120.30
2	F	191	ARG	NE-CZ-NH2	-6.49	117.06	120.30
3	G	254	ARG	NE-CZ-NH2	-5.62	117.49	120.30
1	C	423	ARG	CD-NE-CZ	5.33	131.06	123.60
1	B	146	MET	CG-SD-CE	5.20	108.51	100.20
2	E	97	VAL	CB-CA-C	-5.18	101.55	111.40

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	G	254	ARG	NE-CZ-NH1	5.15	122.87	120.30
2	D	97	VAL	CB-CA-C	-5.14	101.62	111.40
1	C	291	ARG	NE-CZ-NH2	-5.10	117.75	120.30

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
2	D	194	ASN	Mainchain

## 5.2 Too-close contacts [\(i\)](#)

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	3748	0	3844	76	0
1	B	3748	0	3844	106	0
1	C	3748	0	3844	75	0
2	D	3538	0	3592	83	0
2	E	3530	0	3587	89	0
2	F	3530	0	3586	88	0
3	G	2051	0	2115	108	0
4	H	970	0	972	55	0
5	I	369	0	395	20	0
6	A	31	0	12	0	0
6	C	31	0	12	1	0
7	A	1	0	0	0	0
7	B	1	0	0	0	0
7	C	1	0	0	0	0
7	D	1	0	0	0	0
7	F	1	0	0	0	0
8	B	27	0	12	0	0
8	D	27	0	12	0	0
8	F	27	0	12	0	0
9	B	6	0	8	1	0
10	D	16	0	23	6	0
11	E	5	0	0	0	0
12	A	163	0	0	4	0

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
12	B	140	0	0	3	0
12	C	167	0	0	2	0
12	D	148	0	0	9	0
12	E	95	0	0	0	0
12	F	164	0	0	4	0
12	G	25	0	0	1	0
12	H	5	0	0	0	0
12	I	4	0	0	0	0
All	All	26318	0	25870	651	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 (651) 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:D:199:GLU:HG2	10:D:700:DCW:H71C	1.32	1.08
2:D:199:GLU:CG	10:D:700:DCW:H71C	1.85	1.06
3:G:90:LYS:HB3	3:G:116:LEU:HD11	1.38	1.01
1:B:406:PHE:HB2	1:B:409:ASP:HB2	1.44	1.00
2:F:282:GLN:H	2:F:282:GLN:HE21	1.00	0.98
2:E:181:SER:HB2	2:E:215:VAL:HG12	1.45	0.96
4:H:62:LEU:HD11	4:H:144:ALA:HB2	1.49	0.92
2:E:282:GLN:H	2:E:282:GLN:HE21	1.16	0.91
2:E:257:ASN:HD21	2:E:259:PHE:HB3	1.35	0.91
4:H:85:ASN:HD21	4:H:91:GLN:HE22	1.13	0.90
2:D:282:GLN:H	2:D:282:GLN:HE21	0.91	0.88
3:G:20:THR:HG22	3:G:236:SER:HB3	1.57	0.87
2:D:282:GLN:H	2:D:282:GLN:NE2	1.71	0.86
2:F:282:GLN:H	2:F:282:GLN:NE2	1.77	0.81
4:H:105:LEU:HD22	4:H:109:LYS:HE3	1.63	0.81
1:B:47:VAL:HG12	1:B:90:ARG:HG2	1.62	0.81
3:G:161:ILE:HG12	3:G:175:GLU:HG2	1.63	0.81
3:G:89:MET:HB3	3:G:116:LEU:HD22	1.63	0.80
2:E:388:ILE:HG12	2:E:396:LEU:HD11	1.62	0.80
3:G:178:ILE:HG22	3:G:180:SER:HB2	1.65	0.79
2:D:275:ILE:HD13	3:G:272:LEU:HD12	1.64	0.79
2:D:200:MET:HE1	2:D:217:LEU:HD21	1.65	0.79
3:G:137:THR:HG21	5:I:39:GLY:H	1.48	0.78
2:D:282:GLN:HE21	2:D:282:GLN:N	1.76	0.77
2:F:130:GLN:HB3	2:F:357:ILE:HD11	1.68	0.76

*Continued on next page...*



*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:G:117:HIS:ND1	3:G:118:ARG:N	2.34	0.76
2:D:10:THR:HG21	2:D:74:LYS:HE3	1.68	0.75
1:B:97:VAL:HB	1:B:98:PRO:HD2	1.68	0.75
4:H:138:ASN:HA	4:H:141:LEU:HD12	1.68	0.74
3:G:121:SER:C	3:G:123:GLN:H	1.91	0.74
1:C:423:ARG:HD2	1:C:461:ILE:HD11	1.70	0.74
2:F:223:ASN:HD22	2:F:223:ASN:H	1.36	0.73
4:H:34:ARG:HH22	4:H:70:GLY:HA2	1.52	0.73
2:D:220:GLY:HA3	2:D:232:VAL:HG11	1.70	0.73
4:H:85:ASN:HD21	4:H:91:GLN:NE2	1.87	0.72
2:F:89:GLU:HB2	2:F:110:THR:HG22	1.71	0.72
1:C:183:ILE:HD12	1:C:201:CYS:HB3	1.69	0.72
2:D:181:SER:HB2	2:D:215:VAL:HG22	1.71	0.72
3:G:57:ILE:CG2	3:G:184:ILE:HD12	2.19	0.72
1:B:406:PHE:CE1	1:B:410:LEU:HB2	2.25	0.72
4:H:84:VAL:HG12	4:H:90:VAL:HG22	1.72	0.72
1:C:179:ALA:HB1	1:C:267:ILE:HD13	1.71	0.71
2:D:89:GLU:HG3	2:D:110:THR:HA	1.71	0.71
2:E:390:ILE:O	2:E:391:LEU:HB2	1.90	0.71
4:H:133:ILE:HD11	5:I:4:TRP:HB3	1.73	0.71
1:A:246:ALA:HB3	1:A:247:PRO:HD3	1.72	0.70
1:B:102:GLU:HG3	1:B:123:SER:HA	1.74	0.69
1:B:343:ILE:HD12	1:B:349:GLN:HG2	1.75	0.69
1:B:246:ALA:HB3	1:B:247:PRO:HD3	1.74	0.68
2:E:170:ILE:HD13	2:E:215:VAL:HG11	1.75	0.67
2:E:220:GLY:HA3	2:E:232:VAL:HG21	1.77	0.67
3:G:137:THR:HG22	3:G:139:GLY:H	1.60	0.67
1:C:34:ILE:HD11	1:C:79:ASP:HB2	1.75	0.67
1:A:180:ILE:HD11	1:A:216:LEU:HD21	1.76	0.67
1:B:289:PRO:HG2	3:G:263:ILE:HD12	1.76	0.67
3:G:14:LYS:HG3	3:G:243:ILE:HD12	1.76	0.67
1:A:141:SER:O	1:A:143:ARG:HD3	1.95	0.67
1:B:30:ARG:NH1	1:B:32:LEU:HD23	2.10	0.67
2:E:282:GLN:H	2:E:282:GLN:NE2	1.92	0.66
2:E:408:ARG:O	2:E:412:ARG:HG2	1.94	0.66
2:F:444:ILE:HD11	2:F:463:ILE:HD11	1.78	0.66
2:F:410:ILE:HG13	2:F:444:ILE:HG21	1.78	0.66
2:E:9:THR:HG21	2:E:27:GLU:HG3	1.78	0.66
2:F:208:LEU:O	2:F:209:LYS:HE2	1.96	0.65
5:I:35:MET:C	5:I:37:THR:H	1.99	0.65
2:E:185:GLY:HA3	2:E:188:GLU:HG2	1.79	0.65

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:338:ILE:HB	1:C:339:PRO:HD3	1.79	0.65
2:F:440:GLY:O	2:F:444:ILE:HD13	1.97	0.65
2:D:266:SER:HB3	2:D:282:GLN:HE22	1.62	0.64
2:E:89:GLU:HG2	2:E:110:THR:HG22	1.79	0.64
2:F:471:ASP:C	2:F:473:LEU:H	2.01	0.64
3:G:115:ILE:C	3:G:117:HIS:H	2.01	0.64
4:H:54:THR:N	4:H:84:VAL:HG23	2.13	0.64
1:C:211:SER:HB3	2:F:126:MET:CE	2.28	0.63
3:G:39:LYS:HB3	3:G:40:PRO:HD3	1.80	0.63
1:B:168:ILE:HD11	1:B:329:THR:CG2	2.28	0.63
2:F:172:ASN:ND2	2:F:431:LEU:HD11	2.14	0.63
2:F:321:ALA:HB3	2:F:322:PRO:HD3	1.80	0.63
3:G:141:ALA:HB1	3:G:213:ILE:HG23	1.81	0.63
2:F:63:MET:CE	2:F:228:ALA:HA	2.29	0.63
1:A:179:ALA:HB1	1:A:267:ILE:HD13	1.79	0.63
2:D:139:VAL:HA	12:D:2048:HOH:O	1.99	0.63
1:B:410:LEU:HD21	1:B:414:THR:HB	1.80	0.63
3:G:61:GLU:OE1	3:G:101:LYS:HG2	1.99	0.62
2:D:258:ILE:HD11	2:D:292:MET:SD	2.39	0.62
1:C:52:MET:HE2	1:C:52:MET:HA	1.80	0.62
4:H:65:VAL:C	4:H:72:THR:HG23	2.19	0.62
2:D:101:PRO:HB3	2:D:108:ILE:HD11	1.81	0.62
4:H:54:THR:H	4:H:84:VAL:HG23	1.65	0.62
1:C:97:VAL:HB	1:C:98:PRO:HD2	1.82	0.61
1:A:180:ILE:CD1	1:A:216:LEU:HD21	2.30	0.61
1:B:80:LYS:HD2	2:E:33:LEU:HD12	1.82	0.61
1:C:91:THR:HG23	1:C:93:ALA:H	1.65	0.61
3:G:178:ILE:C	3:G:180:SER:H	2.04	0.61
2:D:321:ALA:HB3	2:D:322:PRO:HD3	1.83	0.61
1:B:30:ARG:O	1:B:31:VAL:HB	2.01	0.61
2:D:143:LEU:HG	12:D:2048:HOH:O	2.00	0.61
2:D:136:GLY:HA3	2:D:431:LEU:CD1	2.32	0.60
2:E:147:ALA:HB2	2:E:357:ILE:HD13	1.82	0.60
2:F:63:MET:HE3	2:F:228:ALA:HA	1.83	0.60
1:A:183:ILE:HD12	1:A:201:CYS:HB3	1.83	0.60
2:E:136:GLY:HA3	2:E:431:LEU:HD13	1.84	0.60
1:A:362:ARG:HA	1:A:363:PRO:C	2.21	0.60
1:B:44:LEU:HB3	1:B:47:VAL:HG13	1.83	0.60
2:D:292:MET:HE2	2:D:293:GLN:HG2	1.83	0.60
2:D:393:MET:HG3	2:D:396:LEU:HD12	1.84	0.60
1:B:180:ILE:HD11	1:B:216:LEU:HD21	1.84	0.59

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:338:ILE:HB	1:B:339:PRO:HD3	1.84	0.59
2:E:358:MET:HE2	2:E:368:TYR:HD1	1.68	0.59
1:B:20:ASP:HB3	1:B:22:SER:H	1.67	0.59
1:B:442:VAL:HG21	1:B:489:ILE:HD11	1.84	0.59
3:G:57:ILE:CG2	3:G:184:ILE:CD1	2.81	0.59
1:B:440:GLU:HB3	1:B:469:LEU:HD11	1.84	0.59
4:H:37:ASP:HB2	4:H:64:VAL:HB	1.85	0.59
2:F:419:GLN:NE2	2:F:431:LEU:HD13	2.17	0.59
1:C:91:THR:CG2	1:C:93:ALA:H	2.16	0.59
1:C:381:ARG:H	1:C:381:ARG:HD2	1.68	0.59
3:G:207:TYR:HA	5:I:12:ILE:HD11	1.84	0.59
2:E:80:ALA:HB1	2:E:81:PRO:HD2	1.83	0.58
1:A:151:LYS:HD3	1:A:436:MET:SD	2.43	0.58
2:E:390:ILE:CG2	3:G:29:ALA:HB2	2.33	0.58
3:G:156:ASP:HA	3:G:181:LEU:HD13	1.85	0.58
1:C:240:ALA:HB3	1:C:241:PRO:HD3	1.84	0.58
2:D:419:GLN:HA	2:D:429:GLY:HA3	1.85	0.58
2:E:404:VAL:O	2:E:408:ARG:HG3	2.03	0.58
1:A:44:LEU:O	1:A:47:VAL:HG22	2.04	0.58
3:G:87:LYS:O	3:G:90:LYS:HG2	2.04	0.58
4:H:64:VAL:HG13	4:H:72:THR:HG21	1.85	0.58
1:A:383:MET:HE2	1:A:387:ALA:HB2	1.85	0.58
3:G:180:SER:O	3:G:205:GLN:HG3	2.04	0.58
1:B:362:ARG:HA	1:B:363:PRO:C	2.23	0.57
5:I:5:ARG:C	5:I:7:ALA:H	2.06	0.57
2:D:199:GLU:CG	10:D:700:DCW:C7	2.63	0.57
2:F:321:ALA:HB3	2:F:322:PRO:CD	2.33	0.57
2:F:419:GLN:HE21	2:F:431:LEU:HD13	1.67	0.57
4:H:96:GLU:OE2	5:I:23:ARG:NE	2.38	0.57
1:B:146:MET:HE1	1:B:186:GLN:NE2	2.20	0.57
3:G:57:ILE:HG23	3:G:184:ILE:CD1	2.35	0.57
3:G:164:ARG:NH2	3:G:166:ARG:HD3	2.20	0.57
1:B:423:ARG:HH21	1:B:458:PRO:HD3	1.70	0.57
2:F:32:ILE:HD12	2:F:51:GLN:HA	1.86	0.56
1:A:96:ASP:OD1	1:A:126:ARG:NH1	2.38	0.56
1:A:499:GLU:HG2	1:A:500:ILE:N	2.20	0.56
3:G:209:LEU:O	3:G:213:ILE:HG22	2.05	0.56
2:E:339:ILE:HD12	2:E:349:ASP:HA	1.86	0.56
1:A:211:SER:HB3	2:D:126:MET:CE	2.35	0.56
1:A:240:ALA:HB3	1:A:241:PRO:HD3	1.87	0.56
3:G:57:ILE:HG22	3:G:184:ILE:HD12	1.87	0.56

