



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 3, 2024 – 06:03 PM EST

PDB ID : 6DHM
Title : Bovine glutamate dehydrogenase complexed with zinc
Authors : Smith, T.J.
Deposited on : 2018-05-20
Resolution : 3.00 Å(reported)

This is a Full wwPDB X-ray Structure Validation Report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

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

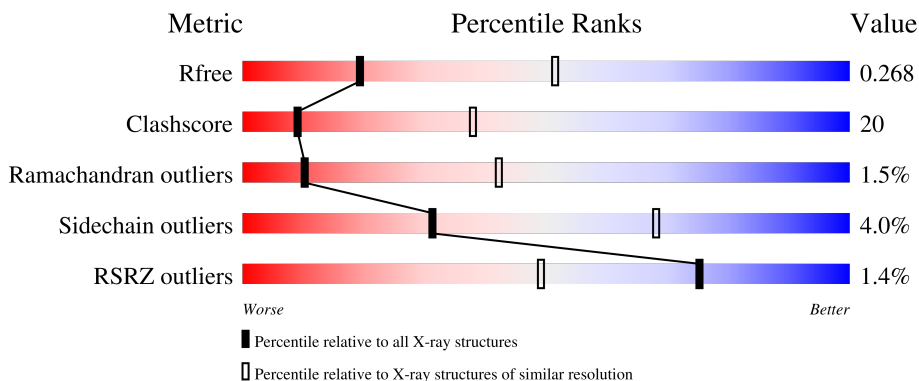
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.00 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	2092 (3.00-3.00)
Clashscore	141614	2416 (3.00-3.00)
Ramachandran outliers	138981	2333 (3.00-3.00)
Sidechain outliers	138945	2336 (3.00-3.00)
RSRZ outliers	127900	1990 (3.00-3.00)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments of the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	582	
1	B	582	
1	C	582	
1	D	582	
1	E	582	

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Mol	Chain	Length	Quality of chain
1	F	582	<p>%</p> <p>51% 33% 14%</p>

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
2	GLU	A	601	-	-	X	-
2	GLU	C	601	-	-	X	-

2 Entry composition [i](#)

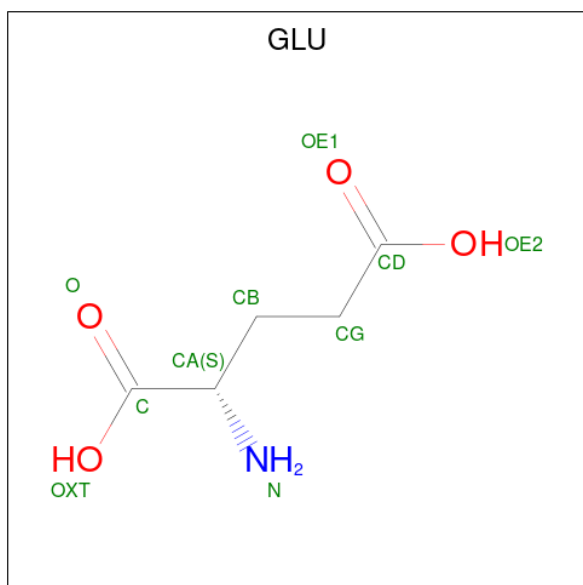
There are 5 unique types of molecules in this entry. The entry contains 23838 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 Glutamate dehydrogenase 1, mitochondrial.

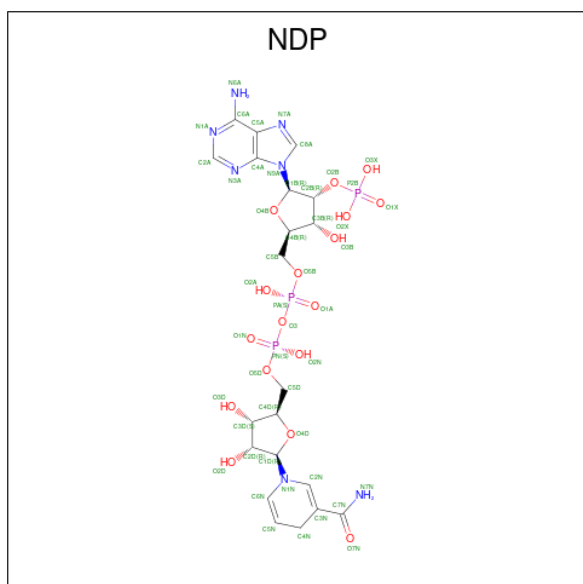
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	495	Total 3874	C 2446	N 681	O 728	S 19	0	0	0
1	B	495	Total 3874	C 2446	N 681	O 728	S 19	0	0	0
1	C	495	Total 3874	C 2446	N 681	O 728	S 19	0	0	0
1	D	495	Total 3874	C 2446	N 681	O 728	S 19	0	0	0
1	E	495	Total 3874	C 2446	N 681	O 728	S 19	0	0	0
1	F	501	Total 3916	C 2473	N 687	O 737	S 19	0	0	0

- Molecule 2 is GLUTAMIC ACID (three-letter code: GLU) (formula: C₅H₉NO₄).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	A	1	Total	C	N	O	0	0
			10	5	1	4		
2	B	1	Total	C	N	O	0	0
			10	5	1	4		
2	C	1	Total	C	N	O	0	0
			10	5	1	4		
2	D	1	Total	C	N	O	0	0
			10	5	1	4		
2	E	1	Total	C	N	O	0	0
			10	5	1	4		
2	F	1	Total	C	N	O	0	0
			10	5	1	4		

- Molecule 3 is NADPH DIHYDRO-NICOTINAMIDE-ADENINE-DINUCLEOTIDE PHOSPHATE (three-letter code: NDP) (formula: $C_{21}H_{30}N_7O_{17}P_3$).



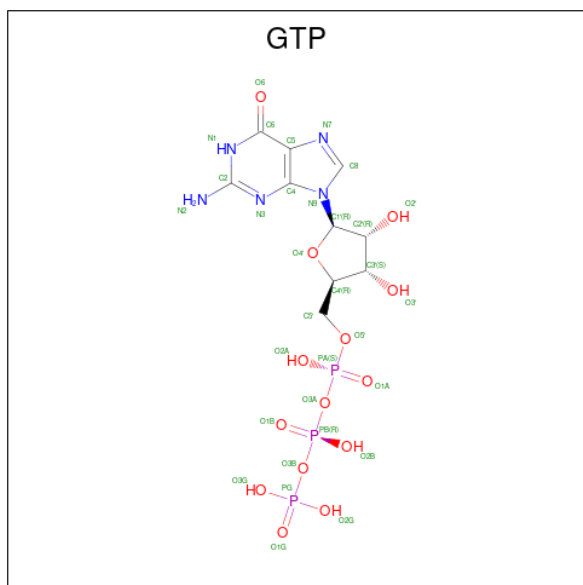
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
3	A	1	Total	C	N	O	P	0	0
			48	21	7	17	3		
3	B	1	Total	C	N	O	P	0	0
			48	21	7	17	3		
3	C	1	Total	C	N	O	P	0	0
			48	21	7	17	3		
3	D	1	Total	C	N	O	P	0	0
			48	21	7	17	3		
3	E	1	Total	C	N	O	P	0	0
			48	21	7	17	3		

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Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	
			Total	C	N	O			P
3	F	1	48	21	7	17	3	0	0

- Molecule 4 is GUANOSINE-5'-TRIPHOSPHATE (three-letter code: GTP) (formula: $C_{10}H_{16}N_5O_{14}P_3$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	
			Total	C	N	O			P
4	A	1	32	10	5	14	3	0	0
4	B	1	32	10	5	14	3	0	0
4	C	1	32	10	5	14	3	0	0
4	D	1	32	10	5	14	3	0	0
4	E	1	32	10	5	14	3	0	0
4	F	1	32	10	5	14	3	0	0

- Molecule 5 is ZINC ION (three-letter code: ZN) (formula: Zn).

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

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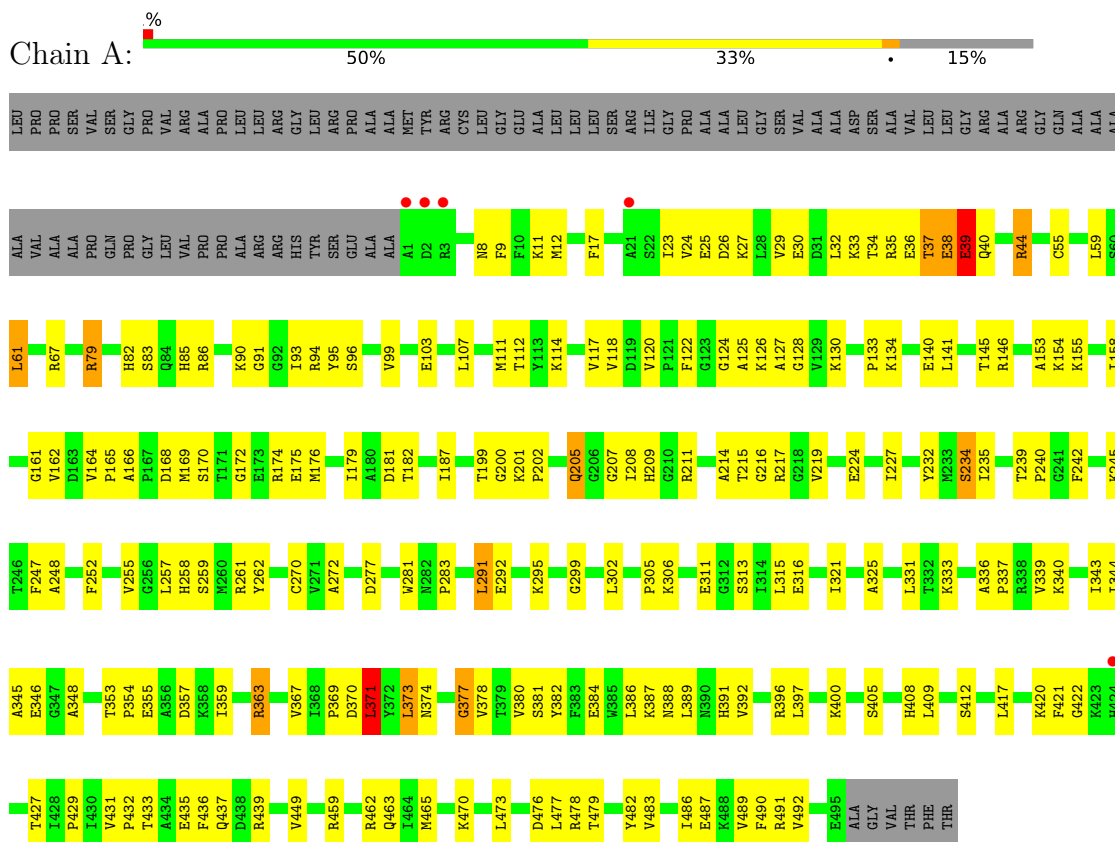
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	C	2	Total 2	Zn 2	0	0
5	D	2	Total 2	Zn 2	0	0
5	E	2	Total 2	Zn 2	0	0
5	F	2	Total 2	Zn 2	0	0