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:H:65:VAL:O	4:H:72:THR:HG23	2.05	0.56
1:B:99:VAL:HG22	1:B:253:MET:HA	1.88	0.56
1:C:246:ALA:HB3	1:C:247:PRO:HD3	1.88	0.56
3:G:137:THR:HG21	5:I:39:GLY:N	2.19	0.56
1:B:295:PRO:O	1:B:298:VAL:HG22	2.06	0.56
2:E:321:ALA:HB3	2:E:322:PRO:HD3	1.86	0.56
1:B:190:ASN:HA	1:B:198:LYS:HG2	1.87	0.56
2:D:188:GLU:H	2:D:221:GLN:NE2	2.04	0.56
1:A:49:ALA:O	1:A:50:GLU:HB2	2.07	0.55
1:A:392:LEU:HG	1:A:396:GLN:HE21	1.71	0.55
1:B:171:ARG:NH1	1:B:171:ARG:HB2	2.21	0.55
3:G:184:ILE:C	3:G:186:SER:H	2.08	0.55
1:C:49:ALA:O	1:C:50:GLU:HB2	2.05	0.55
2:F:433:PRO:HD2	2:F:436:GLU:HG3	1.88	0.55
3:G:160:ILE:CG2	3:G:176:LYS:HB2	2.36	0.55
2:E:223:ASN:HD22	2:E:223:ASN:H	1.55	0.55
2:F:470:ALA:HA	2:F:473:LEU:HD12	1.87	0.55
3:G:181:LEU:HG	3:G:183:THR:HB	1.89	0.55
1:A:151:LYS:HE3	1:A:427:LEU:O	2.06	0.55
2:E:89:GLU:HG2	2:E:110:THR:CG2	2.35	0.55
3:G:207:TYR:HA	5:I:12:ILE:CD1	2.37	0.55
1:B:168:ILE:HD13	1:B:169:GLY:N	2.21	0.55
12:G:2006:HOH:O	5:I:41:THR:HG21	2.06	0.55
1:A:211:SER:HB3	2:D:126:MET:HE2	1.87	0.55
1:B:142:VAL:HG13	12:B:2038:HOH:O	2.06	0.55
2:F:25:PHE:HB2	2:F:29:LEU:HD12	1.88	0.55
2:F:130:GLN:HB3	2:F:357:ILE:CD1	2.37	0.55
2:F:225:PRO:HG3	12:F:2025:HOH:O	2.05	0.55
3:G:121:SER:C	3:G:123:GLN:N	2.60	0.55
1:C:362:ARG:HA	1:C:363:PRO:C	2.26	0.55
3:G:117:HIS:ND1	3:G:118:ARG:HA	2.22	0.54
3:G:117:HIS:CE1	3:G:121:SER:HB2	2.42	0.54
1:B:185:ASN:OD1	1:B:188:ARG:NH1	2.39	0.54
3:G:181:LEU:HB3	3:G:184:ILE:HG22	1.89	0.54
2:F:282:GLN:HE21	2:F:282:GLN:N	1.85	0.54
1:C:488:LYS:HG2	1:C:489:ILE:N	2.23	0.54
2:F:245:ASP:C	2:F:247:GLU:H	2.11	0.54
3:G:144:ILE:HD13	3:G:213:ILE:HD11	1.90	0.54
3:G:181:LEU:O	3:G:184:ILE:HG22	2.08	0.54
1:C:99:VAL:HG22	1:C:253:MET:HA	1.90	0.54
2:F:87:GLY:HA2	2:F:242:TYR:CE1	2.43	0.54

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:F:471:ASP:C	2:F:473:LEU:N	2.61	0.54
3:G:164:ARG:HD3	3:G:174:GLU:OE2	2.07	0.54
1:C:215:GLN:HE22	2:F:128:VAL:HA	1.73	0.54
2:E:31:PRO:HD2	2:E:34:ASN:ND2	2.22	0.54
1:B:410:LEU:HG	1:B:411:ASP:H	1.72	0.54
1:B:416:GLN:O	1:B:419:SER:HB3	2.07	0.54
1:C:52:MET:HB3	1:C:91:THR:HG21	1.90	0.54
2:F:360:PRO:HD3	2:F:368:TYR:CD1	2.43	0.54
3:G:71:VAL:HG13	3:G:108:VAL:HG22	1.88	0.54
4:H:22:SER:HB2	4:H:23:PRO:HD2	1.89	0.54
2:D:139:VAL:HB	12:D:2047:HOH:O	2.06	0.53
2:D:142:LEU:HD23	12:D:2048:HOH:O	2.08	0.53
3:G:39:LYS:HB3	3:G:40:PRO:CD	2.38	0.53
1:B:168:ILE:HD11	1:B:329:THR:HG21	1.89	0.53
2:D:63:MET:HE3	2:D:228:ALA:HA	1.89	0.53
1:C:441:GLN:O	1:C:445:ILE:HG12	2.08	0.53
5:I:28:THR:O	5:I:29:GLU:HB2	2.08	0.53
1:C:211:SER:HB3	2:F:126:MET:HE1	1.90	0.53
1:C:211:SER:HB3	2:F:126:MET:HE2	1.90	0.53
1:B:406:PHE:CZ	1:B:410:LEU:HD22	2.43	0.53
1:B:482:LYS:NZ	1:B:496:LYS:NZ	2.56	0.53
1:C:347:ASP:C	1:C:373:ARG:HG3	2.28	0.53
2:D:321:ALA:HB3	2:D:322:PRO:CD	2.38	0.53
2:E:408:ARG:HH21	2:E:412:ARG:HH22	1.56	0.53
2:F:172:ASN:HD21	2:F:431:LEU:HD11	1.73	0.53
1:B:168:ILE:HD11	1:B:329:THR:HG23	1.91	0.53
3:G:137:THR:HG22	3:G:138:PHE:N	2.24	0.53
3:G:249:THR:HA	3:G:252:ARG:NH1	2.24	0.53
1:A:381:ARG:HD2	1:A:487:GLY:O	2.08	0.52
1:B:65:ASN:ND2	2:F:17:ILE:HG23	2.25	0.52
2:D:63:MET:CE	2:D:97:VAL:HG11	2.39	0.52
2:D:310:ILE:HD13	2:D:325:THR:HG21	1.91	0.52
2:D:366:GLU:O	2:D:370:VAL:HG23	2.09	0.52
2:F:84:ILE:HD13	2:F:235:THR:HG23	1.91	0.52
4:H:127:THR:O	4:H:131:ILE:HG12	2.10	0.52
5:I:5:ARG:O	5:I:6:GLN:HB3	2.10	0.52
1:C:114:ALA:HB2	1:C:121:ILE:HD12	1.91	0.52
2:D:63:MET:CE	2:D:228:ALA:HA	2.39	0.52
2:E:51:GLN:HE21	2:E:272:LEU:HD22	1.74	0.52
2:F:63:MET:CE	2:F:97:VAL:HG11	2.40	0.52
4:H:40:THR:HG23	4:H:42:THR:H	1.75	0.52

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:F:292:MET:CE	2:F:296:ILE:HD11	2.40	0.52
1:C:179:ALA:O	1:C:183:ILE:HG12	2.09	0.52
2:E:257:ASN:ND2	2:E:259:PHE:H	2.08	0.52
1:A:362:ARG:HH22	2:D:372:ARG:HD3	1.74	0.52
1:B:64:LEU:HG	1:B:65:ASN:ND2	2.24	0.52
2:D:420:VAL:HG13	10:D:700:DCW:H8	1.92	0.52
2:D:63:MET:HE1	2:D:97:VAL:HG11	1.91	0.52
3:G:19:ILE:HG22	3:G:23:MET:CE	2.40	0.52
3:G:23:MET:SD	3:G:232:MET:HE2	2.50	0.52
3:G:117:HIS:ND1	3:G:118:ARG:CA	2.73	0.52
3:G:117:HIS:O	3:G:120:HIS:N	2.35	0.52
4:H:34:ARG:HG2	4:H:66:HIS:O	2.10	0.51
1:B:24:ASP:O	1:B:28:THR:HB	2.11	0.51
1:A:336:ALA:HB3	1:A:339:PRO:HG2	1.92	0.51
1:B:469:LEU:O	1:B:473:ILE:HG12	2.10	0.51
1:C:419:SER:O	1:C:423:ARG:HG2	2.10	0.51
1:C:74:VAL:HG13	1:C:241:PRO:HB3	1.93	0.51
2:F:337:ARG:O	2:F:341:GLU:HG3	2.10	0.51
2:E:358:MET:HE2	2:E:368:TYR:CD1	2.46	0.51
2:F:440:GLY:HA2	2:F:463:ILE:HG13	1.91	0.51
2:D:397:SER:O	2:D:401:LYS:HD2	2.10	0.51
2:E:80:ALA:HB1	2:E:81:PRO:CD	2.40	0.51
3:G:49:LEU:HD21	3:G:212:ILE:CD1	2.41	0.51
1:C:185:ASN:OD1	1:C:435:PRO:HB2	2.11	0.51
2:D:97:VAL:HG13	2:D:232:VAL:HG13	1.93	0.51
2:E:94:ILE:HD11	2:E:197:TYR:CD1	2.45	0.51
2:D:139:VAL:HG22	2:D:414:LEU:HD22	1.92	0.51
1:C:52:MET:HE3	1:C:76:PHE:HE2	1.76	0.51
1:B:26:GLU:HA	1:B:45:ARG:HB2	1.93	0.51
1:C:211:SER:O	1:C:215:GLN:HG2	2.11	0.51
4:H:83:THR:HB	4:H:91:GLN:HE21	1.75	0.51
1:B:457:GLU:OE1	1:B:460:LYS:HG3	2.10	0.50
1:C:418:LEU:O	1:C:422:VAL:HG23	2.10	0.50
4:H:58:LEU:HD13	4:H:77:VAL:HG11	1.92	0.50
2:D:95:MET:HG3	12:D:2063:HOH:O	2.11	0.50
4:H:18:PHE:CZ	4:H:20:PHE:HB2	2.46	0.50
2:D:136:GLY:HA3	2:D:431:LEU:HD12	1.92	0.50
2:F:63:MET:HE1	2:F:97:VAL:HG11	1.92	0.50
2:D:167:MET:HG3	10:D:700:DCW:H131	1.94	0.50
2:F:80:ALA:HB1	2:F:81:PRO:HD2	1.94	0.50
2:F:408:ARG:NE	2:F:454:GLU:OE2	2.44	0.50