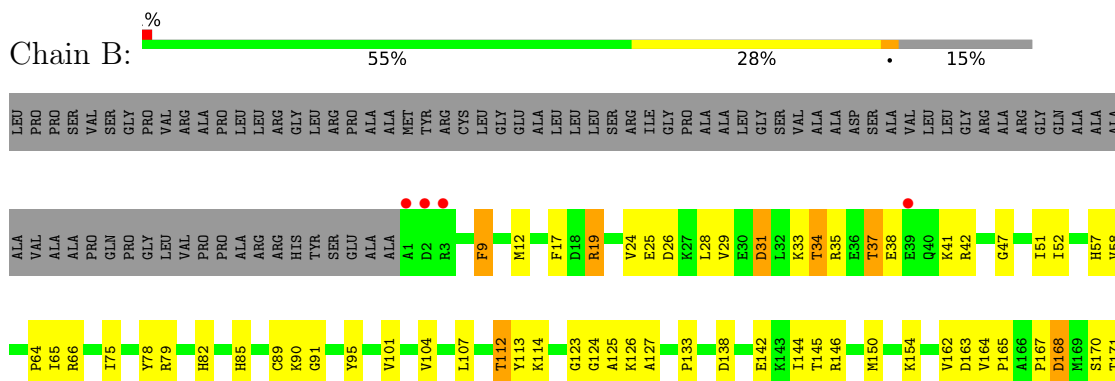
3 Residue-property plots [i](#)

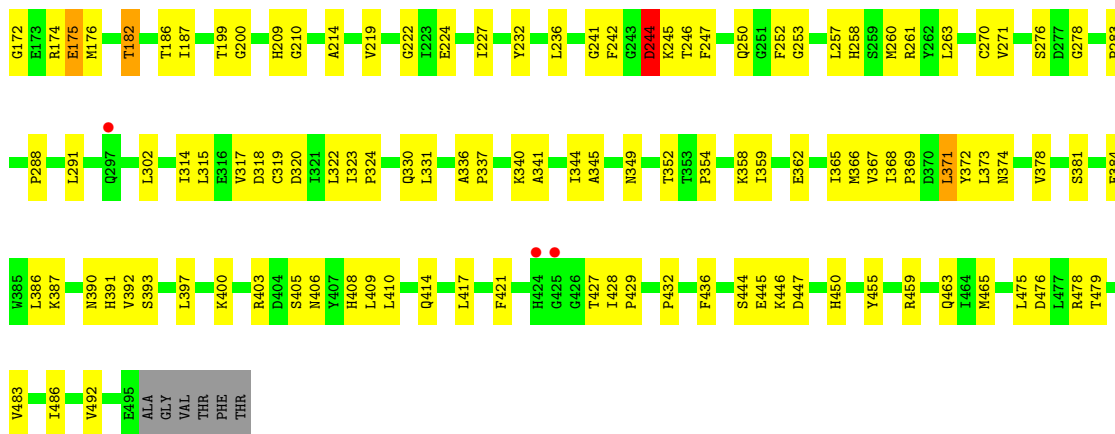
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red dot above a residue indicates a poor fit to the electron density ($RSRZ > 2$). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

- Molecule 1: Glutamate dehydrogenase 1, mitochondrial

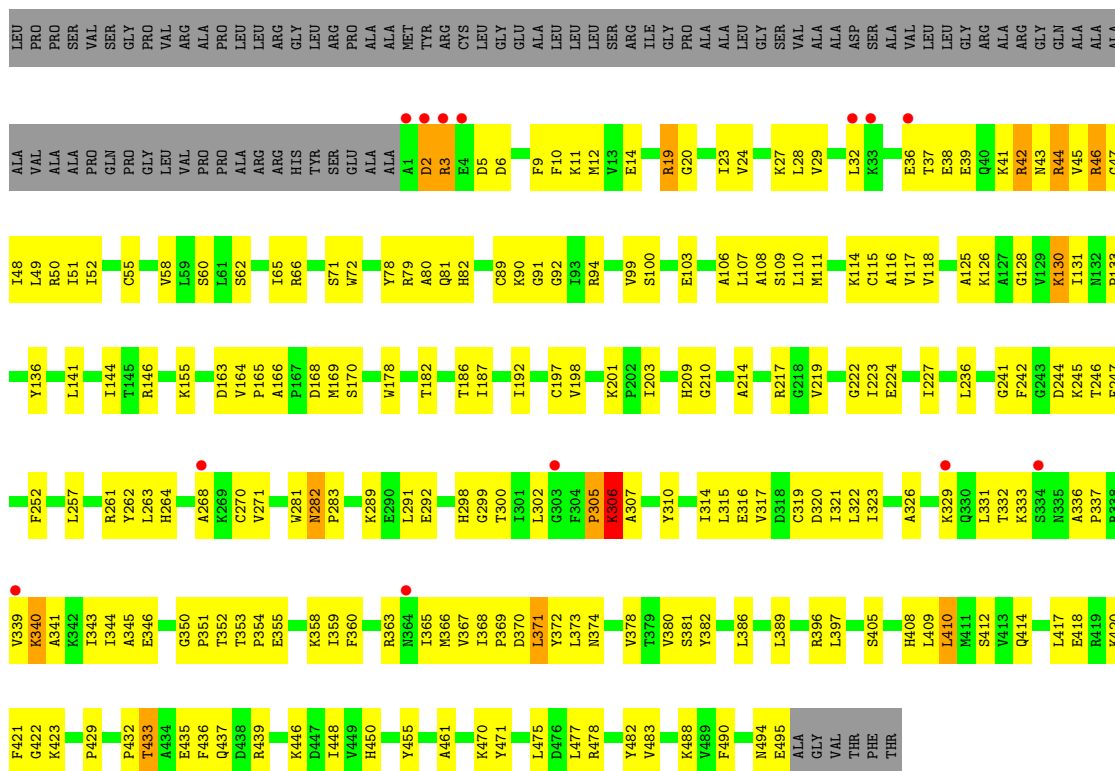


- Molecule 1: Glutamate dehydrogenase 1, mitochondrial

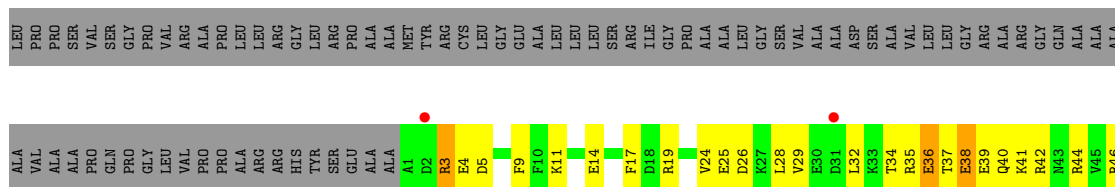


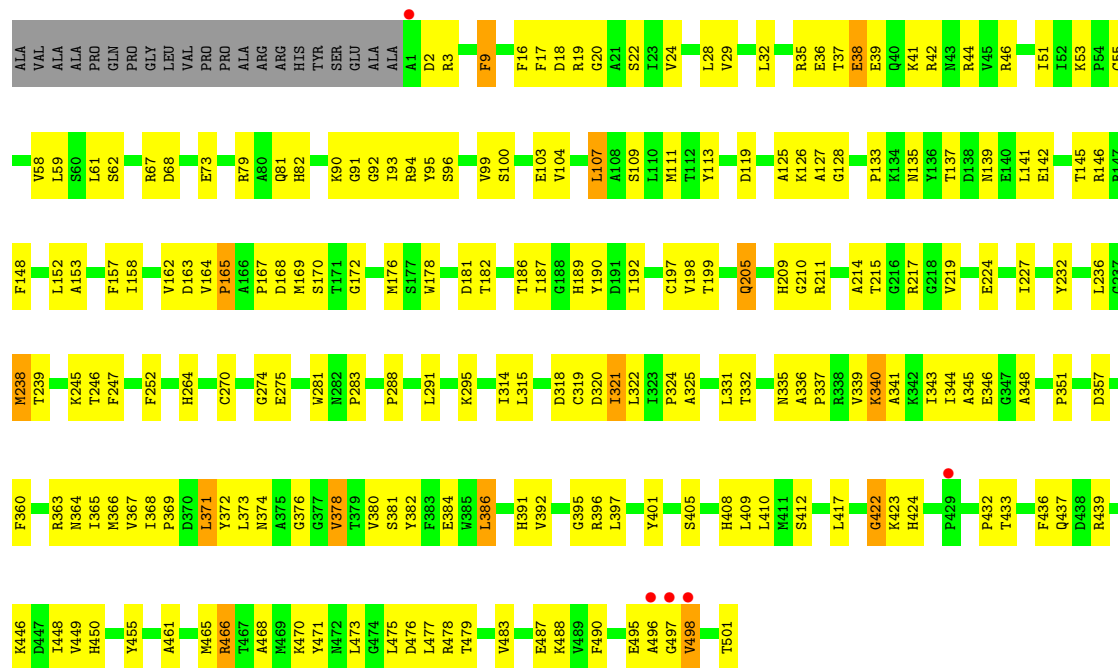


• Molecule 1: Glutamate dehydrogenase 1, mitochondrial



• Molecule 1: Glutamate dehydrogenase 1, mitochondrial





4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	121.11Å 98.76Å 165.64Å 90.00° 101.55° 90.00°	Depositor
Resolution (Å)	45.88 – 3.00 47.44 – 2.94	Depositor EDS
% Data completeness (in resolution range)	92.9 (45.88-3.00) 93.0 (47.44-2.94)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.76 (at 2.96Å)	Xtrriage
Refinement program	PHENIX (1.12_2829: ???)	Depositor
R, R_{free}	0.197 , 0.270 0.198 , 0.268	Depositor DCC
R_{free} test set	3825 reflections (5.04%)	wwPDB-VP
Wilson B-factor (Å ²)	34.5	Xtrriage
Anisotropy	0.301	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 38.5	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
F_o, F_c correlation	0.90	EDS
Total number of atoms	23838	wwPDB-VP
Average B, all atoms (Å ²)	34.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.36% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: GTP, NDP, ZN

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	A	0.47	0/3956	0.64	0/5338
1	B	0.46	0/3956	0.63	0/5338
1	C	0.46	0/3956	0.63	0/5338
1	D	0.49	0/3956	0.64	0/5338
1	E	0.48	0/3956	0.65	3/5338 (0.1%)
1	F	0.49	0/3999	0.66	1/5396 (0.0%)
All	All	0.47	0/23779	0.64	4/32086 (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
1	A	0	2
1	B	0	1
All	All	0	3

There are no bond length outliers.

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	E	371	LEU	CB-CG-CD2	-6.50	99.95	111.00
1	E	24	VAL	CB-CA-C	-6.15	99.72	111.40
1	E	371	LEU	CA-CB-CG	6.12	129.37	115.30
1	F	238	MET	C-N-CA	6.07	136.87	121.70

There are no chirality outliers.

All (3) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	37	THR	Peptide
1	A	39	GLU	Peptide
1	B	244	ASP	Peptide

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	3874	0	3840	176	0
1	B	3874	0	3840	141	0
1	C	3874	0	3840	196	0
1	D	3874	0	3840	140	0
1	E	3874	0	3840	181	0
1	F	3916	0	3880	178	0
2	A	10	0	5	5	0
2	B	10	0	5	1	0
2	C	10	0	5	4	0
2	D	10	0	5	2	0
2	E	10	0	5	1	0
2	F	10	0	5	3	0
3	A	48	0	26	6	0
3	B	48	0	25	4	0
3	C	48	0	26	5	0
3	D	48	0	26	0	0
3	E	48	0	26	4	0
3	F	48	0	26	4	0
4	A	32	0	12	0	0
4	B	32	0	12	2	0
4	C	32	0	12	3	0
4	D	32	0	12	2	0
4	E	32	0	12	2	0
4	F	32	0	12	0	0
5	A	2	0	0	0	0
5	B	2	0	0	0	0
5	C	2	0	0	0	0
5	D	2	0	0	0	0
5	E	2	0	0	0	0
5	F	2	0	0	0	0
All	All	23838	0	23337	946	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 20.

All (946) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:321:ILE:HD13	1:A:343:ILE:HB	1.32	1.05
1:E:112:THR:HG22	1:E:124:GLY:H	1.25	1.01
1:B:244:ASP:HB3	1:B:245:LYS:HG3	1.46	0.97
1:D:153:ALA:HB1	1:D:187:ILE:HG13	1.47	0.96
1:C:38:GLU:HG2	1:C:39:GLU:H	1.31	0.95
1:F:24:VAL:HG13	1:F:483:VAL:HG13	1.50	0.93
1:B:95:TYR:OH	1:B:145:THR:HG22	1.70	0.91
1:C:300:THR:HG22	1:C:302:LEU:H	1.34	0.90
1:D:19:ARG:HH12	1:D:358:LYS:HE3	1.37	0.90
1:F:24:VAL:CG1	1:F:483:VAL:HG13	2.03	0.89
1:A:34:THR:HG21	1:A:44:ARG:HH22	1.38	0.89
1:B:37:THR:HA	1:B:41:LYS:HD3	1.55	0.88
1:E:107:LEU:HB3	1:E:126:LYS:HG2	1.56	0.88
1:A:112:THR:HG22	1:A:124:GLY:H	1.39	0.87
1:B:331:LEU:HD12	1:B:352:THR:HG22	1.55	0.87
1:F:186:THR:O	1:F:189:HIS:ND1	2.06	0.87
1:A:112:THR:HG22	1:A:124:GLY:N	1.91	0.85
1:F:432:PRO:HB2	1:F:437:GLN:HG2	1.57	0.85
1:D:341:ALA:O	1:D:365:ILE:HD12	1.77	0.84
1:D:95:TYR:OH	1:D:145:THR:HG22	1.78	0.84
1:B:82:HIS:CD2	1:B:112:THR:HG21	2.13	0.83
1:E:435:GLU:HG3	1:E:439:ARG:HH12	1.42	0.83
1:E:94:ARG:NH1	1:E:169:MET:SD	2.51	0.83
1:B:406:ASN:O	1:B:410:LEU:HD13	1.79	0.83
1:C:114:LYS:HE2	1:C:374:ASN:OD1	1.80	0.81
1:E:112:THR:HG22	1:E:124:GLY:N	1.94	0.81
1:A:112:THR:HG22	1:A:124:GLY:CA	2.10	0.81
1:A:79:ARG:HD2	1:A:127:ALA:HB2	1.62	0.81
1:A:199:THR:HG21	1:A:381:SER:HA	1.61	0.81
1:A:12:MET:HG3	1:A:354:PRO:HD3	1.62	0.80
1:A:24:VAL:CG1	1:A:483:VAL:HG13	2.12	0.80
1:D:425:GLY:O	1:E:420:LYS:NZ	2.15	0.79
1:C:433:THR:HG22	1:C:435:GLU:H	1.46	0.79
1:D:238:MET:HE3	1:D:342:LYS:HD3	1.63	0.79
1:B:417:LEU:HD21	1:C:417:LEU:HD13	1.65	0.79
1:A:432:PRO:HB2	1:A:437:GLN:HG2	1.63	0.79
1:A:357:ASP:OD1	1:A:478:ARG:NH2	2.17	0.78