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:338:ILE:N	1:A:339:PRO:CD	2.75	0.50
1:B:156:LEU:HD22	1:B:391:LYS:HD3	1.94	0.50
2:F:96:ASN:ND2	2:F:100:GLU:H	2.09	0.50
2:E:408:ARG:HH21	2:E:412:ARG:NH2	2.10	0.50
2:F:246:GLN:O	2:F:247:GLU:HG3	2.12	0.49
4:H:35:GLN:HB3	4:H:66:HIS:HD2	1.77	0.49
1:B:137:ILE:HB	1:B:138:PRO:HD3	1.94	0.49
2:F:345:TYR:HA	2:F:346:PRO:C	2.33	0.49
1:B:30:ARG:HH11	1:B:32:LEU:HD23	1.76	0.49
1:B:171:ARG:HB2	1:B:171:ARG:HH11	1.76	0.49
1:A:270:ASP:HB2	1:A:326:VAL:O	2.13	0.49
1:B:180:ILE:CD1	1:B:216:LEU:HD21	2.42	0.49
1:C:36:ASP:HB3	1:C:284:LEU:HD13	1.93	0.49
4:H:138:ASN:O	4:H:141:LEU:HB2	2.12	0.49
1:A:205:ALA:C	1:A:206:ILE:HG13	2.33	0.49
1:A:496:LYS:HA	1:A:499:GLU:CD	2.32	0.49
1:B:240:ALA:HB3	1:B:241:PRO:HD3	1.93	0.49
2:D:15:ALA:HB3	2:D:22:ASP:HB2	1.94	0.49
2:D:399:GLU:O	2:D:403:THR:HG23	2.12	0.49
3:G:71:VAL:HG13	3:G:108:VAL:CG2	2.43	0.49
1:A:395:ALA:HA	1:A:398:ARG:NH1	2.27	0.49
2:F:153:GLY:HA3	2:F:329:LEU:HD13	1.95	0.49
3:G:179:PHE:C	3:G:181:LEU:N	2.66	0.49
1:C:278:TYR:CE2	1:C:295:PRO:HG2	2.46	0.49
2:E:258:ILE:HD13	2:E:258:ILE:O	2.13	0.49
2:F:292:MET:HE2	2:F:296:ILE:HD11	1.94	0.49
4:H:105:LEU:CD2	4:H:109:LYS:HE3	2.41	0.49
1:B:339:PRO:O	1:B:343:ILE:HG12	2.13	0.49
1:A:496:LYS:HA	1:A:499:GLU:OE2	2.13	0.49
1:A:496:LYS:HD2	1:A:499:GLU:OE2	2.13	0.49
1:B:388:GLY:O	1:B:392:LEU:HD23	2.13	0.49
4:H:41:GLN:HG2	4:H:57:VAL:HG12	1.94	0.49
2:D:10:THR:CG2	2:D:74:LYS:HE3	2.39	0.48
3:G:203:ASN:CB	4:H:57:VAL:HG21	2.42	0.48
2:E:408:ARG:O	2:E:411:GLN:HG2	2.13	0.48
1:B:240:ALA:N	1:B:241:PRO:CD	2.76	0.48
2:D:136:GLY:HA3	2:D:431:LEU:HD11	1.94	0.48
2:F:266:SER:HB2	2:F:282:GLN:HE22	1.79	0.48
3:G:136:PRO:HD3	3:G:221:THR:HG21	1.95	0.48
3:G:156:ASP:O	3:G:181:LEU:HB2	2.13	0.48
4:H:34:ARG:HH22	4:H:70:GLY:CA	2.24	0.48

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:195:GLU:HA	1:A:198:LYS:HG3	1.94	0.48
1:C:180:ILE:HD11	1:C:216:LEU:CD2	2.44	0.48
1:B:78:ASN:ND2	2:E:119:GLU:OE2	2.46	0.48
1:B:468:PHE:CZ	1:B:501:VAL:HG12	2.48	0.48
1:C:183:ILE:HD11	1:C:267:ILE:CD1	2.43	0.48
2:E:48:GLU:HB3	2:E:61:ILE:CD1	2.44	0.48
2:E:48:GLU:O	2:E:61:ILE:HD13	2.14	0.48
2:E:359:ASP:OD2	2:E:361:ASN:HB2	2.13	0.48
3:G:197:ASP:O	3:G:200:VAL:HG12	2.13	0.48
4:H:105:LEU:HG	4:H:145:LEU:HB3	1.94	0.48
1:B:130:GLY:HA2	9:B:701:GOL:H11	1.96	0.48
1:C:99:VAL:CG2	1:C:253:MET:HA	2.43	0.48
3:G:160:ILE:HG22	3:G:176:LYS:HB2	1.95	0.48
1:B:211:SER:HB3	2:E:126:MET:HE1	1.96	0.48
1:C:105:GLY:HA2	1:C:226:MET:O	2.12	0.48
2:D:139:VAL:HG21	12:D:2115:HOH:O	2.14	0.48
2:D:420:VAL:HG22	10:D:700:DCW:H31C	1.96	0.48
2:E:339:ILE:CD1	2:E:349:ASP:HA	2.44	0.48
2:D:237:LEU:HD11	2:D:295:ARG:NE	2.29	0.48
2:D:276:PRO:HG3	3:G:268:GLY:HA3	1.94	0.48
2:E:89:GLU:HG3	2:E:109:LYS:O	2.14	0.48
2:E:282:GLN:HE21	2:E:282:GLN:N	1.98	0.48
2:E:321:ALA:HB3	2:E:322:PRO:CD	2.44	0.48
3:G:39:LYS:N	3:G:40:PRO:HD2	2.28	0.48
2:E:367:HIS:CE1	2:E:434:LEU:HD11	2.48	0.48
2:F:357:ILE:HD12	2:F:362:ILE:HG21	1.96	0.48
2:D:9:THR:HG21	2:D:28:GLY:O	2.14	0.48
1:C:183:ILE:HD11	1:C:267:ILE:HD12	1.95	0.47
2:F:360:PRO:HD3	2:F:368:TYR:CE1	2.49	0.47
3:G:179:PHE:HB3	3:G:184:ILE:HG21	1.96	0.47
2:F:391:LEU:HD13	2:F:395:GLU:HG2	1.95	0.47
2:F:400:ASP:O	2:F:404:VAL:HG23	2.14	0.47
1:B:99:VAL:HG13	1:B:256:TYR:HB2	1.95	0.47
3:G:78:CYS:O	3:G:81:ILE:HD13	2.15	0.47
3:G:89:MET:CB	3:G:116:LEU:HD22	2.38	0.47
4:H:57:VAL:HG13	5:I:11:TYR:CZ	2.50	0.47
5:I:37:THR:HG22	5:I:38:SER:H	1.80	0.47
1:B:49:ALA:O	1:B:50:GLU:HB2	2.15	0.47
1:B:292:GLU:O	1:B:293:ALA:HB3	2.14	0.47
3:G:117:HIS:ND1	3:G:117:HIS:C	2.67	0.47
1:B:185:ASN:O	1:B:188:ARG:HG2	2.15	0.47

*Continued on next page...*



*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:D:360:PRO:HD3	2:D:368:TYR:CD1	2.50	0.47
2:D:390:ILE:HD12	3:G:16:ILE:CD1	2.44	0.47
3:G:129:LYS:HG2	3:G:130:GLU:OE1	2.14	0.47
1:B:338:ILE:N	1:B:339:PRO:CD	2.77	0.47
1:C:283:LEU:HD21	1:C:289:PRO:HB3	1.96	0.47
1:C:338:ILE:N	1:C:339:PRO:CD	2.77	0.47
2:D:87:GLY:HA2	2:D:242:TYR:CE1	2.50	0.47
2:E:183:PHE:HB3	2:E:217:LEU:CD2	2.45	0.47
2:E:367:HIS:ND1	2:E:438:ILE:HD11	2.30	0.47
2:F:196:LEU:HD11	2:F:200:MET:CE	2.45	0.47
3:G:125:LEU:HD11	3:G:151:SER:HB2	1.96	0.47
3:G:179:PHE:O	3:G:181:LEU:N	2.48	0.47
1:B:457:GLU:O	1:B:460:LYS:N	2.42	0.47
2:F:394:ASP:HB2	12:F:2143:HOH:O	2.14	0.47
2:D:139:VAL:HG23	12:D:2133:HOH:O	2.15	0.47
2:D:224:GLU:HB3	2:D:225:PRO:HD2	1.97	0.47
2:E:179:GLY:HA3	2:E:250:ASP:O	2.14	0.47
4:H:47:ILE:HD12	4:H:47:ILE:H	1.79	0.47
2:D:369:ASP:OD1	2:D:372:ARG:NH2	2.47	0.47
2:E:345:TYR:HA	2:E:346:PRO:C	2.35	0.47
3:G:19:ILE:HG22	3:G:23:MET:HE2	1.96	0.46
3:G:207:TYR:CZ	4:H:80:GLY:HA2	2.50	0.46
1:A:34:ILE:HD12	1:A:38:ILE:O	2.16	0.46
2:D:84:ILE:HB	2:D:85:PRO:HD2	1.96	0.46
2:F:188:GLU:O	2:F:222:MET:HG2	2.15	0.46
1:C:201:CYS:O	1:C:229:THR:HA	2.15	0.46
2:F:80:ALA:HB1	2:F:81:PRO:CD	2.44	0.46
2:E:406:ARG:O	2:E:410:ILE:HG12	2.16	0.46
3:G:144:ILE:HG21	3:G:213:ILE:HD13	1.97	0.46
1:C:188:ARG:NH2	1:C:437:ALA:N	2.64	0.46
2:E:237:LEU:HD21	2:E:295:ARG:HB2	1.98	0.46
2:F:366:GLU:O	2:F:370:VAL:HG23	2.16	0.46
1:A:497:LEU:O	1:A:501:VAL:HG12	2.15	0.46
1:C:288:PRO:HG2	2:D:270:ALA:HB1	1.98	0.46
2:D:348:VAL:O	2:D:350:PRO:HD3	2.15	0.46
1:A:32:LEU:HD21	1:A:42:HIS:HB2	1.96	0.46
1:A:299:PHE:CZ	1:A:345:ILE:HD11	2.50	0.46
2:F:443:GLN:HE21	2:F:449:TYR:HE2	1.62	0.46
1:B:357:PHE:C	1:B:359:LYS:H	2.19	0.46
1:B:380:THR:HG22	1:B:383:MET:H	1.81	0.46
2:E:87:GLY:HA2	2:E:242:TYR:CE2	2.51	0.46

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:E:380:ASP:O	2:E:384:LEU:HG	2.15	0.46
2:E:471:ASP:O	2:E:472:LYS:C	2.54	0.46
4:H:70:GLY:O	4:H:71:THR:C	2.53	0.46
4:H:99:THR:O	4:H:102:MET:HG2	2.15	0.46
1:A:213:VAL:O	1:A:216:LEU:HB3	2.16	0.46
1:A:392:LEU:HG	1:A:396:GLN:NE2	2.30	0.46
1:B:44:LEU:HB3	1:B:47:VAL:CG1	2.45	0.46
1:B:354:THR:HG23	1:B:358:TYR:CE1	2.51	0.46
1:B:409:ASP:HB3	3:G:169:ILE:HD11	1.98	0.46
2:E:393:MET:C	2:E:395:GLU:H	2.19	0.46
2:F:16:VAL:O	2:F:17:ILE:HD13	2.16	0.46
2:F:225:PRO:HB2	12:F:2020:HOH:O	2.15	0.46
2:D:97:VAL:HG22	12:D:2064:HOH:O	2.16	0.45
2:E:163:THR:O	2:E:167:MET:HG3	2.16	0.45
2:F:63:MET:HE1	2:F:228:ALA:HA	1.98	0.45
2:F:405:SER:O	2:F:409:LYS:HG3	2.16	0.45
4:H:35:GLN:HB3	4:H:66:HIS:CD2	2.50	0.45
2:E:27:GLU:CD	2:E:27:GLU:H	2.19	0.45
5:I:35:MET:C	5:I:37:THR:N	2.68	0.45
1:C:129:VAL:HG21	1:C:245:LEU:HD11	1.98	0.45
3:G:206:GLU:O	5:I:12:ILE:HD11	2.17	0.45
1:B:87:ILE:HD12	1:B:87:ILE:H	1.82	0.45
1:B:399:GLU:C	1:B:400:VAL:HG23	2.36	0.45
1:B:403:PHE:O	1:B:404:ALA:C	2.53	0.45
2:D:279:VAL:HG12	2:D:279:VAL:O	2.16	0.45
2:E:181:SER:HB2	2:E:215:VAL:CG1	2.33	0.45
1:A:481:GLY:HA2	1:A:484:ARG:NH1	2.31	0.45
3:G:259:THR:O	3:G:263:ILE:HG12	2.17	0.45
1:B:410:LEU:HB3	1:B:415:GLN:CG	2.46	0.45
2:D:345:TYR:HA	2:D:346:PRO:C	2.37	0.45
4:H:112:LEU:HD21	4:H:135:ILE:HG23	1.99	0.45
1:B:289:PRO:CG	3:G:263:ILE:HD12	2.46	0.45
3:G:51:LEU:HD13	4:H:55:LEU:HD21	1.97	0.45
1:A:114:ALA:HB2	1:A:121:ILE:CD1	2.47	0.45
3:G:86:ALA:HA	3:G:89:MET:HE2	1.99	0.45
3:G:228:ARG:O	3:G:232:MET:HG2	2.17	0.45
1:B:47:VAL:CG1	1:B:90:ARG:HG2	2.41	0.45
1:C:30:ARG:HA	1:C:86:ASP:O	2.15	0.45
2:E:135:THR:OG1	2:E:137:ILE:HB	2.17	0.45
2:E:400:ASP:O	2:E:404:VAL:HG23	2.17	0.45
1:B:295:PRO:HB2	1:B:297:ASP:OD1	2.16	0.45