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:141:LEU:O	1:F:145:THR:HG23	1.83	0.78
1:B:107:LEU:HB3	1:B:126:LYS:HE3	1.66	0.77
1:C:337:PRO:HD3	1:C:359:ILE:HD13	1.66	0.77
1:B:91:GLY:HA3	1:B:125:ALA:O	1.85	0.77
1:D:146:ARG:NH2	1:D:181:ASP:OD2	2.18	0.76
1:C:257:LEU:HD11	1:C:292:GLU:HG3	1.66	0.76
1:C:432:PRO:HB2	1:C:437:GLN:HG2	1.68	0.76
1:D:408:HIS:HB3	1:F:436:PHE:HB2	1.68	0.75
1:E:439:ARG:HG3	1:E:439:ARG:HH11	1.50	0.75
1:E:93:ILE:HD11	1:E:95:TYR:CE1	2.23	0.73
1:E:463:GLN:OE1	1:E:488:LYS:NZ	2.20	0.73
1:D:423:LYS:HA	1:D:426:GLY:HA2	1.71	0.73
1:C:48:ILE:HA	1:C:51:ILE:HD12	1.71	0.73
1:A:255:VAL:HG22	3:A:602:NDP:O2N	1.89	0.73
1:A:357:ASP:CG	1:A:478:ARG:HH21	1.93	0.72
1:A:479:THR:O	1:A:483:VAL:HG23	1.90	0.72
1:E:5:ASP:OD2	1:E:353:THR:HG21	1.90	0.71
1:F:178:TRP:O	1:F:182:THR:HG22	1.89	0.71
1:B:219:VAL:HG22	1:B:373:LEU:HD22	1.73	0.71
1:E:107:LEU:HG	1:E:126:LYS:HE3	1.71	0.71
1:E:386:LEU:HD21	1:F:392:VAL:CG2	2.21	0.71
1:C:223:ILE:HD12	1:C:263:LEU:HD11	1.73	0.71
1:B:400:LYS:HB2	1:C:455:TYR:HB2	1.73	0.71
1:A:24:VAL:HG13	1:A:483:VAL:HG13	1.73	0.70
1:F:29:VAL:HG21	1:F:42:ARG:HG3	1.73	0.70
1:E:82:HIS:CD2	1:E:112:THR:HG21	2.27	0.70
1:E:386:LEU:HD21	1:F:392:VAL:HG22	1.72	0.70
1:D:238:MET:CE	1:D:342:LYS:HD3	2.21	0.69
1:F:214:ALA:HB3	1:F:380:VAL:HG21	1.74	0.69
1:C:29:VAL:HG21	1:C:42:ARG:HG3	1.72	0.69
1:F:322:LEU:HG	1:F:324:PRO:HD3	1.74	0.69
1:A:340:LYS:H	1:A:363:ARG:HH22	1.38	0.69
1:C:363:ARG:NH1	1:C:365:ILE:HD11	2.07	0.69
1:B:79:ARG:NH1	1:B:163:ASP:OD2	2.25	0.69
1:E:95:TYR:HB3	1:E:133:PRO:HG3	1.74	0.69
1:E:117:VAL:HG21	1:E:371:LEU:HD21	1.74	0.69
1:F:81:GLN:NE2	1:F:163:ASP:OD1	2.25	0.69
1:B:241:GLY:O	1:B:245:LYS:NZ	2.22	0.69
1:A:344:ILE:HB	1:A:367:VAL:HG12	1.74	0.68
1:D:433:THR:HG23	1:E:412:SER:HA	1.76	0.68
1:A:112:THR:HG22	1:A:124:GLY:HA3	1.75	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:A:601:GLU:HA	3:A:602:NDP:H41N	1.74	0.68
1:A:174:ARG:NH2	1:A:175:GLU:OE1	2.27	0.68
1:E:99:VAL:HG21	1:E:128:GLY:HA3	1.75	0.68
1:A:82:HIS:CD2	1:A:112:THR:HG21	2.29	0.68
1:A:91:GLY:HA3	1:A:125:ALA:O	1.93	0.68
2:B:601:GLU:HA	3:B:602:NDP:H41N	1.75	0.68
1:E:417:LEU:HD13	1:F:417:LEU:HD21	1.75	0.68
1:B:258:HIS:HD2	1:B:261:ARG:HH11	1.40	0.67
1:E:29:VAL:HG13	1:E:41:LYS:HB3	1.76	0.67
1:B:114:LYS:NZ	1:B:374:ASN:OD1	2.22	0.67
1:F:37:THR:O	1:F:38:GLU:HB3	1.95	0.67
1:D:334:SER:O	1:D:338:ARG:NH1	2.28	0.67
1:E:435:GLU:HG2	1:F:408:HIS:NE2	2.09	0.67
1:A:24:VAL:HG11	1:A:483:VAL:HG13	1.77	0.67
1:A:321:ILE:HD13	1:A:343:ILE:CB	2.17	0.67
1:B:252:PHE:CZ	1:B:291:LEU:HD12	2.30	0.67
1:C:368:ILE:CG2	1:C:373:LEU:HG	2.25	0.67
1:B:112:THR:HG22	1:B:124:GLY:HA3	1.77	0.66
1:E:303:GLY:H	1:E:309:ILE:HD11	1.61	0.66
1:B:133:PRO:HG2	1:B:170:SER:HB3	1.77	0.66
1:E:8:ASN:ND2	1:E:11:LYS:HG2	2.10	0.66
1:C:65:ILE:HG13	1:C:144:ILE:HG12	1.76	0.66
1:E:336:ALA:O	1:E:339:VAL:HG23	1.96	0.66
1:D:94:ARG:HD3	1:D:169:MET:HB2	1.78	0.66
1:C:420:LYS:HG2	1:C:421:PHE:CD2	2.31	0.66
1:F:232:TYR:CE2	1:F:465:MET:HG2	2.31	0.65
1:F:18:ASP:OD1	1:F:53:LYS:HE2	1.95	0.65
1:B:75:ILE:HD12	1:B:144:ILE:HG12	1.77	0.65
1:D:107:LEU:HB3	1:D:126:LYS:HE3	1.78	0.65
1:F:281:TRP:CZ2	1:F:283:PRO:HG3	2.31	0.65
1:A:436:PHE:CZ	1:C:409:LEU:HD12	2.32	0.65
1:B:24:VAL:HG13	1:B:483:VAL:HG13	1.78	0.65
1:C:281:TRP:CZ2	1:C:283:PRO:HG3	2.31	0.65
1:E:413:VAL:HG12	1:E:430:ILE:HG13	1.79	0.65
1:A:199:THR:HG22	1:A:200:GLY:N	2.12	0.65
1:A:490:PHE:O	1:A:491:ARG:HB3	1.96	0.65
1:B:331:LEU:CD1	1:B:352:THR:HG22	2.27	0.65
1:B:323:ILE:HG12	1:B:345:ALA:HB3	1.79	0.64
1:A:141:LEU:O	1:A:145:THR:HG23	1.98	0.64
1:E:94:ARG:HG3	1:E:169:MET:HB2	1.79	0.64
1:B:85:HIS:HD2	1:B:492:VAL:HG21	1.63	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:345:ALA:HB1	1:A:373:LEU:HD11	1.77	0.64
1:C:99:VAL:HG21	1:C:128:GLY:HA3	1.79	0.64
1:A:133:PRO:HG2	1:A:170:SER:HB3	1.78	0.64
1:A:400:LYS:HB2	1:B:455:TYR:HB2	1.80	0.64
1:E:337:PRO:HD3	1:E:359:ILE:HD13	1.78	0.64
1:A:337:PRO:HD3	1:A:359:ILE:HD13	1.81	0.63
1:B:344:ILE:HB	1:B:367:VAL:HG12	1.80	0.63
1:E:386:LEU:HD23	1:F:397:LEU:HD11	1.78	0.63
1:C:71:SER:HA	1:F:44:ARG:NH2	2.13	0.63
1:E:492:VAL:O	1:F:205:GLN:NE2	2.32	0.63
1:F:99:VAL:HA	1:F:103:GLU:OE1	1.98	0.63
1:A:281:TRP:CZ2	1:A:283:PRO:HG3	2.33	0.63
1:E:244:ASP:HB2	1:E:245:LYS:HE3	1.80	0.63
1:D:418:GLU:HG2	1:D:428:ILE:HD12	1.80	0.63
1:E:63:PHE:CD1	1:E:147:ARG:HG3	2.34	0.63
1:C:44:ARG:HH22	1:C:494:ASN:HB2	1.64	0.63
1:F:91:GLY:HA3	1:F:125:ALA:O	1.99	0.63
1:A:311:GLU:OE1	1:A:311:GLU:N	2.29	0.63
1:C:433:THR:HG22	1:C:435:GLU:N	2.13	0.63
1:E:37:THR:O	1:E:40:GLN:NE2	2.31	0.63
1:B:25:GLU:O	1:B:29:VAL:HG23	1.99	0.62
1:B:219:VAL:HA	1:B:373:LEU:CD2	2.30	0.62
1:A:199:THR:HG21	1:A:381:SER:CA	2.28	0.62
1:F:345:ALA:HB1	1:F:373:LEU:HD21	1.81	0.62
1:B:79:ARG:NH2	1:B:91:GLY:O	2.32	0.62
1:C:366:MET:HG3	1:C:475:LEU:HD22	1.82	0.62
2:C:601:GLU:HA	3:C:602:NDP:H41N	1.81	0.62
1:A:94:ARG:NH1	1:A:103:GLU:OE2	2.33	0.62
1:C:72:TRP:HB3	1:F:51:ILE:HD11	1.81	0.62
1:A:95:TYR:OH	1:A:145:THR:HG22	2.00	0.62
1:C:38:GLU:HG2	1:C:39:GLU:N	2.09	0.62
1:D:38:GLU:HG2	1:D:39:GLU:H	1.65	0.62
1:E:89:CYS:HB3	1:E:125:ALA:HB2	1.80	0.61
1:A:381:SER:OG	2:A:601:GLU:OE2	2.11	0.61
1:C:321:ILE:HD13	1:C:343:ILE:HB	1.81	0.61
1:E:91:GLY:O	1:E:165:PRO:HA	2.00	0.61
1:E:142:GLU:OE2	1:E:146:ARG:NH1	2.33	0.61
1:C:107:LEU:HB3	1:C:126:LYS:HE3	1.82	0.61
1:C:322:LEU:HB3	1:C:344:ILE:HD13	1.81	0.61
1:D:341:ALA:O	1:D:365:ILE:CD1	2.47	0.61
1:E:12:MET:HG3	1:E:354:PRO:HD3	1.83	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:281:TRP:CZ2	1:E:283:PRO:HG3	2.36	0.61
1:A:255:VAL:O	1:A:259:SER:OG	2.12	0.61
1:B:392:VAL:HG22	1:C:386:LEU:HD21	1.82	0.61
1:C:210:GLY:O	1:C:214:ALA:HB2	2.01	0.61
1:E:227:ILE:HD11	1:E:245:LYS:HG3	1.80	0.61
1:D:172:GLY:H	1:D:175:GLU:HG2	1.66	0.61
1:E:172:GLY:H	1:E:175:GLU:HG2	1.65	0.61
1:E:450:HIS:CE1	4:E:603:GTP:O2B	2.54	0.60
1:E:24:VAL:CG1	1:E:483:VAL:HG13	2.32	0.60
1:C:271:VAL:HG12	1:C:283:PRO:HA	1.82	0.60
1:D:141:LEU:O	1:D:145:THR:HG23	2.00	0.60
1:E:37:THR:HG22	1:E:41:LYS:HE3	1.82	0.60
1:D:331:LEU:O	1:D:353:THR:HG22	2.02	0.60
1:F:214:ALA:CB	1:F:380:VAL:HG21	2.31	0.60
1:D:331:LEU:HB2	1:D:352:THR:HG22	1.82	0.60
1:D:344:ILE:HB	1:D:367:VAL:HG22	1.84	0.60
1:A:153:ALA:HB1	1:A:187:ILE:HG13	1.83	0.60
1:D:139:ASN:OD1	1:F:501:THR:HG21	2.01	0.60
1:E:91:GLY:HA3	1:E:125:ALA:O	2.02	0.60
1:E:432:PRO:HB3	1:E:436:PHE:HD2	1.67	0.60
1:F:35:ARG:O	1:F:37:THR:N	2.35	0.60
1:D:114:LYS:HZ2	2:D:601:GLU:N	2.00	0.60