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:F:96:ASN:HD21	2:F:100:GLU:H	1.64	0.45
3:G:115:ILE:C	3:G:117:HIS:N	2.68	0.45
3:G:178:ILE:C	3:G:180:SER:N	2.69	0.44
1:A:362:ARG:HH22	2:D:372:ARG:CG	2.31	0.44
2:E:228:ALA:O	2:E:232:VAL:HG22	2.16	0.44
3:G:13:ILE:HD13	3:G:242:MET:SD	2.57	0.44
3:G:105:ILE:HG22	3:G:106:ILE:N	2.32	0.44
1:A:34:ILE:HD13	1:A:39:ALA:HB2	1.99	0.44
1:B:286:ARG:NE	12:B:2079:HOH:O	2.48	0.44
1:B:333:ASP:OD2	3:G:252:ARG:HD3	2.17	0.44
2:F:223:ASN:H	2:F:223:ASN:ND2	2.10	0.44
3:G:117:HIS:CE1	3:G:118:ARG:NE	2.86	0.44
4:H:55:LEU:O	4:H:56:GLN:HG3	2.17	0.44
1:C:411:ASP:OD2	1:C:413:ALA:HB3	2.18	0.44
2:D:145:PRO:HD2	2:D:358:MET:HG2	1.98	0.44
2:E:61:ILE:HD13	2:E:61:ILE:H	1.83	0.44
2:E:422:GLU:HG2	2:E:427:HIS:O	2.17	0.44
2:E:259:PHE:CE1	2:E:313:PRO:HG3	2.52	0.44
2:E:397:SER:O	2:E:401:LYS:HG3	2.18	0.44
3:G:84:SER:HB3	3:G:173:THR:OG1	2.17	0.44
1:A:183:ILE:HD11	1:A:267:ILE:HD12	2.00	0.44
1:A:291:ARG:HA	3:G:262:LEU:HD22	1.99	0.44
1:A:338:ILE:N	1:A:339:PRO:HD2	2.33	0.44
2:E:223:ASN:HD22	2:E:223:ASN:N	2.15	0.44
2:E:381:TYR:CE1	2:E:404:VAL:HG13	2.52	0.44
2:F:432:VAL:HA	2:F:433:PRO:HD3	1.83	0.44
1:A:165:GLU:O	1:A:325:PRO:HD2	2.17	0.44
1:A:383:MET:CE	1:A:386:VAL:HG23	2.47	0.44
1:B:297:ASP:HB3	2:F:267:GLU:HG2	1.99	0.44
1:B:359:LYS:HD2	1:B:361:ILE:CD1	2.48	0.44
1:C:23:VAL:HG12	1:C:23:VAL:O	2.18	0.44
2:E:183:PHE:HB3	2:E:217:LEU:HD23	2.00	0.44
3:G:128:PHE:HB3	5:I:42:ILE:CD1	2.48	0.44
4:H:33:VAL:HG11	4:H:65:VAL:HG13	1.99	0.44
1:C:33:SER:HB2	2:F:52:HIS:O	2.17	0.44
2:D:97:VAL:HG13	2:D:232:VAL:CG1	2.47	0.44
3:G:113:ARG:O	3:G:117:HIS:HB2	2.18	0.44
1:A:345:ILE:HD13	2:E:222:MET:SD	2.58	0.44
1:B:209:LYS:HD2	2:E:328:HIS:HA	2.00	0.44
1:B:482:LYS:NZ	1:B:496:LYS:H22	2.15	0.44
2:D:142:LEU:HB3	12:D:2048:HOH:O	2.17	0.44

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:362:ARG:HD3	6:C:600:ATP:C2	2.53	0.43
1:C:381:ARG:HD2	1:C:381:ARG:N	2.32	0.43
1:C:404:ALA:C	1:C:406:PHE:H	2.21	0.43
1:C:444:VAL:HG12	1:C:469:LEU:HD13	2.00	0.43
2:D:32:ILE:O	2:D:33:LEU:HB2	2.18	0.43
2:E:374:VAL:HG13	2:E:410:ILE:HG21	1.99	0.43
1:A:422:VAL:O	1:A:426:GLU:HG2	2.18	0.43
1:B:410:LEU:HG	1:B:414:THR:OG1	2.18	0.43
2:E:63:MET:HE3	2:E:97:VAL:HG21	1.99	0.43
2:E:257:ASN:HD22	2:E:260:ARG:H	1.65	0.43
1:A:20:ASP:O	1:A:22:SER:N	2.51	0.43
1:A:240:ALA:N	1:A:241:PRO:CD	2.81	0.43
1:B:99:VAL:CG1	1:B:256:TYR:HB2	2.48	0.43
1:B:168:ILE:HD13	1:B:168:ILE:C	2.38	0.43
2:D:237:LEU:HD11	2:D:295:ARG:CZ	2.48	0.43
1:B:158:PRO:O	1:B:375:GLY:HA3	2.19	0.43
1:C:62:MET:HG2	1:C:64:LEU:HD13	2.01	0.43
2:E:358:MET:CE	2:E:368:TYR:HA	2.49	0.43
2:E:415:SER:HB2	2:E:459:MET:H	1.84	0.43
2:F:223:ASN:HD22	2:F:223:ASN:N	2.07	0.43
3:G:6:ILE:HG21	3:G:250:PHE:HB2	2.00	0.43
1:A:440:GLU:O	1:A:444:VAL:HG13	2.19	0.43
2:D:139:VAL:HG22	2:D:414:LEU:HB3	2.00	0.43
2:E:419:GLN:N	2:E:429:GLY:HA3	2.33	0.43
2:F:245:ASP:O	2:F:247:GLU:N	2.50	0.43
1:B:406:PHE:CZ	1:B:410:LEU:HD13	2.53	0.43
2:D:89:GLU:HB2	2:D:110:THR:HG23	2.01	0.43
2:F:348:VAL:O	2:F:350:PRO:HD3	2.18	0.43
1:A:67:GLU:HB3	1:A:68:PRO:HD2	1.99	0.43
1:B:148:THR:HA	1:B:182:THR:HG23	2.01	0.43
1:B:508:PHE:CE2	1:B:510:ALA:HA	2.53	0.43
2:E:170:ILE:CD1	2:E:215:VAL:HG11	2.46	0.43
4:H:41:GLN:CG	4:H:57:VAL:HG12	2.48	0.43
1:A:487:GLY:O	1:A:488:LYS:HB3	2.19	0.43
1:C:410:LEU:O	1:C:415:GLN:NE2	2.51	0.43
2:D:188:GLU:O	2:D:221:GLN:HB3	2.18	0.43
4:H:79:SER:O	4:H:94:ALA:HA	2.18	0.43
1:A:446:TYR:O	1:A:449:VAL:HG12	2.19	0.43
1:C:151:LYS:HA	1:C:441:GLN:OE1	2.17	0.43
2:F:51:GLN:HG2	2:F:59:ARG:HB3	2.00	0.43
2:F:141:ASP:HB3	2:F:434:LEU:HD13	2.01	0.43

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:G:86:ALA:O	3:G:116:LEU:HD13	2.18	0.43
4:H:35:GLN:HG2	4:H:36:VAL:N	2.34	0.43
3:G:239:ALA:O	3:G:243:ILE:HG12	2.18	0.43
4:H:20:PHE:CD1	4:H:92:LEU:HD23	2.54	0.43
4:H:131:ILE:HG23	4:H:134:ARG:HH21	1.84	0.43
1:A:157:VAL:N	1:A:158:PRO:CD	2.82	0.42
1:A:423:ARG:NH2	1:A:458:PRO:HD3	2.33	0.42
1:B:269:ASP:HA	1:B:270:ASP:HA	1.74	0.42
1:B:286:ARG:HG2	2:E:275:ILE:CD1	2.49	0.42
1:C:240:ALA:N	1:C:241:PRO:CD	2.82	0.42
2:E:48:GLU:HB3	2:E:61:ILE:HD11	1.99	0.42
2:E:221:GLN:N	2:E:224:GLU:OE2	2.48	0.42
3:G:192:ILE:HG22	4:H:53:PRO:HG2	2.00	0.42
1:A:49:ALA:O	1:A:50:GLU:CB	2.66	0.42
1:B:156:LEU:HD13	1:B:367:VAL:HG11	2.00	0.42
1:C:189:PHE:HB3	1:C:197:LYS:HB3	2.01	0.42
2:E:335:LEU:HA	2:E:347:ALA:O	2.19	0.42
2:E:387:ILE:O	2:E:391:LEU:HB3	2.18	0.42
3:G:180:SER:O	3:G:182:ASP:N	2.52	0.42
1:A:183:ILE:HD12	1:A:201:CYS:SG	2.58	0.42
1:B:157:VAL:N	1:B:158:PRO:CD	2.81	0.42
2:D:404:VAL:O	2:D:408:ARG:HG3	2.19	0.42
2:E:154:LEU:HD21	2:E:162:LYS:HG3	2.01	0.42
2:E:358:MET:HE3	2:E:358:MET:HA	2.01	0.42
2:F:228:ALA:O	2:F:232:VAL:HG22	2.19	0.42
4:H:39:PRO:HG3	4:H:62:LEU:N	2.34	0.42
2:F:321:ALA:CB	2:F:322:PRO:CD	2.96	0.42
3:G:86:ALA:HA	3:G:89:MET:CE	2.49	0.42
3:G:87:LYS:HA	3:G:90:LYS:HE2	2.02	0.42
1:A:102:GLU:HG2	1:A:122:GLY:O	2.19	0.42
1:B:413:ALA:O	1:B:417:LEU:HG	2.20	0.42
2:D:186:VAL:HG13	2:D:232:VAL:HG23	2.00	0.42
1:B:303:SER:HA	1:B:345:ILE:HD12	2.01	0.42
2:F:188:GLU:H	2:F:221:GLN:NE2	2.18	0.42
3:G:180:SER:O	3:G:181:LEU:C	2.56	0.42
1:A:99:VAL:CG2	1:A:253:MET:HA	2.49	0.42
1:B:97:VAL:HB	1:B:98:PRO:CD	2.46	0.42
1:B:171:ARG:HG2	12:B:2107:HOH:O	2.19	0.42
1:C:204:VAL:HG12	1:C:206:ILE:CD1	2.50	0.42
2:F:32:ILE:CD1	2:F:51:GLN:HA	2.50	0.42
2:F:422:GLU:HG2	2:F:427:HIS:O	2.19	0.42

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:I:5:ARG:C	5:I:7:ALA:N	2.72	0.42
1:A:338:ILE:HB	1:A:339:PRO:HD3	2.02	0.42
1:A:362:ARG:HH22	2:D:372:ARG:CD	2.33	0.42
2:D:155:PHE:O	2:D:335:LEU:HB2	2.19	0.42
2:E:321:ALA:N	2:E:322:PRO:HD2	2.35	0.42
2:F:97:VAL:HG22	12:F:2073:HOH:O	2.18	0.42
2:F:416:GLN:HA	2:F:417:PRO:HD3	1.89	0.42
2:F:444:ILE:HD12	2:F:449:TYR:HD2	1.85	0.42
1:B:390:MET:O	1:B:394:LEU:HB2	2.19	0.42
1:C:406:PHE:CE1	2:D:389:ALA:HA	2.54	0.42
3:G:56:ASP:C	3:G:57:ILE:HG12	2.41	0.42
3:G:106:ILE:HG12	3:G:126:VAL:HG23	2.02	0.42
1:A:97:VAL:HB	1:A:98:PRO:HD2	2.02	0.42
1:A:269:ASP:HA	1:A:270:ASP:HA	1.77	0.42
1:C:171:ARG:NH1	12:C:2053:HOH:O	2.53	0.42
2:D:242:TYR:CD2	2:D:246:GLN:HG3	2.55	0.42
5:I:5:ARG:O	5:I:6:GLN:CB	2.68	0.42
1:A:48:GLN:HG2	2:E:70:VAL:HG22	2.02	0.41
1:A:183:ILE:HD12	1:A:201:CYS:CB	2.47	0.41
1:B:45:ARG:HA	1:B:45:ARG:HD3	1.88	0.41
1:B:397:TYR:CG	1:B:421:GLY:HA3	2.55	0.41
1:B:404:ALA:O	1:B:406:PHE:CD1	2.74	0.41
3:G:203:ASN:HB3	4:H:57:VAL:HG21	2.02	0.41
4:H:34:ARG:NH2	4:H:70:GLY:HA2	2.28	0.41
1:A:241:PRO:O	1:A:244:TYR:HB3	2.20	0.41
1:B:168:ILE:HD11	1:B:334:VAL:HG12	2.03	0.41
2:F:94:ILE:HG12	2:F:217:LEU:HD12	2.01	0.41
3:G:184:ILE:C	3:G:186:SER:N	2.72	0.41
1:A:20:ASP:O	1:A:21:THR:C	2.59	0.41
2:E:319:ASP:O	2:E:322:PRO:HD2	2.20	0.41
2:F:314:ALA:O	2:F:315:ASP:HB2	2.21	0.41
3:G:203:ASN:HB2	4:H:57:VAL:HG21	2.02	0.41
1:C:194:ASP:OD2	1:C:197:LYS:HG3	2.20	0.41
3:G:12:SER:O	3:G:16:ILE:HD12	2.20	0.41
1:A:62:MET:HE1	1:A:64:LEU:HD21	2.01	0.41
1:B:406:PHE:HD1	1:B:407:GLY:N	2.18	0.41
1:C:180:ILE:HD11	1:C:216:LEU:HD21	2.01	0.41
2:F:471:ASP:O	2:F:473:LEU:N	2.54	0.41
4:H:62:LEU:CD1	4:H:144:ALA:HB2	2.34	0.41
1:A:168:ILE:HD11	1:A:329:THR:CG2	2.51	0.41
1:C:189:PHE:CD1	1:C:197:LYS:HD3	2.55	0.41