1:F:146:ARG:NH2	1:F:181:ASP:OD1	2.35	0.59
1:E:169:MET:HG3	3:E:602:NDP:H3D	1.82	0.59
1:E:117:VAL:HG21	1:E:371:LEU:CD2	2.33	0.59
1:F:17:PHE:CE2	1:F:53:LYS:HE3	2.37	0.59
1:F:37:THR:HG22	1:F:38:GLU:H	1.66	0.59
1:C:146:ARG:HD3	1:C:182:THR:CG2	2.33	0.59
1:E:435:GLU:HG3	1:E:439:ARG:NH1	2.16	0.59
1:B:246:THR:HG22	1:B:320:ASP:OD1	2.02	0.59
1:E:153:ALA:HB1	1:E:187:ILE:HG13	1.85	0.59
1:E:409:LEU:HD13	1:F:409:LEU:HD11	1.83	0.59
1:F:247:PHE:CZ	1:F:270:CYS:HB2	2.37	0.59
1:C:470:LYS:HD3	1:C:471:TYR:CE2	2.38	0.59
1:E:253:GLY:HA3	3:E:602:NDP:O5B	2.02	0.59
1:A:346:GLU:OE1	1:A:478:ARG:NH1	2.34	0.59
1:B:409:LEU:HD11	1:C:409:LEU:HD22	1.85	0.59
1:C:222:GLY:HA3	1:C:373:LEU:CD2	2.33	0.59
1:F:29:VAL:HG11	1:F:42:ARG:NH1	2.18	0.59
1:B:253:GLY:HA3	3:B:602:NDP:O5B	2.03	0.59
1:D:332:THR:HA	1:D:353:THR:CG2	2.32	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:12:MET:HG3	1:C:354:PRO:HD3	1.83	0.59
1:D:186:THR:O	1:D:189:HIS:ND1	2.32	0.59
1:C:315:LEU:HD23	1:C:331:LEU:HG	1.84	0.58
1:D:95:TYR:HB2	1:D:170:SER:HB2	1.84	0.58
1:B:209:HIS:CE1	1:B:446:LYS:HG3	2.38	0.58
1:C:90:LYS:HD2	1:C:164:VAL:HB	1.86	0.58
1:C:262:TYR:OH	4:C:603:GTP:O2G	2.12	0.58
1:F:374:ASN:HB2	3:F:603:NDP:H5N	1.85	0.58
1:D:459:ARG:O	1:D:463:GLN:HG3	2.02	0.58
1:C:49:LEU:HD23	1:C:52:ILE:HD12	1.86	0.58
1:C:178:TRP:O	1:C:182:THR:HG23	2.03	0.58
1:C:222:GLY:HA3	1:C:373:LEU:HD21	1.86	0.58
1:D:258:HIS:HD2	1:D:261:ARG:HH11	1.51	0.58
1:D:342:LYS:HA	1:D:365:ILE:HD13	1.85	0.58
1:D:232:TYR:HA	1:D:235:ILE:HG22	1.86	0.58
1:C:38:GLU:O	1:C:41:LYS:NZ	2.37	0.57
1:D:190:TYR:HD1	1:F:162:VAL:HG21	1.68	0.57
1:D:281:TRP:HB2	1:D:310:TYR:HB2	1.85	0.57
1:D:432:PRO:HB2	1:D:437:GLN:HG2	1.85	0.57
1:F:79:ARG:NH2	1:F:91:GLY:O	2.37	0.57
1:C:323:ILE:HG12	1:C:345:ALA:HB3	1.84	0.57
1:E:259:SER:O	1:E:263:LEU:HD12	2.04	0.57
1:E:55:CYS:HA	1:E:82:HIS:HA	1.87	0.57
1:A:107:LEU:HD13	1:A:126:LYS:HE3	1.86	0.57
1:A:95:TYR:HB3	1:A:133:PRO:HG3	1.86	0.57
1:B:172:GLY:H	1:B:175:GLU:HG2	1.69	0.57
1:C:38:GLU:CG	1:C:39:GLU:H	2.13	0.57
1:E:115:CYS:SG	1:E:378:VAL:HG11	2.44	0.57
1:D:94:ARG:HG2	1:D:99:VAL:HG12	1.87	0.57
1:F:344:ILE:HD12	1:F:367:VAL:HG22	1.86	0.57
1:E:331:LEU:HD12	1:E:352:THR:HG22	1.86	0.56
1:B:349:ASN:ND2	3:B:602:NDP:O2D	2.37	0.56
1:C:378:VAL:O	1:C:382:TYR:N	2.26	0.56
1:E:38:GLU:HG3	1:E:39:GLU:HG2	1.87	0.56
1:E:133:PRO:HG2	1:E:170:SER:HB3	1.86	0.56
1:F:113:TYR:HB2	1:F:371:LEU:HD21	1.87	0.56
1:F:232:TYR:HE2	1:F:465:MET:HG2	1.69	0.56
1:F:346:GLU:HG2	1:F:351:PRO:HG2	1.87	0.56
1:A:357:ASP:CG	1:A:478:ARG:NH2	2.57	0.56
1:C:368:ILE:HG21	1:C:373:LEU:HG	1.87	0.56
1:E:489:VAL:O	1:E:492:VAL:HG13	2.04	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:242:PHE:HA	1:B:245:LYS:NZ	2.21	0.56
1:C:24:VAL:HG13	1:C:483:VAL:HG13	1.88	0.56
1:C:378:VAL:HA	1:C:381:SER:HB2	1.87	0.56
1:E:232:TYR:O	1:E:236:LEU:HB2	2.04	0.56
1:D:36:GLU:HG2	1:D:40:GLN:HB3	1.86	0.56
1:F:368:ILE:HG21	1:F:373:LEU:HD13	1.88	0.56
1:B:232:TYR:HE2	1:B:465:MET:HG2	1.70	0.56
1:F:238:MET:HE3	1:F:245:LYS:HE3	1.88	0.56
1:A:117:VAL:HG21	1:A:371:LEU:HD22	1.87	0.56
1:C:146:ARG:HD3	1:C:182:THR:HG22	1.88	0.56
1:C:126:LYS:HZ3	2:C:601:GLU:N	2.04	0.56
1:C:236:LEU:HD21	1:C:343:ILE:HG12	1.87	0.56
1:C:369:PRO:HG3	1:C:478:ARG:HA	1.88	0.56
1:B:314:ILE:O	1:B:317:VAL:HG23	2.06	0.55
1:E:291:LEU:HD11	1:E:301:ILE:HG22	1.88	0.55
1:D:369:PRO:HG3	1:D:478:ARG:HA	1.87	0.55
1:A:470:LYS:O	1:A:470:LYS:HD3	2.07	0.55
1:C:71:SER:HA	1:F:44:ARG:HH22	1.71	0.55
1:E:171:THR:HB	1:E:175:GLU:HG3	1.88	0.55
1:C:3:ARG:H	1:C:3:ARG:HD3	1.71	0.55
1:E:215:THR:HG21	1:E:255:VAL:HG12	1.89	0.55
1:F:20:GLY:O	1:F:24:VAL:HG22	2.07	0.55
1:F:79:ARG:NH1	1:F:163:ASP:OD2	2.40	0.55
1:A:435:GLU:HG2	1:C:408:HIS:NE2	2.22	0.55
1:D:3:ARG:HD2	1:D:4:GLU:HB2	1.89	0.55
1:A:371:LEU:HD12	1:A:482:TYR:CE1	2.41	0.55
1:C:99:VAL:HA	1:C:103:GLU:OE2	2.07	0.55
1:C:146:ARG:HH11	1:C:182:THR:HG22	1.72	0.55
1:A:219:VAL:HA	1:A:373:LEU:HD22	1.88	0.55
1:C:305:PRO:O	1:C:307:ALA:N	2.38	0.55
1:F:42:ARG:HG3	1:F:42:ARG:HH11	1.71	0.55
1:A:392:VAL:HG21	1:A:397:LEU:HD11	1.87	0.55
1:D:308:LYS:HD2	1:D:309:ILE:O	2.07	0.55
1:E:38:GLU:CG	1:E:39:GLU:N	2.70	0.55
1:A:82:HIS:HD2	1:A:112:THR:HG21	1.72	0.54
1:A:158:ILE:HG13	1:A:165:PRO:HD3	1.89	0.54
1:A:202:PRO:HB2	1:A:205:GLN:HG3	1.89	0.54
1:D:95:TYR:HB3	1:D:133:PRO:HG3	1.88	0.54
1:E:224:GLU:HB2	1:E:242:PHE:HE2	1.73	0.54
1:A:234:SER:OG	1:A:235:ILE:N	2.39	0.54
1:D:178:TRP:HE1	1:F:498:VAL:HG23	1.73	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:24:VAL:CG1	1:C:483:VAL:HG13	2.37	0.54
1:C:370:ASP:HB2	1:C:374:ASN:HD21	1.72	0.54
1:B:260:MET:HG2	1:B:288:PRO:HG3	1.90	0.54
1:D:24:VAL:HG12	1:D:28:LEU:HG	1.90	0.54
1:D:119:ASP:O	1:E:396:ARG:NH1	2.41	0.54
1:E:59:LEU:O	1:E:78:TYR:HA	2.08	0.54
1:A:55:CYS:HA	1:A:82:HIS:HA	1.90	0.54
1:A:258:HIS:HD2	1:A:261:ARG:HH11	1.55	0.54
1:B:12:MET:HG3	1:B:354:PRO:HD3	1.90	0.54
1:B:450:HIS:CE1	4:B:603:GTP:O1B	2.61	0.54
1:C:331:LEU:HD12	1:C:352:THR:HG22	1.90	0.54
1:B:250:GLN:NE2	1:B:315:LEU:HD21	2.22	0.54
1:C:115:CYS:HA	1:C:118:VAL:HG12	1.89	0.54
1:C:186:THR:OG1	1:C:187:ILE:N	2.35	0.54
1:D:90:LYS:HE2	1:D:164:VAL:HG12	1.89	0.54
1:A:146:ARG:HH12	1:A:181:ASP:HB3	1.73	0.54
1:B:199:THR:HG22	1:B:384:GLU:HG2	1.89	0.54
1:B:219:VAL:HA	1:B:373:LEU:HD23	1.89	0.54
1:C:133:PRO:HG2	1:C:170:SER:HB3	1.90	0.53
1:E:112:THR:HG22	1:E:124:GLY:CA	2.37	0.53
1:E:439:ARG:HG3	1:E:439:ARG:NH1	2.23	0.53
1:A:25:GLU:O	1:A:29:VAL:HG23	2.08	0.53
1:A:378:VAL:HA	1:A:381:SER:HB2	1.89	0.53
1:B:24:VAL:CG1	1:B:483:VAL:HG13	2.37	0.53
1:B:427:THR:O	1:B:429:PRO:HD3	2.08	0.53
1:C:163:ASP:O	1:C:165:PRO:HD3	2.08	0.53
1:D:90:LYS:HD2	1:D:164:VAL:HB	1.90	0.53
1:B:126:LYS:NZ	1:B:168:ASP:OD2	2.41	0.53
1:B:89:CYS:HB3	1:B:125:ALA:HB2	1.91	0.53
1:B:95:TYR:HH	1:B:145:THR:HG22	1.70	0.53
1:C:81:GLN:NE2	1:C:163:ASP:OD1	2.23	0.53
1:C:198:VAL:O	1:C:201:LYS:NZ	2.40	0.53
1:D:90:LYS:HZ1	1:D:166:ALA:HB2	1.73	0.53
1:D:412:SER:OG	1:F:433:THR:HG23	2.08	0.53
1:B:138:ASP:OD1	1:B:174:ARG:NH1	2.42	0.53
1:B:387:LYS:HE3	1:B:445:GLU:OE1	2.08	0.53
1:D:186:THR:OG1	1:D:187:ILE:N	2.35	0.53
1:E:164:VAL:HG11	1:E:199:THR:HG23	1.91	0.53
1:A:211:ARG:HH12	1:A:377:GLY:CA	2.22	0.53
1:D:345:ALA:HB1	1:D:373:LEU:HD21	1.90	0.53
1:F:55:CYS:HA	1:F:82:HIS:HA	1.89	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:107:LEU:HB3	1:F:126:LYS:HG2	1.90	0.53
1:F:211:ARG:HH22	3:F:603:NDP:H72N	1.56	0.53
1:A:90:LYS:HD3	1:A:122:PHE:CE1	2.43	0.53
1:B:209:HIS:CE1	4:B:603:GTP:O1B	2.62	0.53
1:F:153:ALA:HA	1:F:158:ILE:HG22	1.90	0.53
1:F:325:ALA:HA	1:F:348:ALA:HB2	1.91	0.53
1:C:55:CYS:O	1:F:62:SER:HB2	2.09	0.53
1:A:118:VAL:HG23	1:A:120:VAL:HG23	1.89	0.52
1:A:239:THR:HG22	1:A:240:PRO:O	2.09	0.52
1:A:333:LYS:HD2	1:A:355:GLU:HG2	1.92	0.52
1:E:137:THR:OG1	1:E:140:GLU:HG3	2.09	0.52
1:E:473:LEU:HB3	1:E:476:ASP:HB3	1.91	0.52
1:C:344:ILE:HB	1:C:367:VAL:HG12	1.91	0.52
1:D:370:ASP:OD1	1:D:371:LEU:N	2.41	0.52
1:A:85:HIS:HB2	1:A:492:VAL:HG11	1.92	0.52
1:E:241:GLY:O	1:E:245:LYS:NZ	2.42	0.52
1:F:199:THR:HG22	1:F:384:GLU:HG2	1.91	0.52
1:A:169:MET:HG2	3:A:602:NDP:H52N	1.92	0.52
1:A:208:ILE:HB	1:A:384:GLU:HB2	1.90	0.52
1:A:277:ASP:O	1:A:302:LEU:HD11	2.09	0.52
1:D:142:GLU:OE2	1:F:498:VAL:HG21	2.10	0.52
1:F:339:VAL:C	1:F:341:ALA:H	2.13	0.52
1:A:38:GLU:HG3	1:A:39:GLU:N	2.25	0.52
1:B:24:VAL:HB	1:B:28:LEU:HD13	1.90	0.52
1:A:382:TYR:CE1	1:A:386:LEU:HD11	2.45	0.52
1:B:337:PRO:HD3	1:B:359:ILE:HD13	1.91	0.52
1:D:432:PRO:HB3	1:D:436:PHE:HD2	1.74	0.52
1:A:247:PHE:CZ	1:A:270:CYS:HB2	2.45	0.52
1:B:358:LYS:O	1:B:362:GLU:HG2	2.10	0.52
1:B:476:ASP:OD1	1:B:479:THR:HG23	2.09	0.52
1:C:91:GLY:O	1:C:165:PRO:HA	2.10	0.52
1:F:42:ARG:O	1:F:46:ARG:HG2	2.10	0.52
1:C:114:LYS:HZ3	2:C:601:GLU:C	2.10	0.52
1:E:423:LYS:HD2	1:E:423:LYS:O	2.10	0.52
1:A:217:ARG:HB2	1:A:262:TYR:CE1	2.45	0.51
1:A:370:ASP:OD1	1:A:371:LEU:N	2.31	0.51
1:C:217:ARG:CZ	1:C:450:HIS:CD2	2.93	0.51
1:D:265:ARG:NH2	4:D:603:GTP:O1G	2.43	0.51
1:E:224:GLU:HA	1:E:227:ILE:HG22	1.92	0.51
1:E:403:ARG:CZ	1:E:407:TYR:HE1	2.23	0.51
1:B:113:TYR:HB2	1:B:371:LEU:HD21	1.91	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:91:GLY:HA2	1:F:111:MET:SD	2.51	0.51
1:A:409:LEU:HD13	1:C:409:LEU:HD11	1.92	0.51
1:C:44:ARG:NH2	1:C:494:ASN:HB2	2.26	0.51
1:C:282:ASN:ND2	1:C:306:LYS:O	2.40	0.51
1:E:346:GLU:HG2	1:E:351:PRO:HG2	1.92	0.51
1:A:114:LYS:HA	1:A:371:LEU:HD23	1.90	0.51
1:E:16:PHE:CD2	1:E:478:ARG:HD2	2.46	0.51
1:F:90:LYS:HD2	1:F:164:VAL:HB	1.91	0.51
1:F:372:TYR:OH	1:F:461:ALA:HB2	2.10	0.51
1:B:91:GLY:O	1:B:165:PRO:HA	2.10	0.51
1:B:107:LEU:HB3	1:B:126:LYS:HG2	1.93	0.51
1:C:363:ARG:HH11	1:C:365:ILE:HD11	1.76	0.51
1:C:374:ASN:HB2	3:C:602:NDP:C5N	2.41	0.51
1:A:111:MET:HE1	1:A:378:VAL:CG1	2.41	0.51
1:B:95:TYR:HB3	1:B:133:PRO:HG3	1.92	0.51
1:D:32:LEU:HD13	1:D:494:ASN:OD1	2.10	0.51
1:E:61:LEU:HD13	1:E:151:GLU:HB3	1.92	0.51
1:F:67:ARG:NH2	1:F:135:ASN:O	2.43	0.51
1:F:376:GLY:O	1:F:380:VAL:HG22	2.11	0.51
1:A:114:LYS:NZ	2:A:601:GLU:O	2.43	0.51
1:B:29:VAL:HG13	1:B:41:LYS:HB3	1.92	0.51
1:D:340:LYS:HD2	1:D:363:ARG:HH22	1.76	0.51
1:E:38:GLU:CG	1:E:39:GLU:H	2.23	0.51
1:E:38:GLU:HG2	1:E:39:GLU:H	1.75	0.51
1:F:16:PHE:CD2	1:F:478:ARG:HD3	2.45	0.51
1:F:94:ARG:NH1	1:F:103:GLU:OE2	2.43	0.51
1:C:368:ILE:HG22	1:C:373:LEU:HG	1.93	0.51
1:F:126:LYS:HZ3	2:F:602:GLU:N	2.09	0.51
1:A:155:LYS:HD2	1:D:155:LYS:O	2.10	0.51
1:B:95:TYR:CZ	1:B:145:THR:HG22	2.45	0.51
1:B:247:PHE:CZ	1:B:270:CYS:HB2	2.46	0.51
1:B:224:GLU:HA	1:B:227:ILE:HG22	1.93	0.50
1:E:142:GLU:O	1:E:146:ARG:HG3	2.12	0.50
1:F:32:LEU:O	1:F:41:LYS:HE2	2.10	0.50
1:A:96:SER:O	1:A:130:LYS:HA	2.11	0.50
1:C:219:VAL:HA	1:C:373:LEU:HD22	1.94	0.50
1:F:318:ASP:HA	1:F:340:LYS:HB3	1.92	0.50
1:D:24:VAL:HG22	1:D:483:VAL:HG13	1.93	0.50
1:D:443:ALA:HB2	1:E:401:TYR:CD2	2.45	0.50
1:F:163:ASP:O	1:F:165:PRO:HD3	2.11	0.50
1:D:423:LYS:HD2	1:D:423:LYS:N	2.27	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:432:PRO:HB3	1:E:436:PHE:CD2	2.47	0.50
1:A:146:ARG:HD3	1:A:182:THR:OG1	2.10	0.50
1:A:417:LEU:HD13	1:C:417:LEU:HD21	1.94	0.50
1:E:10:PHE:HA	1:E:106:ALA:HB2	1.93	0.50
1:F:2:ASP:HB2	1:F:332:THR:HG21	1.93	0.50
1:C:146:ARG:NH1	1:C:182:THR:HG22	2.27	0.50
1:C:310:TYR:CZ	1:C:317:VAL:HG22	2.46	0.50
1:C:62:SER:HB2	1:F:55:CYS:O	2.11	0.50
1:D:241:GLY:O	1:D:245:LYS:NZ	2.42	0.50
1:D:336:ALA:HB2	1:D:356:ALA:HB1	1.94	0.50
1:E:94:ARG:HH21	1:E:107:LEU:HD21	1.77	0.50
1:B:167:PRO:HB3	1:B:172:GLY:HA2	1.94	0.50
1:C:92:GLY:O	1:C:126:LYS:HD3	2.12	0.50
1:C:414:GLN:O	1:C:418:GLU:HG3	2.12	0.50
1:F:369:PRO:HG3	1:F:478:ARG:HA	1.93	0.50
1:C:374:ASN:HB2	3:C:602:NDP:H5N	1.93	0.49
1:C:396:ARG:HG3	1:C:397:LEU:HD23	1.94	0.49
1:F:336:ALA:N	1:F:337:PRO:HD2	2.26	0.49
1:D:436:PHE:HB2	1:E:408:HIS:HB3	1.94	0.49
1:E:386:LEU:HD21	1:F:392:VAL:HG21	1.95	0.49
1:A:255:VAL:HG23	1:A:325:ALA:HB1	1.93	0.49
1:C:90:LYS:NZ	1:C:166:ALA:HB2	2.27	0.49
1:D:379:THR:O	1:D:382:TYR:HB3	2.11	0.49
1:B:142:GLU:OE2	1:B:146:ARG:NH1	2.45	0.49
1:F:90:LYS:HE3	1:F:381:SER:HB3	1.93	0.49
1:D:167:PRO:HD3	1:D:200:GLY:HA3	1.95	0.49
1:D:468:ALA:HA	1:D:473:LEU:HD12	1.94	0.49
1:E:79:ARG:NH2	1:E:163:ASP:OD2	2.39	0.49
1:E:103:GLU:O	1:E:107:LEU:HB2	2.13	0.49
1:E:386:LEU:CD2	1:F:397:LEU:HD11	2.42	0.49
1:A:37:THR:O	1:A:38:GLU:HG2	2.11	0.49
1:B:146:ARG:HA	1:B:182:THR:HG21	1.95	0.49
1:C:315:LEU:HD12	1:C:315:LEU:H	1.78	0.49
1:C:339:VAL:HG21	1:C:360:PHE:CE1	2.48	0.49
1:F:495:GLU:O	1:F:497:GLY:N	2.46	0.49
1:A:408:HIS:HB3	1:B:436:PHE:HB2	1.94	0.49
1:E:255:VAL:HG23	1:E:325:ALA:HB1	1.94	0.49
1:F:315:LEU:HB3	1:F:331:LEU:HD21	1.95	0.49
1:F:382:TYR:O	1:F:386:LEU:HD22	2.12	0.49
1:B:391:HIS:O	1:C:382:TYR:OH	2.21	0.49
1:C:224:GLU:HB2	1:C:242:PHE:CE2	2.47	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:211:ARG:O	1:E:211:ARG:NH1	2.33	0.49
1:F:366:MET:HG3	1:F:475:LEU:HD22	1.95	0.49
1:A:117:VAL:CG2	1:A:371:LEU:HD22	2.43	0.49
1:C:494:ASN:OD1	1:C:495:GLU:N	2.46	0.49
1:F:111:MET:HE1	2:F:602:GLU:HG2	1.94	0.49
1:C:298:HIS:O	1:C:300:THR:N	2.46	0.49
1:D:38:GLU:CG	1:D:39:GLU:H	2.26	0.49
1:D:89:CYS:HB3	1:D:125:ALA:HB2	1.95	0.49
1:D:96:SER:O	1:D:99:VAL:HG13	2.13	0.49
1:E:85:HIS:HD2	1:E:492:VAL:HG11	1.77	0.49
1:E:368:ILE:CG2	1:E:373:LEU:HG	2.43	0.49
1:F:67:ARG:HD2	1:F:73:GLU:OE1	2.13	0.49
1:A:90:LYS:HE3	1:A:381:SER:HB3	1.95	0.48
1:A:459:ARG:O	1:A:463:GLN:HG2	2.13	0.48
1:C:241:GLY:O	1:C:245:LYS:HD3	2.13	0.48
1:E:432:PRO:HA	1:F:412:SER:HB3	1.95	0.48
1:A:17:PHE:CE1	1:A:486:ILE:HG12	2.47	0.48
1:D:332:THR:HA	1:D:353:THR:HG21	1.95	0.48
1:F:339:VAL:O	1:F:341:ALA:N	2.44	0.48
1:A:199:THR:CG2	1:A:200:GLY:N	2.76	0.48
1:B:57:HIS:HD2	1:E:61:LEU:HD22	1.78	0.48
1:B:378:VAL:HA	1:B:381:SER:HB2	1.95	0.48
1:E:67:ARG:NH1	1:E:73:GLU:OE1	2.47	0.48
1:E:224:GLU:HB2	1:E:242:PHE:CE2	2.48	0.48
1:E:431:VAL:O	1:F:412:SER:HB3	2.13	0.48
1:F:19:ARG:HG2	1:F:479:THR:CG2	2.44	0.48
1:A:205:GLN:NE2	1:B:492:VAL:O	2.47	0.48
1:B:242:PHE:HA	1:B:245:LYS:HZ3	1.77	0.48
1:C:5:ASP:HB3	1:C:332:THR:HB	1.96	0.48