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:452:TYR:CD2	1:C:501:VAL:HG21	2.56	0.41
1:A:213:VAL:O	1:A:217:VAL:HG13	2.20	0.41
1:B:404:ALA:O	1:B:405:GLN:C	2.59	0.41
1:C:400:VAL:HG11	1:C:417:LEU:HD23	2.03	0.41
2:E:63:MET:CE	2:E:228:ALA:HA	2.51	0.41
2:F:384:LEU:O	2:F:386:ASP:N	2.54	0.41
3:G:120:HIS:HB3	3:G:123:GLN:HB2	2.03	0.41
5:I:35:MET:O	5:I:37:THR:N	2.52	0.41
1:A:279:ARG:HG3	12:A:2097:HOH:O	2.20	0.41
1:B:158:PRO:HG2	1:B:376:SER:HA	2.03	0.41
1:B:473:ILE:O	1:B:477:GLN:HG2	2.21	0.41
1:C:362:ARG:NH1	12:C:2122:HOH:O	2.54	0.41
2:E:95:MET:HG3	2:E:99:GLY:HA2	2.01	0.41
2:F:398:GLU:HA	2:F:401:LYS:HD2	2.02	0.41
4:H:54:THR:O	4:H:55:LEU:HD23	2.20	0.41
12:A:2128:HOH:O	2:D:354:THR:HG22	2.20	0.41
1:B:168:ILE:CD1	1:B:334:VAL:HG12	2.50	0.41
1:C:304:ARG:HH11	1:C:304:ARG:HD3	1.71	0.41
2:D:274:ARG:O	3:G:272:LEU:HD11	2.21	0.41
2:F:357:ILE:CD1	2:F:362:ILE:HD13	2.51	0.41
1:A:307:GLU:HG3	2:E:223:ASN:HB3	2.03	0.40
1:B:410:LEU:HG	1:B:411:ASP:N	2.36	0.40
1:C:114:ALA:HB2	1:C:121:ILE:CD1	2.52	0.40
1:C:144:GLU:HA	1:C:145:PRO:HD3	1.92	0.40
1:C:263:HIS:HD2	1:C:320:SER:OG	2.04	0.40
1:C:452:TYR:OH	1:C:498:LYS:HG3	2.21	0.40
2:D:382:LYS:HA	2:D:385:GLN:HE21	1.86	0.40
2:E:32:ILE:O	2:E:33:LEU:HB2	2.21	0.40
3:G:73:SER:O	3:G:111:LYS:HB2	2.21	0.40
4:H:62:LEU:HD23	4:H:75:TYR:O	2.22	0.40
1:A:295:PRO:HD3	12:A:2097:HOH:O	2.21	0.40
1:B:185:ASN:OD1	1:B:435:PRO:HB2	2.21	0.40
1:B:268:TYR:O	1:B:270:ASP:HA	2.20	0.40
2:D:246:GLN:O	2:D:247:GLU:HG3	2.21	0.40
3:G:2:THR:HG22	3:G:4:LYS:H	1.86	0.40
3:G:180:SER:O	3:G:205:GLN:NE2	2.50	0.40
1:A:138:PRO:HB3	1:A:316:PHE:CE1	2.55	0.40
1:A:398:ARG:NH2	12:A:2137:HOH:O	2.45	0.40
1:C:237:SER:HB3	2:F:294:GLU:HG3	2.03	0.40
1:C:269:ASP:HA	1:C:270:ASP:HA	1.74	0.40
2:D:428:LEU:HD12	2:D:428:LEU:HA	1.97	0.40

*Continued on next page...*

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:G:2:THR:C	3:G:4:LYS:N	2.75	0.40
3:G:51:LEU:HD23	3:G:52:TYR:CZ	2.57	0.40
3:G:184:ILE:O	3:G:184:ILE:HD13	2.22	0.40
4:H:78:SER:HB3	5:I:22:VAL:HG21	2.03	0.40
1:C:48:GLN:HB2	1:C:51:GLU:HB2	2.02	0.40
2:F:443:GLN:NE2	2:F:449:TYR:OH	2.54	0.40
4:H:40:THR:HG23	4:H:42:THR:N	2.36	0.40
1:A:168:ILE:HD11	1:A:329:THR:HG21	2.03	0.40
1:A:183:ILE:HD11	1:A:267:ILE:CD1	2.51	0.40
1:C:404:ALA:C	1:C:406:PHE:N	2.74	0.40
4:H:95:GLU:O	4:H:96:GLU:HG2	2.22	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	490/510 (96%)	468 (96%)	19 (4%)	3 (1%)	25 36
1	B	490/510 (96%)	451 (92%)	31 (6%)	8 (2%)	9 13
1	C	490/510 (96%)	468 (96%)	21 (4%)	1 (0%)	47 62
2	D	465/482 (96%)	437 (94%)	27 (6%)	1 (0%)	47 62
2	E	464/482 (96%)	434 (94%)	23 (5%)	7 (2%)	10 14
2	F	464/482 (96%)	433 (93%)	27 (6%)	4 (1%)	17 25
3	G	257/272 (94%)	223 (87%)	26 (10%)	8 (3%)	4 3
4	H	129/146 (88%)	118 (92%)	8 (6%)	3 (2%)	6 7
5	I	45/50 (90%)	36 (80%)	4 (9%)	5 (11%)	0 0
All	All	3294/3444 (96%)	3068 (93%)	186 (6%)	40 (1%)	13 19

All (40) Ramachandran outliers are listed below:



Mol	Chain	Res	Type
1	A	23	VAL
1	B	404	ALA
1	B	405	GLN
1	B	406	PHE
1	B	411	ASP
2	E	391	LEU
2	E	472	LYS
4	H	71	THR
5	I	29	GLU
1	A	488	LYS
1	C	407	GLY
2	F	28	GLY
2	F	246	GLN
2	F	385	GLN
3	G	51	LEU
3	G	56	ASP
1	A	21	THR
1	B	408	SER
1	B	452	TYR
2	D	448	GLU
2	E	389	ALA
3	G	72	SER
3	G	180	SER
5	I	36	LYS
1	B	31	VAL
2	E	109	LYS
3	G	122	ASP
4	H	49	ALA
5	I	40	SER
1	B	400	VAL
2	E	394	ASP
2	E	455	GLN
3	G	116	LEU
3	G	179	PHE
3	G	185	SER
4	H	79	SER
5	I	28	THR
5	I	42	ILE
2	E	279	VAL
2	F	279	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	397/412 (96%)	380 (96%)	17 (4%)	29	46
1	B	397/412 (96%)	378 (95%)	19 (5%)	25	41
1	C	397/412 (96%)	374 (94%)	23 (6%)	20	32
2	D	377/386 (98%)	367 (97%)	10 (3%)	44	65
2	E	376/386 (97%)	359 (96%)	17 (4%)	27	44
2	F	376/386 (97%)	363 (96%)	13 (4%)	36	55
3	G	225/230 (98%)	210 (93%)	15 (7%)	16	26
4	H	104/109 (95%)	100 (96%)	4 (4%)	33	51
5	I	38/41 (93%)	35 (92%)	3 (8%)	12	19
All	All	2687/2774 (97%)	2566 (96%)	121 (4%)	27	44

All (121) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	21	THR
1	A	50	GLU
1	A	52	MET
1	A	59	LEU
1	A	79	ASP
1	A	80	LYS
1	A	99	VAL
1	A	141	SER
1	A	143	ARG
1	A	164	ARG
1	A	168	ILE
1	A	371	VAL
1	A	438	ILE
1	A	444	VAL
1	A	469	LEU
1	A	479	LEU
1	A	493	SER
1	B	21	THR

*Continued on next page...*

*Continued from previous page...*

<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
1	B	30	ARG
1	B	99	VAL
1	B	146	MET
1	B	167	ILE
1	B	168	ILE
1	B	171	ARG
1	B	216	LEU
1	B	244	TYR
1	B	276	VAL
1	B	298	VAL
1	B	344	SER
1	B	371	VAL
1	B	384	LYS
1	B	400	VAL
1	B	406	PHE
1	B	449	VAL
1	B	505	LEU
1	B	509	GLU
1	C	34	ILE
1	C	52	MET
1	C	56	SER
1	C	57	SER
1	C	64	LEU
1	C	74	VAL
1	C	91	THR
1	C	99	VAL
1	C	140	ILE
1	C	164	ARG
1	C	206	ILE
1	C	216	LEU
1	C	298	VAL
1	C	334	VAL
1	C	349	GLN
1	C	381	ARG
1	C	408	SER
1	C	414	THR
1	C	434	SER
1	C	470	SER
1	C	479	LEU
1	C	485	THR
1	C	505	LEU
2	D	9	THR

*Continued on next page...*

*Continued from previous page...*

<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
2	D	61	ILE
2	D	97	VAL
2	D	132	ILE
2	D	250	ASP
2	D	258	ILE
2	D	274	ARG
2	D	282	GLN
2	D	335	LEU
2	D	384	LEU
2	E	9	THR
2	E	27	GLU
2	E	61	ILE
2	E	67	GLU
2	E	84	ILE
2	E	96	ASN
2	E	97	VAL
2	E	139	VAL
2	E	151	LYS
2	E	223	ASN
2	E	232	VAL
2	E	252	LEU
2	E	257	ASN
2	E	258	ILE
2	E	282	GLN
2	E	391	LEU
2	E	431	LEU
2	F	51	GLN
2	F	76	LEU
2	F	96	ASN
2	F	97	VAL
2	F	139	VAL
2	F	223	ASN
2	F	232	VAL
2	F	274	ARG
2	F	282	GLN
2	F	420	VAL
2	F	436	GLU
2	F	444	ILE
2	F	463	ILE
3	G	35	GLU
3	G	67	LEU
3	G	110	ASP

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Res	Type
3	G	113	ARG
3	G	118	ARG
3	G	125	LEU
3	G	126	VAL
3	G	130	GLU
3	G	180	SER
3	G	184	ILE
3	G	190	MET
3	G	205	GLN
3	G	212	ILE
3	G	213	ILE
3	G	262	LEU
4	H	54	THR
4	H	57	VAL
4	H	91	GLN
4	H	112	LEU
5	I	37	THR
5	I	41	THR
5	I	42	ILE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (49) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	260	ASN
1	A	379	GLN
1	A	396	GLN
1	A	405	GLN
1	A	477	GLN
1	B	65	ASN
1	B	186	GLN
1	B	349	GLN
1	B	466	ASN
1	B	475	GLN
1	B	503	ASN
1	C	48	GLN
1	C	215	GLN
1	C	260	ASN
1	C	263	HIS
1	C	349	GLN
1	C	416	GLN
1	C	432	GLN
2	D	130	GLN

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Res	Type
2	D	194	ASN
2	D	198	HIS
2	D	221	GLN
2	D	282	GLN
2	D	385	GLN
2	D	411	GLN
2	E	51	GLN
2	E	96	ASN
2	E	194	ASN
2	E	223	ASN
2	E	257	ASN
2	E	263	GLN
2	E	282	GLN
2	E	411	GLN
2	F	51	GLN
2	F	96	ASN
2	F	194	ASN
2	F	221	GLN
2	F	223	ASN
2	F	282	GLN
2	F	419	GLN
2	F	443	GLN
3	G	82	HIS
3	G	88	GLN
3	G	225	GLN
3	G	234	ASN
4	H	91	GLN
4	H	111	ASN
4	H	132	GLN
5	I	16	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 [i](#)

There are no monosaccharides in this entry.

## 5.6 Ligand geometry [i](#)

Of 13 ligands modelled in this entry, 5 are monoatomic - leaving 8 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
10	DCW	D	700	2	17,17,17	1.14	1 (5%)	21,21,21	1.22	1 (4%)
6	ATP	C	600	7	26,33,33	0.87	0	31,52,52	0.96	1 (3%)
8	ADP	D	600	7	24,29,29	0.91	0	29,45,45	0.96	1 (3%)
8	ADP	B	600	7	24,29,29	0.86	0	29,45,45	0.91	1 (3%)
11	SO4	E	630	-	4,4,4	0.64	0	6,6,6	0.08	0
8	ADP	F	600	7	24,29,29	0.84	0	29,45,45	0.98	1 (3%)
6	ATP	A	600	7	26,33,33	0.81	0	31,52,52	0.87	0
9	GOL	B	701	-	5,5,5	0.26	0	5,5,5	0.38	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
10	DCW	D	700	2	-	3/8/24/24	0/2/2/2
6	ATP	C	600	7	-	4/18/38/38	0/3/3/3
8	ADP	D	600	7	-	3/12/32/32	0/3/3/3
8	ADP	B	600	7	-	2/12/32/32	0/3/3/3
8	ADP	F	600	7	-	2/12/32/32	0/3/3/3
6	ATP	A	600	7	-	7/18/38/38	0/3/3/3
9	GOL	B	701	-	-	2/4/4/4	-

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
10	D	700	DCW	C1-N1	2.48	1.40	1.35

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
10	D	700	DCW	C8-N2-C1	3.37	130.15	123.02
8	F	600	ADP	C5-C6-N6	2.78	124.58	120.35
8	B	600	ADP	C5-C6-N6	2.68	124.43	120.35
8	D	600	ADP	C5-C6-N6	2.37	123.95	120.35
6	C	600	ATP	C5-C6-N6	2.31	123.87	120.35

There are no chirality outliers.