1:C:41:LYS:O	1:C:45:VAL:HG23	2.13	0.48
1:D:14:GLU:OE2	1:D:53:LYS:HE2	2.14	0.48
1:D:400:LYS:HB2	1:F:455:TYR:HB2	1.94	0.48
1:C:203:ILE:HD11	1:C:209:HIS:HA	1.93	0.48
1:C:246:THR:HG23	1:C:319:CYS:HA	1.95	0.48
1:E:94:ARG:O	1:E:128:GLY:HA2	2.13	0.48
1:A:433:THR:HG23	1:C:412:SER:OG	2.13	0.48
1:B:236:LEU:HD11	1:B:366:MET:HB2	1.95	0.48
1:E:246:THR:HG22	1:E:320:ASP:H	1.78	0.48
1:A:199:THR:HG21	1:A:381:SER:CB	2.43	0.48
1:A:315:LEU:HB3	1:A:331:LEU:HD21	1.96	0.48
1:C:346:GLU:HG2	1:C:351:PRO:HG2	1.96	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:90:LYS:HD2	1:E:164:VAL:HB	1.95	0.48
1:C:32:LEU:HD13	1:C:494:ASN:HD22	1.77	0.48
1:C:333:LYS:HB2	1:C:355:GLU:HB3	1.96	0.48
1:A:313:SER:HB3	1:A:316:GLU:HG3	1.95	0.48
1:B:186:THR:OG1	1:B:187:ILE:N	2.46	0.48
1:C:478:ARG:HG3	1:C:482:TYR:HE1	1.78	0.48
1:E:90:LYS:HD3	1:E:122:PHE:CE1	2.47	0.48
1:F:93:ILE:HG12	1:F:127:ALA:HB3	1.95	0.48
1:F:133:PRO:HG2	1:F:170:SER:HB3	1.95	0.48
1:F:142:GLU:O	1:F:146:ARG:HG3	2.14	0.48
1:F:495:GLU:C	1:F:497:GLY:H	2.16	0.48
1:B:47:GLY:O	1:B:51:ILE:HG13	2.13	0.48
1:C:46:ARG:HA	1:C:49:LEU:HB2	1.95	0.48
1:F:210:GLY:O	1:F:214:ALA:HB2	2.14	0.48
1:A:348:ALA:O	1:A:374:ASN:ND2	2.47	0.47
1:B:232:TYR:CE2	1:B:465:MET:HG2	2.48	0.47
1:C:339:VAL:HG21	1:C:360:PHE:CZ	2.49	0.47
1:A:224:GLU:HB2	1:A:242:PHE:HE2	1.80	0.47
1:B:52:ILE:O	1:B:82:HIS:NE2	2.47	0.47
1:C:60:SER:HB2	1:F:58:VAL:HB	1.96	0.47
1:C:421:PHE:CD2	1:C:421:PHE:N	2.81	0.47
1:F:44:ARG:HA	1:F:44:ARG:CZ	2.45	0.47
1:F:275:GLU:OE1	1:F:295:LYS:HE2	2.14	0.47
1:A:33:LYS:NZ	1:A:35:ARG:HG3	2.29	0.47
1:C:10:PHE:HA	1:C:106:ALA:HB2	1.95	0.47
1:C:336:ALA:N	1:C:337:PRO:HD2	2.29	0.47
1:A:439:ARG:HD3	1:C:405:SER:HA	1.95	0.47
1:A:85:HIS:CD2	1:A:86:ARG:HG2	2.49	0.47
1:E:339:VAL:HG21	1:E:360:PHE:CE1	2.49	0.47
1:F:29:VAL:HG21	1:F:42:ARG:CG	2.42	0.47
1:A:199:THR:HG22	1:A:200:GLY:H	1.79	0.47
2:A:601:GLU:CA	3:A:602:NDP:H41N	2.44	0.47
1:B:246:THR:HG22	1:B:320:ASP:CG	2.35	0.47
1:B:414:GLN:OE1	1:B:429:PRO:HA	2.15	0.47
1:C:214:ALA:HB1	1:C:380:VAL:HG21	1.97	0.47
1:C:420:LYS:HG2	1:C:421:PHE:CE2	2.48	0.47
1:D:91:GLY:HA3	1:D:125:ALA:O	2.14	0.47
1:D:142:GLU:OE1	1:D:146:ARG:NH1	2.46	0.47
1:E:24:VAL:HG13	1:E:483:VAL:HG13	1.96	0.47
1:E:158:ILE:HG12	1:E:159:GLY:N	2.29	0.47
1:E:274:GLY:O	1:E:275:GLU:HG2	2.15	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:17:PHE:HE2	1:F:53:LYS:HE3	1.80	0.47
1:F:19:ARG:HG2	1:F:479:THR:HG21	1.97	0.47
1:F:28:LEU:HD22	1:F:490:PHE:CD2	2.49	0.47
1:B:366:MET:HG3	1:B:475:LEU:HD22	1.96	0.47
1:D:24:VAL:CG2	1:D:483:VAL:HG22	2.44	0.47
1:D:37:THR:O	1:D:38:GLU:HG2	2.15	0.47
1:D:113:TYR:HB2	1:D:371:LEU:HD11	1.97	0.47
1:C:446:LYS:HG3	1:C:450:HIS:CE1	2.50	0.47
1:F:35:ARG:O	1:F:37:THR:OG1	2.33	0.47
1:B:278:GLY:HA3	1:B:302:LEU:HD21	1.97	0.47
1:D:5:ASP:OD2	1:D:353:THR:HG21	2.15	0.47
1:D:450:HIS:CE1	4:D:603:GTP:O2B	2.67	0.47
1:A:433:THR:HG23	1:C:412:SER:HA	1.96	0.46
1:C:373:LEU:HD23	1:C:373:LEU:HA	1.53	0.46
1:D:239:THR:HG23	1:D:245:LYS:HZ1	1.80	0.46
1:F:68:ASP:OD1	1:F:137:THR:OG1	2.22	0.46
1:A:333:LYS:HB2	1:A:355:GLU:HB3	1.97	0.46
1:D:26:ASP:HA	1:D:42:ARG:NH2	2.30	0.46
1:B:219:VAL:HG22	1:B:373:LEU:CD2	2.44	0.46
1:B:246:THR:HG23	1:B:319:CYS:HA	1.98	0.46
1:B:250:GLN:NE2	1:B:330:GLN:OE1	2.48	0.46
1:B:390:ASN:O	1:B:392:VAL:HG23	2.15	0.46
1:D:175:GLU:HA	1:D:178:TRP:CE3	2.51	0.46
1:D:263:LEU:CD1	1:D:323:ILE:HD11	2.45	0.46
1:B:9:PHE:HD2	1:B:9:PHE:O	1.99	0.46
1:B:340:LYS:HB3	1:B:340:LYS:HE3	1.73	0.46
1:C:11:LYS:HA	1:C:14:GLU:HB2	1.98	0.46
1:E:25:GLU:OE1	1:E:46:ARG:NH1	2.49	0.46
1:E:93:ILE:HB	1:E:127:ALA:HB3	1.98	0.46
1:A:169:MET:CG	3:A:602:NDP:H52N	2.46	0.46
1:C:82:HIS:CG	1:C:109:SER:HA	2.51	0.46
1:C:131:ILE:HB	1:C:136:TYR:CE2	2.50	0.46
1:D:58:VAL:HG11	1:D:101:VAL:HG23	1.97	0.46
1:D:114:LYS:O	1:D:118:VAL:HG22	2.15	0.46
1:E:246:THR:CG2	1:E:320:ASP:H	2.28	0.46
1:F:165:PRO:HD2	1:F:197:CYS:O	2.15	0.46
1:F:331:LEU:HA	1:F:335:ASN:HD21	1.79	0.46
1:A:67:ARG:HD2	1:A:140:GLU:OE1	2.16	0.46
1:E:99:VAL:HG21	1:E:128:GLY:CA	2.44	0.46
1:F:236:LEU:HD21	1:F:343:ILE:HG12	1.98	0.46
1:E:161:GLY:HA2	1:F:192:ILE:HG13	1.96	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:339:VAL:HG21	1:E:360:PHE:HE1	1.80	0.46
1:A:23:ILE:CD1	1:A:473:LEU:HD21	2.46	0.46
1:A:111:MET:HE1	1:A:378:VAL:HG11	1.97	0.46
1:B:19:ARG:HG2	1:B:479:THR:CG2	2.46	0.46
1:D:101:VAL:HA	1:D:104:VAL:HG12	1.98	0.46
1:E:439:ARG:HH11	1:E:439:ARG:CG	2.25	0.46
1:F:470:LYS:HE2	1:F:471:TYR:CZ	2.50	0.46
1:A:90:LYS:NZ	1:A:166:ALA:HB2	2.30	0.46
1:A:107:LEU:CB	1:A:126:LYS:HG2	2.46	0.46
1:C:353:THR:HB	1:C:354:PRO:HD2	1.98	0.46
1:D:281:TRP:CB	1:D:310:TYR:HB2	2.45	0.46
2:F:602:GLU:HA	3:F:603:NDP:H41N	1.96	0.46
1:A:232:TYR:CE2	1:A:465:MET:HG2	2.50	0.46
1:A:321:ILE:HD11	1:A:343:ILE:HD12	1.98	0.46
1:C:19:ARG:O	1:C:23:ILE:HD12	2.16	0.46
1:C:245:LYS:HD2	1:C:245:LYS:N	2.31	0.46
1:C:410:LEU:HD12	1:C:410:LEU:HA	1.68	0.46
1:F:148:PHE:CE2	1:F:152:LEU:HD11	2.51	0.46
1:F:274:GLY:N	1:F:314:ILE:HD13	2.31	0.46
1:C:246:THR:O	1:C:320:ASP:HB2	2.17	0.45
1:E:59:LEU:HB2	1:E:157:PHE:CZ	2.50	0.45
1:F:172:GLY:O	1:F:176:MET:HG2	2.16	0.45
1:A:172:GLY:O	1:A:176:MET:HG2	2.16	0.45
1:A:389:LEU:O	1:A:391:HIS:ND1	2.48	0.45
1:D:223:ILE:HD11	1:D:345:ALA:CB	2.47	0.45
1:F:321:ILE:HA	1:F:343:ILE:O	2.16	0.45
1:F:378:VAL:HA	1:F:381:SER:HB2	1.98	0.45
1:C:29:VAL:HG13	1:C:41:LYS:HE2	1.98	0.45
1:C:341:ALA:O	1:C:365:ILE:HD12	2.16	0.45
1:C:43:ASN:O	1:C:47:GLY:N	2.47	0.45
1:C:224:GLU:HB2	1:C:242:PHE:HE2	1.80	0.45
1:C:244:ASP:OD1	1:C:244:ASP:N	2.48	0.45
1:C:316:GLU:O	1:C:340:LYS:HD2	2.17	0.45
1:D:95:TYR:OH	1:D:145:THR:CG2	2.59	0.45
1:E:38:GLU:HG3	1:E:39:GLU:CG	2.46	0.45
1:A:412:SER:OG	1:B:432:PRO:HA	2.17	0.45
1:A:436:PHE:HB2	1:C:408:HIS:HB3	1.98	0.45
1:B:90:LYS:HD2	1:B:164:VAL:O	2.16	0.45
1:D:291:LEU:HD23	1:D:291:LEU:HA	1.75	0.45
1:F:422:GLY:C	1:F:423:LYS:HD2	2.37	0.45
1:F:468:ALA:HA	1:F:473:LEU:HD12	1.99	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:107:LEU:CB	1:B:126:LYS:HG2	2.47	0.45
1:D:178:TRP:HE1	1:F:498:VAL:CG2	2.29	0.45
1:E:172:GLY:O	1:E:176:MET:HG2	2.16	0.45
1:A:8:ASN:HD22	1:A:11:LYS:HG3	1.81	0.45
1:B:17:PHE:CE1	1:B:486:ILE:HG12	2.51	0.45
1:B:246:THR:HG23	1:B:320:ASP:H	1.81	0.45
1:D:314:ILE:HA	1:D:317:VAL:HG23	1.97	0.45
1:D:423:LYS:HA	1:D:426:GLY:CA	2.45	0.45
1:E:82:HIS:HD2	1:E:83:SER:HB2	1.82	0.45
1:F:38:GLU:OE1	1:F:39:GLU:HG2	2.16	0.45
1:F:186:THR:OG1	1:F:187:ILE:N	2.48	0.45
1:F:360:PHE:HB3	1:F:365:ILE:HB	1.99	0.45