All (23) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
6	A	600	ATP	PB-O3B-PG-O2G
6	C	600	ATP	PB-O3B-PG-O2G
8	B	600	ADP	PA-O3A-PB-O2B
8	D	600	ADP	PA-O3A-PB-O2B
8	F	600	ADP	PA-O3A-PB-O2B
8	F	600	ADP	PA-O3A-PB-O3B
9	B	701	GOL	C1-C2-C3-O3
9	B	701	GOL	O2-C2-C3-O3
10	D	700	DCW	O1-C1-N1-C2
10	D	700	DCW	N2-C1-N1-C2
10	D	700	DCW	C3-C2-N1-C1
6	A	600	ATP	PA-O3A-PB-O1B
8	B	600	ADP	PA-O3A-PB-O1B
6	C	600	ATP	PA-O3A-PB-O1B
6	A	600	ATP	PB-O3B-PG-O1G
8	D	600	ADP	PA-O3A-PB-O1B
6	A	600	ATP	PB-O3B-PG-O3G
6	C	600	ATP	PB-O3B-PG-O3G
8	D	600	ADP	PA-O3A-PB-O3B
6	A	600	ATP	PG-O3B-PB-O1B
6	A	600	ATP	PG-O3B-PB-O2B
6	A	600	ATP	PA-O3A-PB-O2B
6	C	600	ATP	PB-O3B-PG-O1G

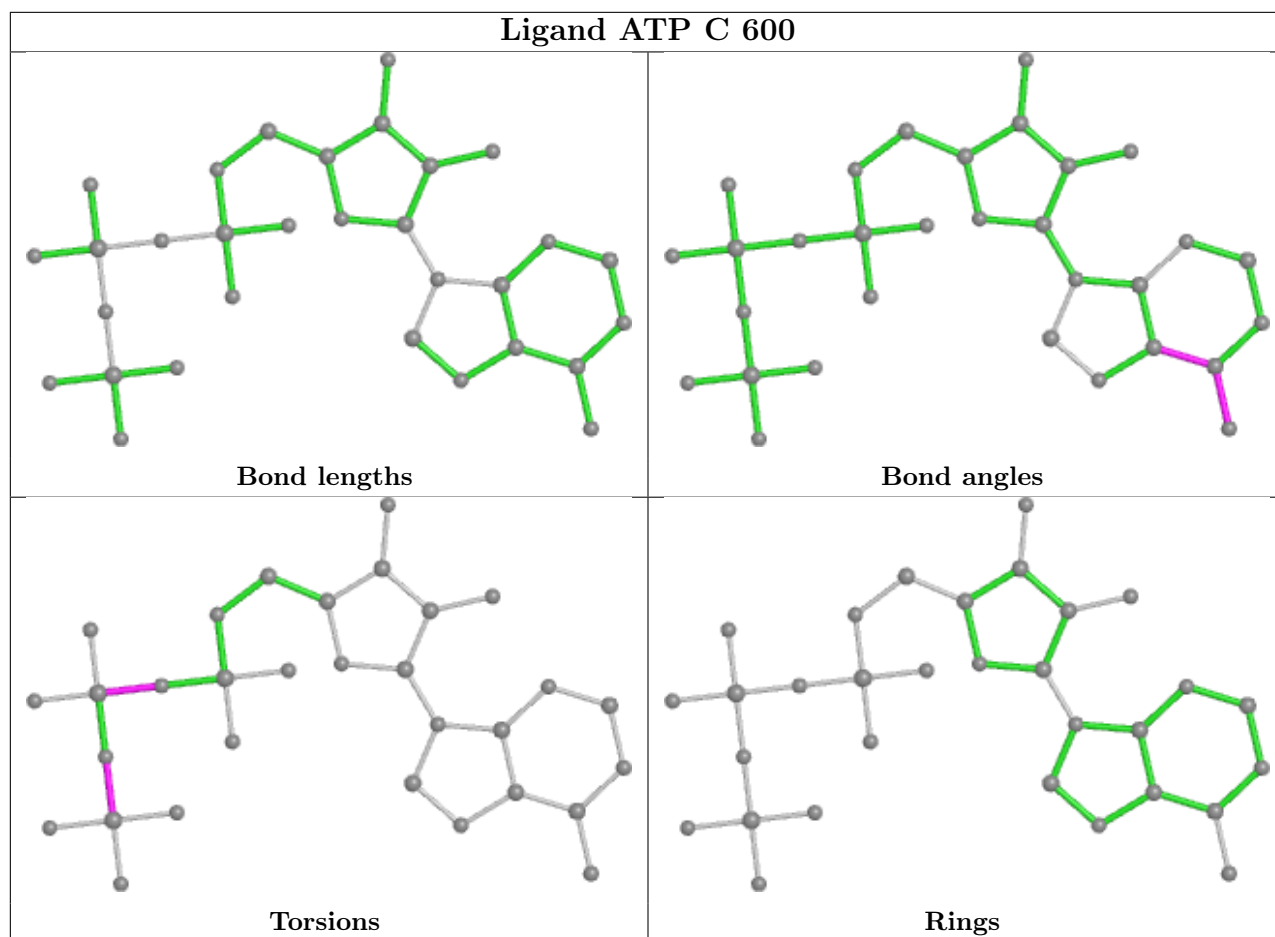
There are no ring outliers.

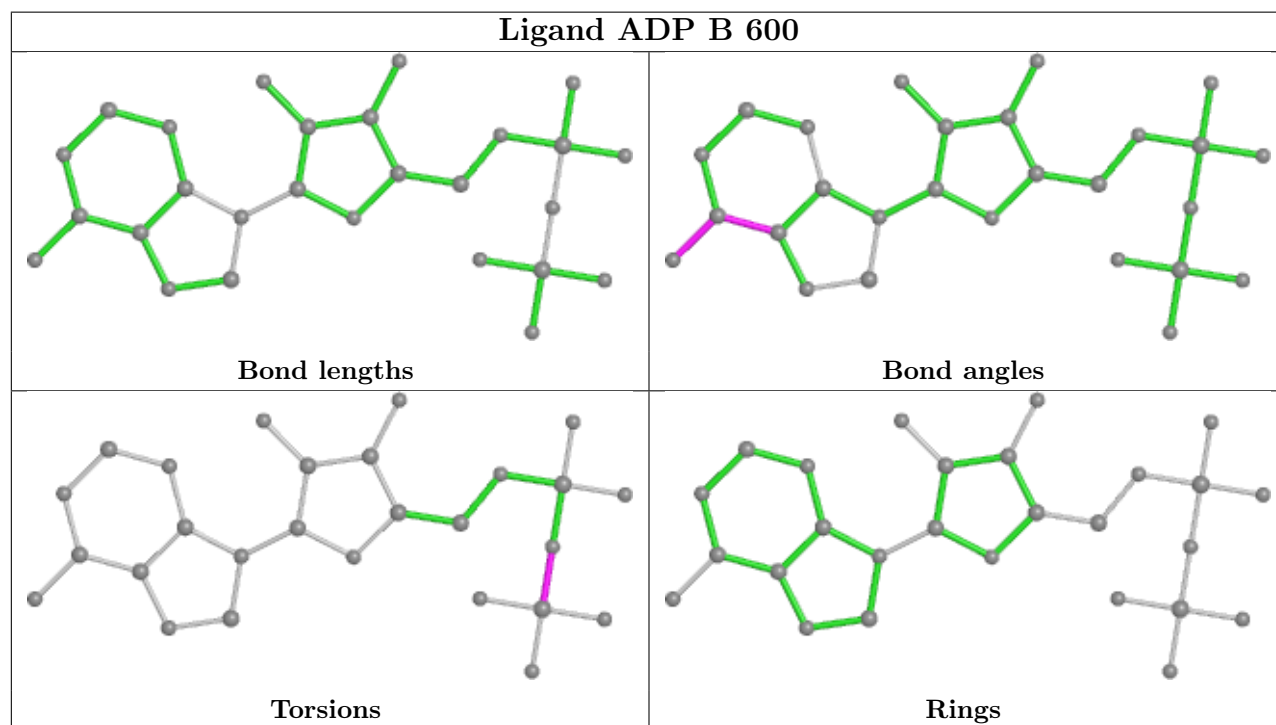
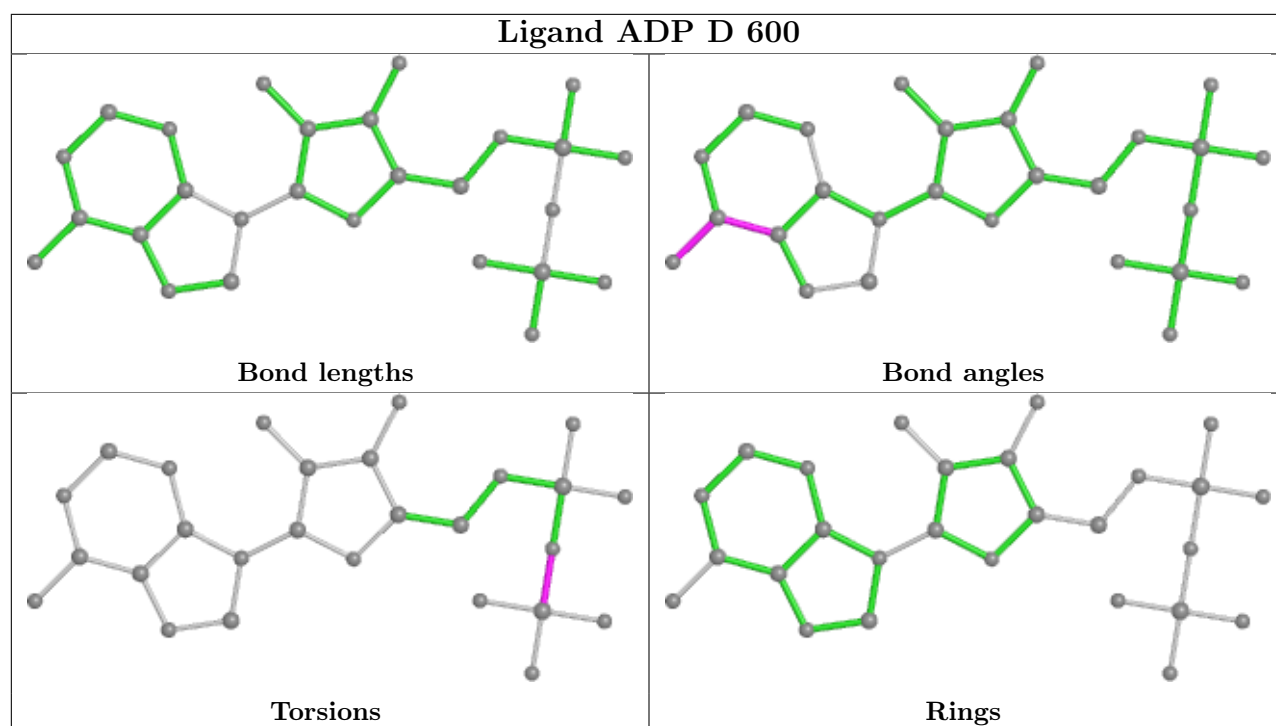
3 monomers are involved in 8 short contacts:

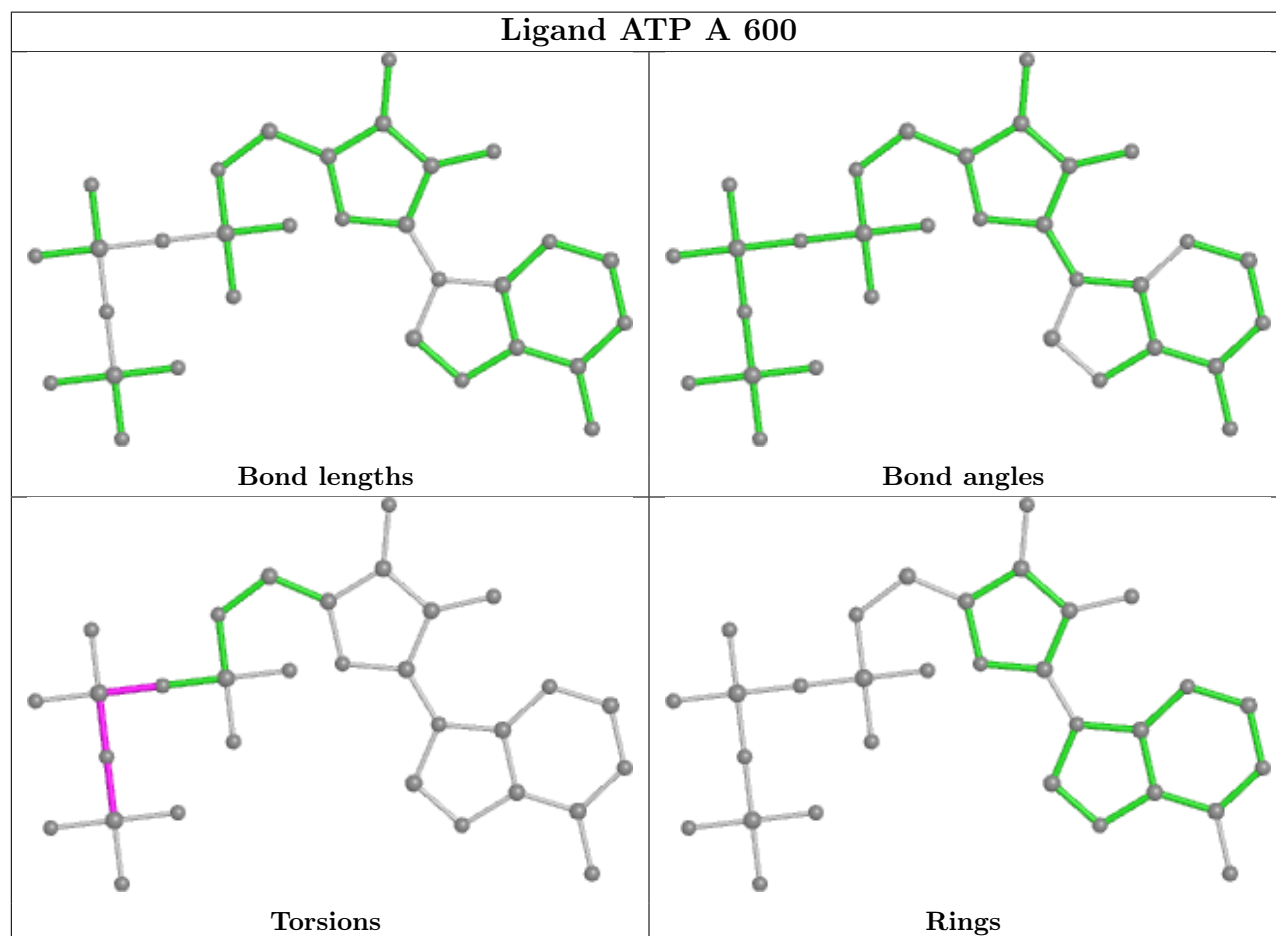
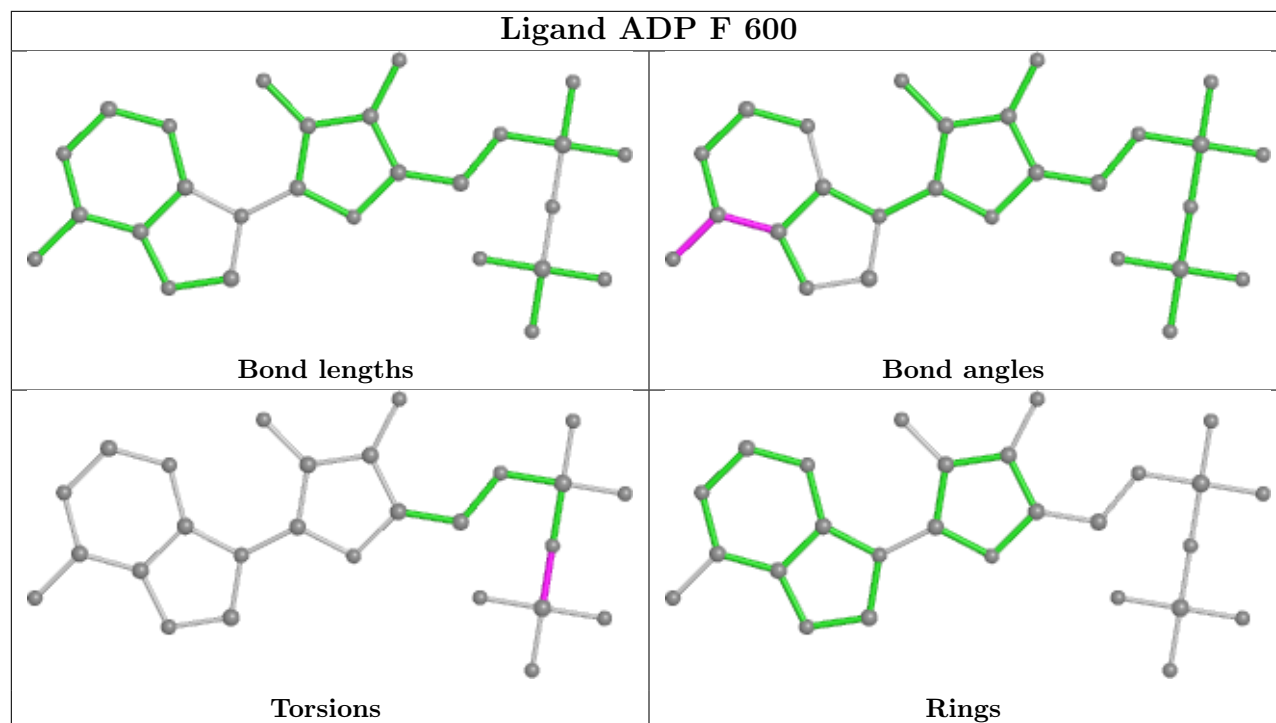


Mol	Chain	Res	Type	Clashes	Symm-Clashes
10	D	700	DCW	6	0
6	C	600	ATP	1	0
9	B	701	GOL	1	0

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 than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.







## 5.7 Other polymers [i](#)

There are no such residues in this entry.

## 5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

## 6 Fit of model and data

### 6.1 Protein, DNA and RNA chains

In the following table, the column labelled ‘#RSRZ > 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 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	492/510 (96%)	-0.16	18 (3%) 41 41	32, 46, 74, 104	0
1	B	492/510 (96%)	0.02	26 (5%) 26 25	32, 48, 95, 143	0
1	C	492/510 (96%)	-0.25	11 (2%) 62 60	30, 44, 63, 102	0
2	D	467/482 (96%)	-0.24	10 (2%) 63 61	31, 45, 69, 100	0
2	E	466/482 (96%)	0.22	38 (8%) 11 10	34, 54, 101, 132	0
2	F	466/482 (96%)	-0.20	11 (2%) 59 57	32, 44, 74, 89	0
3	G	263/272 (96%)	0.67	43 (16%) 1 1	36, 68, 116, 133	0
4	H	131/146 (89%)	1.33	31 (23%) 0 0	67, 97, 131, 136	0
5	I	47/50 (94%)	1.33	11 (23%) 0 0	58, 91, 127, 129	0
All	All	3316/3444 (96%)	0.04	199 (6%) 21 20	30, 48, 102, 143	0

All (199) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	E	473	LEU	8.8
1	C	407	GLY	8.7
2	E	474	ALA	8.4
1	B	400	VAL	8.4
2	E	390	ILE	8.3
1	B	19	ALA	7.9
1	B	21	THR	7.8
2	E	472	LYS	7.0
3	G	60	PRO	6.9
1	B	402	ALA	6.9
1	B	403	PHE	6.6
1	B	405	GLN	6.5
1	A	19	ALA	6.3
1	B	20	ASP	6.3
5	I	47	VAL	6.1

*Continued on next page...*

*Continued from previous page...*

<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>	<b>RSRZ</b>
5	I	35	MET	6.0
1	C	408	SER	5.7
1	C	409	ASP	5.6
2	E	423	VAL	5.5
1	B	406	PHE	5.5
4	H	144	ALA	5.4
1	A	20	ASP	5.4
3	G	199	ASP	5.3
5	I	46	LYS	5.3
1	B	358	TYR	5.1
2	F	248	GLY	5.1
4	H	71	THR	5.1
1	C	193	THR	4.8
3	G	194	ASP	4.8
1	A	21	THR	4.7
2	E	389	ALA	4.5
4	H	15	GLN	4.5
4	H	42	THR	4.4
4	H	69	ASP	4.4
5	I	28	THR	4.3
3	G	117	HIS	4.1
2	E	424	PHE	4.1
1	B	410	LEU	4.0
5	I	40	SER	4.0
1	B	193	THR	4.0
3	G	1	ALA	4.0
1	B	416	GLN	4.0
1	B	408	SER	3.9
3	G	58	LYS	3.9
1	B	22	SER	3.9
2	D	399	GLU	3.9
2	E	386	ASP	3.9
2	D	28	GLY	3.8
3	G	101	LYS	3.8
3	G	116	LEU	3.8
3	G	59	THR	3.8
4	H	67	ALA	3.8
3	G	122	ASP	3.7
5	I	29	GLU	3.7
2	E	42	GLU	3.7
2	E	27	GLU	3.6
3	G	180	SER	3.6

*Continued on next page...*

*Continued from previous page...*

<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>	<b>RSRZ</b>
3	G	193	TYR	3.6
1	C	406	PHE	3.5
2	D	246	GLN	3.5
1	B	404	ALA	3.5
2	E	394	ASP	3.5
2	F	28	GLY	3.4
3	G	39	LYS	3.4
2	D	248	GLY	3.3
2	E	178	GLY	3.3
5	I	30	PHE	3.3
3	G	181	LEU	3.2
4	H	34	ARG	3.2
3	G	87	LYS	3.2
1	B	389	THR	3.2
3	G	195	ASP	3.2
3	G	103	VAL	3.2
4	H	106	GLY	3.2
2	E	337	ARG	3.2
3	G	61	GLU	3.1
3	G	134	ARG	3.1
4	H	109	LYS	3.1
3	G	36	ARG	3.1
3	G	120	HIS	3.1
4	H	45	PHE	3.1
2	F	246	GLN	3.1
3	G	53	GLU	3.1
2	E	451	HIS	3.0
2	E	345	TYR	3.0
3	G	118	ARG	3.0
2	E	395	GLU	3.0
3	G	102	GLU	3.0
2	E	398	GLU	3.0
1	B	412	ALA	2.9
3	G	198	ALA	2.9
4	H	68	GLU	2.9
1	B	506	ALA	2.9
2	E	428	LEU	2.9
1	A	499	GLU	2.9
5	I	36	LYS	2.8
4	H	121	GLY	2.8
4	H	56	GLN	2.8
2	E	159	GLY	2.8

*Continued on next page...*

*Continued from previous page...*

<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>	<b>RSRZ</b>
1	A	22	SER	2.8
1	C	405	GLN	2.8
4	H	142	VAL	2.8
3	G	184	ILE	2.7
4	H	86	ALA	2.7
1	A	315	ALA	2.7
4	H	140	ALA	2.7
2	D	249	GLN	2.7
2	E	427	HIS	2.7
1	A	402	ALA	2.7
1	B	413	ALA	2.7
2	E	338	ALA	2.6
2	F	9	THR	2.6
1	C	194	ASP	2.6
1	A	23	VAL	2.6
2	E	425	THR	2.6
2	D	402	LEU	2.6
1	A	196	LYS	2.6
2	E	43	THR	2.6
1	A	457	GLU	2.6
1	B	457	GLU	2.6
1	C	381	ARG	2.5
2	D	398	GLU	2.5
2	F	42	GLU	2.5
4	H	118	GLU	2.5
4	H	128	ARG	2.5
4	H	32	ASN	2.5
2	F	249	GLN	2.4
2	D	47	LEU	2.4
1	A	404	ALA	2.4
2	E	365	SER	2.4
4	H	83	THR	2.4
5	I	22	VAL	2.4
1	A	122	GLY	2.4
2	E	111	LYS	2.4
2	E	160	VAL	2.4
2	E	399	GLU	2.4
3	G	50	ALA	2.4
2	E	384	LEU	2.4
3	G	105	ILE	2.3
2	E	379	GLN	2.3
1	B	491	GLU	2.3

*Continued on next page...*



*Continued from previous page...*

<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>	<b>RSRZ</b>
2	E	444	ILE	2.3
1	A	193	THR	2.3
3	G	56	ASP	2.3
1	C	19	ALA	2.3
3	G	95	ASN	2.3
3	G	153	TYR	2.3
1	B	355	GLU	2.3
5	I	6	GLN	2.3
1	A	30	ARG	2.3
4	H	70	GLY	2.3
4	H	105	LEU	2.3
1	A	455	LYS	2.2
4	H	37	ASP	2.2
3	G	192	ILE	2.2
1	A	485	THR	2.2
3	G	89	MET	2.2
1	A	25	LEU	2.2
2	E	455	GLN	2.2
2	F	426	GLY	2.2
2	F	178	GLY	2.2
1	B	510	ALA	2.2
1	B	415	GLN	2.2
1	B	455	LYS	2.2
1	C	73	VAL	2.2
3	G	119	THR	2.2
1	C	56	SER	2.2
4	H	16	MET	2.2
2	F	472	LYS	2.2
2	E	391	LEU	2.2
4	H	103	LEU	2.2
2	E	420	VAL	2.1
4	H	72	THR	2.1
2	D	27	GLU	2.1
3	G	70	GLY	2.1
4	H	113	GLU	2.1
3	G	51	LEU	2.1
5	I	1	VAL	2.1
2	E	301	LYS	2.1
3	G	54	LYS	2.1
3	G	107	GLY	2.1
2	E	436	GLU	2.1
2	E	382	LYS	2.1

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Res	Type	RSRZ
2	E	470	ALA	2.1
2	E	362	ILE	2.1
3	G	57	ILE	2.1
2	F	111	LYS	2.1
1	A	413	ALA	2.0
4	H	31	ALA	2.0
4	H	50	ALA	2.0
3	G	52	TYR	2.0
3	G	197	ASP	2.0
4	H	63	VAL	2.0
2	F	385	GLN	2.0
4	H	59	ARG	2.0
3	G	71	VAL	2.0
1	B	122	GLY	2.0
2	D	26	ASP	2.0
3	G	175	GLU	2.0

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

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

## 6.3 Carbohydrates [i](#)

There are no monosaccharides in this entry.

## 6.4 Ligands [i](#)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95<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.

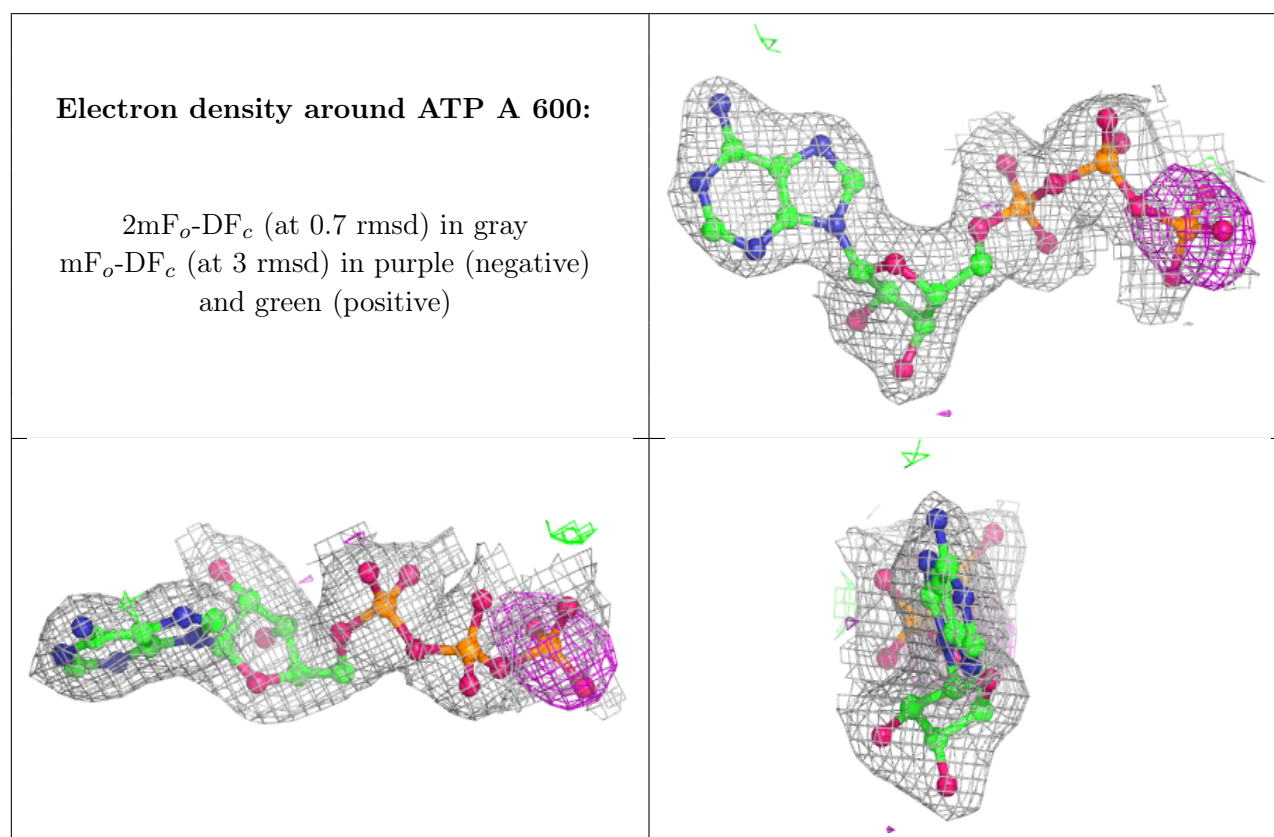
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å <sup>2</sup> )	Q<0.9
10	DCW	D	700	16/16	0.74	0.31	69,73,78,78	0
7	MG	A	601	1/1	0.77	0.12	44,44,44,44	0
11	SO4	E	630	5/5	0.83	0.45	100,100,100,100	0
7	MG	C	601	1/1	0.90	0.15	43,43,43,43	0
6	ATP	A	600	31/31	0.92	0.13	42,44,56,56	0
6	ATP	C	600	31/31	0.94	0.12	36,42,51,52	0
7	MG	F	601	1/1	0.95	0.08	34,34,34,34	0

*Continued on next page...*

Continued from previous page...

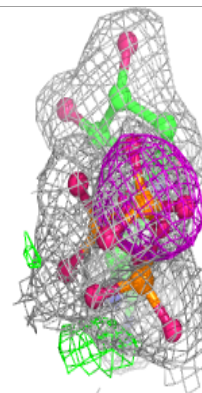
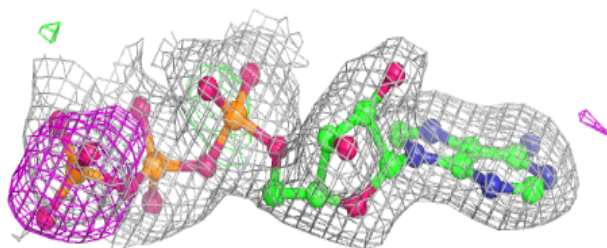
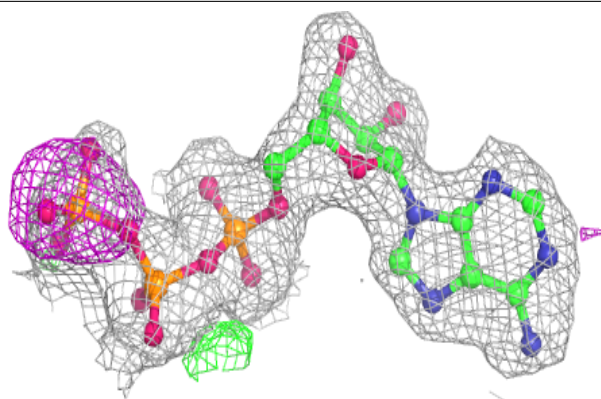
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors( $\text{\AA}^2$ )	Q<0.9
8	ADP	F	600	27/27	0.97	0.10	41,42,45,45	0
9	GOL	B	701	6/6	0.97	0.12	39,43,44,45	0
7	MG	D	601	1/1	0.97	0.18	35,35,35,35	0
7	MG	B	601	1/1	0.97	0.06	46,46,46,46	0
8	ADP	B	600	27/27	0.98	0.10	44,52,56,56	0
8	ADP	D	600	27/27	0.98	0.11	35,37,38,39	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.

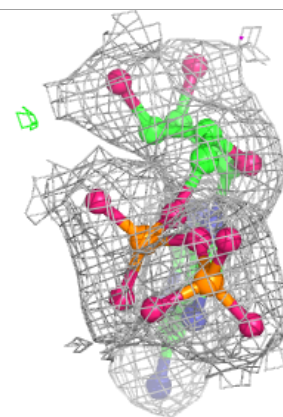
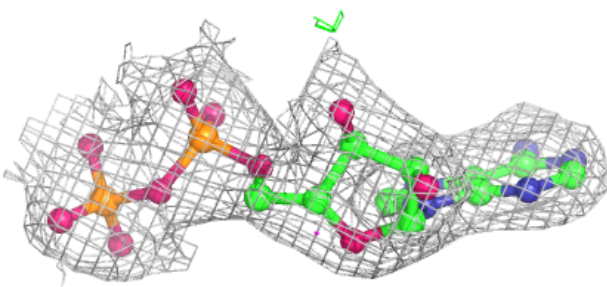
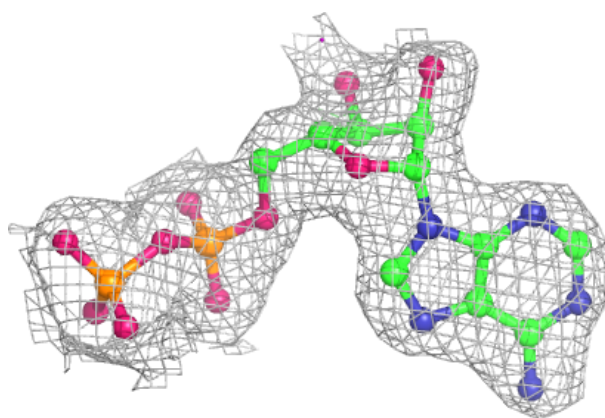


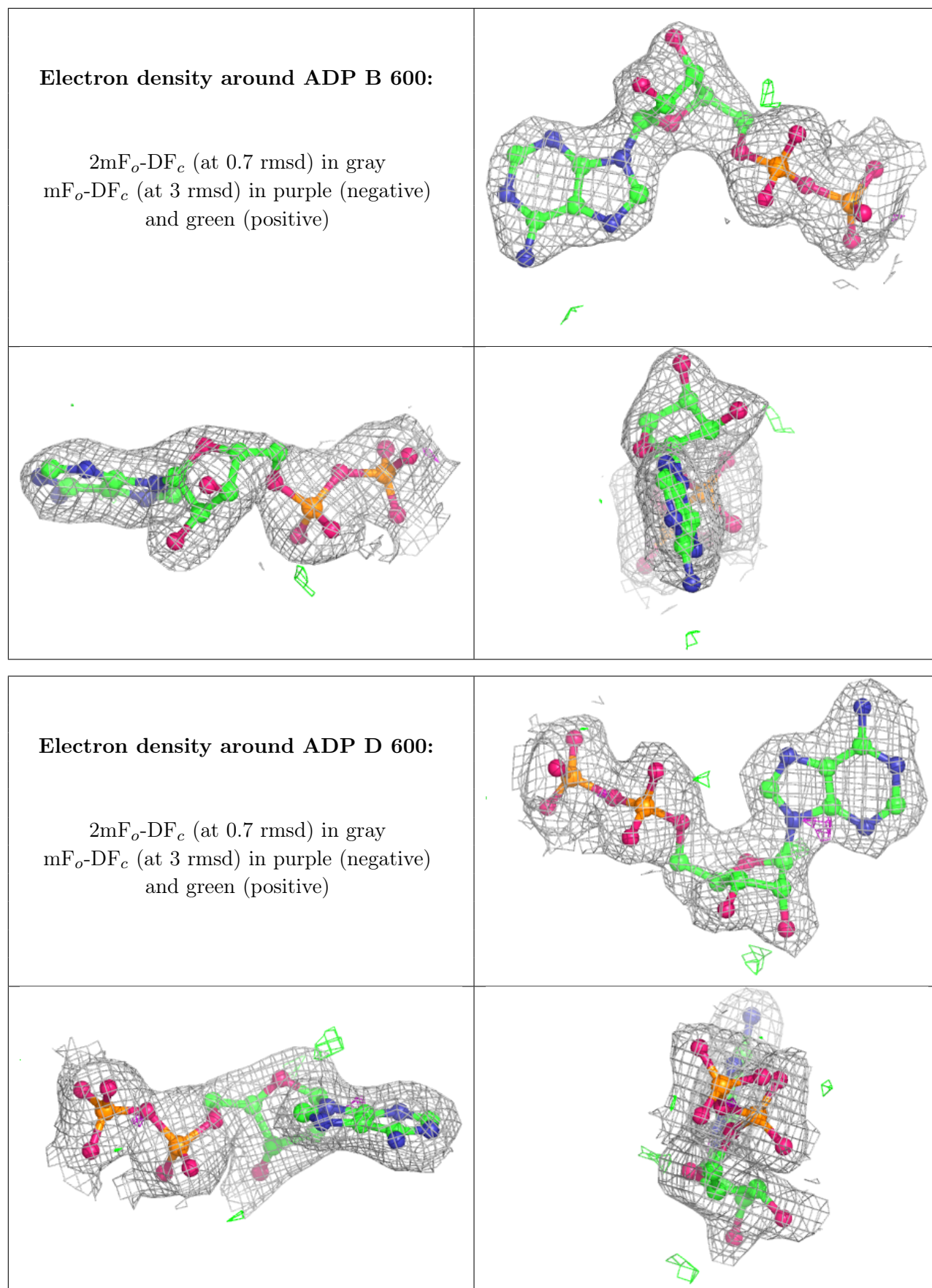
**Electron density around ATP C 600:**

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

**Electron density around ADP F 600:**

$2mF_o-DF_c$  (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.