1:B:34:THR:HB	1:B:41:LYS:HD2	1.98	0.45
1:B:276:SER:HB2	3:B:602:NDP:O2X	2.17	0.45
1:D:65:ILE:HG13	1:D:144:ILE:HG13	1.99	0.45
1:E:150:MET:O	1:E:154:LYS:HG3	2.16	0.45
1:A:27:LYS:O	1:A:30:GLU:HG2	2.17	0.45
1:C:155:LYS:HG3	1:F:157:PHE:CE1	2.51	0.45
1:C:363:ARG:HB3	1:C:365:ILE:HG12	1.98	0.45
1:E:27:LYS:O	1:E:30:GLU:HG2	2.17	0.45
1:E:245:LYS:HA	1:E:245:LYS:HD3	1.67	0.45
1:F:42:ARG:HG3	1:F:42:ARG:NH1	2.28	0.45
1:F:189:HIS:CD2	1:F:190:TYR:CE1	3.05	0.45
1:F:371:LEU:HA	1:F:371:LEU:HD23	1.64	0.45
1:A:489:VAL:O	1:A:492:VAL:HB	2.17	0.45
1:F:380:VAL:HG12	1:F:449:VAL:HG13	1.98	0.45
1:A:93:ILE:HD12	1:A:179:ILE:HD11	1.99	0.44
1:B:222:GLY:HA2	1:B:372:TYR:OH	2.16	0.44
1:C:65:ILE:HA	1:C:65:ILE:HD13	1.81	0.44
1:C:116:ALA:O	1:C:488:LYS:HE3	2.17	0.44
1:D:322:LEU:HG	1:D:324:PRO:HD3	1.97	0.44
1:E:94:ARG:HB2	1:E:168:ASP:OD1	2.16	0.44
1:F:9:PHE:CE1	1:F:107:LEU:HD13	2.52	0.44
1:A:34:THR:HG22	1:A:36:GLU:N	2.33	0.44
1:A:126:LYS:NZ	2:A:601:GLU:N	2.65	0.44
1:C:20:GLY:O	1:C:24:VAL:HG22	2.17	0.44
1:C:146:ARG:HD3	1:C:182:THR:HG21	2.00	0.44
1:C:289:LYS:HD2	1:C:289:LYS:HA	1.68	0.44
1:D:32:LEU:O	1:D:41:LYS:HE2	2.16	0.44
1:D:116:ALA:O	1:D:488:LYS:HD2	2.17	0.44
1:E:146:ARG:NH2	1:E:181:ASP:HB3	2.32	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:165:PRO:HD2	1:E:198:VAL:HG23	1.99	0.44
1:E:368:ILE:HB	1:E:373:LEU:CD1	2.47	0.44
1:C:247:PHE:CZ	1:C:270:CYS:HB2	2.53	0.44
1:D:152:LEU:HD22	1:D:157:PHE:HB3	1.98	0.44
1:F:410:LEU:HD23	1:F:410:LEU:HA	1.75	0.44
1:E:20:GLY:O	1:E:24:VAL:HG22	2.17	0.44
1:E:75:ILE:CD1	1:E:144:ILE:HG12	2.48	0.44
1:A:211:ARG:HA	1:A:214:ALA:HB2	1.98	0.44
1:B:271:VAL:HG12	1:B:283:PRO:HA	2.00	0.44
1:B:381:SER:O	1:B:384:GLU:N	2.50	0.44
1:F:107:LEU:HD12	1:F:107:LEU:HA	1.76	0.44
1:A:154:LYS:HD3	1:E:185:SER:O	2.17	0.44
1:B:58:VAL:HG11	1:B:101:VAL:HG23	1.99	0.44
1:C:28:LEU:HD22	1:C:490:PHE:CD2	2.53	0.44
1:C:372:TYR:OH	1:C:461:ALA:HB2	2.18	0.44
1:D:281:TRP:CH2	1:D:283:PRO:HG3	2.53	0.44
1:F:95:TYR:HB3	1:F:133:PRO:HG3	2.00	0.44
1:F:432:PRO:HG2	1:F:437:GLN:HE21	1.83	0.44
1:A:107:LEU:HB2	1:A:126:LYS:HG2	2.00	0.44
1:B:64:PRO:O	1:B:65:ILE:HD13	2.18	0.44
1:B:245:LYS:NZ	1:B:245:LYS:HB2	2.33	0.44
1:F:79:ARG:HB2	1:F:127:ALA:HB2	1.99	0.44
1:B:368:ILE:HB	1:B:373:LEU:HD12	1.99	0.44
1:C:246:THR:HG22	1:C:320:ASP:OD1	2.18	0.44
1:C:371:LEU:HD23	1:C:371:LEU:HA	1.69	0.44
1:C:389:LEU:HD23	1:C:389:LEU:HA	1.67	0.44
1:E:353:THR:HG23	1:E:354:PRO:HD2	2.00	0.44
1:F:209:HIS:CE1	1:F:446:LYS:HD3	2.52	0.44
1:F:319:CYS:O	1:F:341:ALA:HA	2.18	0.44
1:A:257:LEU:HD11	1:A:292:GLU:HG3	1.99	0.44
1:A:369:PRO:HB3	1:A:478:ARG:HD3	2.00	0.44
1:A:427:THR:O	1:A:429:PRO:HD3	2.18	0.44
1:B:31:ASP:O	1:B:33:LYS:HG2	2.17	0.44
1:B:112:THR:HB	1:B:124:GLY:H	1.82	0.44
1:C:477:LEU:HA	1:C:477:LEU:HD23	1.85	0.44
1:D:230:ALA:HA	1:D:233:MET:HB2	2.00	0.44
1:D:403:ARG:NH1	1:D:407:TYR:HE1	2.16	0.44
1:D:409:LEU:HD13	1:E:409:LEU:HD11	1.99	0.44
1:E:319:CYS:O	1:E:341:ALA:HA	2.17	0.44
1:A:370:ASP:HB2	1:A:374:ASN:HD21	1.83	0.43
1:C:435:GLU:O	1:C:439:ARG:HG3	2.18	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:199:THR:HA	1:F:384:GLU:OE2	2.17	0.43
1:F:357:ASP:OD2	1:F:478:ARG:HD2	2.18	0.43
1:F:466:ARG:HD3	1:F:466:ARG:HA	1.75	0.43
1:A:91:GLY:O	1:A:165:PRO:HA	2.17	0.43
1:A:107:LEU:HB3	1:A:126:LYS:CE	2.47	0.43
1:B:167:PRO:HD3	1:B:200:GLY:HA3	2.01	0.43
1:B:319:CYS:O	1:B:341:ALA:HA	2.19	0.43
1:E:245:LYS:HA	1:E:320:ASP:OD1	2.18	0.43
1:E:275:GLU:HB3	3:E:602:NDP:O2B	2.18	0.43
1:F:224:GLU:HA	1:F:227:ILE:HG22	1.99	0.43
1:A:211:ARG:NH1	1:A:377:GLY:HA2	2.33	0.43
1:B:101:VAL:HA	1:B:104:VAL:HG12	2.00	0.43
1:B:210:GLY:O	1:B:214:ALA:HB2	2.17	0.43
1:C:5:ASP:OD2	1:C:355:GLU:HB2	2.18	0.43
1:C:281:TRP:HB2	1:C:310:TYR:HB2	2.00	0.43
1:C:329:LYS:HG2	1:C:353:THR:HG22	1.99	0.43
1:D:414:GLN:HG3	1:D:428:ILE:O	2.18	0.43
1:E:353:THR:HG22	1:E:355:GLU:N	2.34	0.43
1:F:91:GLY:O	1:F:165:PRO:HA	2.19	0.43
1:F:119:ASP:OD2	1:F:488:LYS:NZ	2.44	0.43
1:B:66:ARG:NH2	1:F:139:ASN:HD21	2.16	0.43
1:B:171:THR:HB	1:B:175:GLU:HG3	2.00	0.43
1:B:258:HIS:HD2	1:B:261:ARG:NH1	2.13	0.43
1:C:350:GLY:N	1:C:370:ASP:OD2	2.43	0.43
1:D:32:LEU:HG	1:D:34:THR:HG22	1.99	0.43
1:D:35:ARG:O	1:D:37:THR:N	2.51	0.43
1:E:152:LEU:HD22	1:E:157:PHE:HB2	1.99	0.43
1:F:395:GLY:O	1:F:397:LEU:N	2.52	0.43
1:A:61:LEU:HD12	1:A:61:LEU:HA	1.75	0.43
1:A:201:LYS:NZ	1:A:388:ASN:OD1	2.36	0.43
1:E:10:PHE:CA	1:E:106:ALA:HB2	2.48	0.43
1:E:78:TYR:O	1:E:127:ALA:HA	2.18	0.43
1:F:82:HIS:CG	1:F:109:SER:HA	2.53	0.43
1:F:252:PHE:CZ	1:F:291:LEU:HD23	2.53	0.43
1:C:32:LEU:HD13	1:C:494:ASN:ND2	2.32	0.43
1:D:11:LYS:HA	1:D:14:GLU:HB2	2.00	0.43
1:D:302:LEU:HA	1:D:302:LEU:HD23	1.73	0.43
1:D:417:LEU:HD21	1:F:417:LEU:HD13	2.00	0.43
1:E:24:VAL:HG11	1:E:483:VAL:HG13	1.99	0.43
1:F:94:ARG:O	1:F:128:GLY:HA2	2.18	0.43
1:A:215:THR:HG23	1:A:216:GLY:H	1.83	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:19:ARG:CD	1:D:479:THR:HG21	2.48	0.43
1:A:38:GLU:CG	1:A:39:GLU:N	2.82	0.43
1:A:90:LYS:HD2	1:A:164:VAL:HB	2.00	0.43
1:A:93:ILE:O	1:A:168:ASP:HB3	2.19	0.43
1:A:199:THR:CG2	1:A:200:GLY:H	2.32	0.43
1:B:444:SER:O	1:B:447:ASP:HB2	2.18	0.43
1:E:66:ARG:HG2	1:E:72:TRP:CZ3	2.54	0.43
1:A:435:GLU:HG2	1:C:408:HIS:CE1	2.54	0.43
1:B:126:LYS:HG3	1:B:127:ALA:N	2.34	0.43
1:D:24:VAL:HG22	1:D:483:VAL:HG22	2.00	0.43
1:E:339:VAL:O	1:E:340:LYS:HB2	2.17	0.43
1:F:165:PRO:HB2	1:F:198:VAL:HG23	2.01	0.43
1:A:95:TYR:CB	1:A:133:PRO:HG3	2.49	0.43
1:B:82:HIS:CG	1:B:112:THR:HG21	2.52	0.43
1:C:37:THR:HB	1:C:38:GLU:H	1.51	0.43
1:C:257:LEU:CD1	1:C:292:GLU:HG3	2.42	0.43
2:E:601:GLU:HA	3:E:602:NDP:H41N	2.01	0.43
1:F:246:THR:HG23	1:F:320:ASP:H	1.84	0.43
1:A:336:ALA:N	1:A:337:PRO:HD2	2.34	0.42
1:B:79:ARG:HB2	1:B:127:ALA:HB2	2.02	0.42
1:B:150:MET:O	1:B:154:LYS:HG3	2.18	0.42
1:B:252:PHE:CZ	1:B:291:LEU:CD1	3.00	0.42
1:B:318:ASP:HB2	1:B:340:LYS:HE2	2.02	0.42
1:C:48:ILE:O	1:C:52:ILE:HG13	2.19	0.42
1:C:242:PHE:HA	1:C:245:LYS:HG2	2.00	0.42
1:C:478:ARG:HG3	1:C:482:TYR:CE1	2.53	0.42
1:D:92:GLY:O	1:D:126:LYS:HD3	2.19	0.42
1:D:458:GLU:HG3	1:D:459:ARG:N	2.33	0.42
1:E:223:ILE:HD11	1:E:345:ALA:CB	2.49	0.42
1:A:24:VAL:CG1	1:A:483:VAL:CG1	2.91	0.42
1:A:227:ILE:HD11	1:A:245:LYS:HG2	2.01	0.42
1:B:369:PRO:HG3	1:B:478:ARG:HA	2.01	0.42
1:C:94:ARG:HB2	1:C:168:ASP:OD1	2.19	0.42
1:D:389:LEU:HD23	1:D:389:LEU:HA	1.74	0.42
1:D:396:ARG:HG3	1:D:397:LEU:HD23	2.01	0.42
1:E:322:LEU:HD23	1:E:344:ILE:HD12	2.01	0.42
1:F:374:ASN:HB2	3:F:603:NDP:C5N	2.48	0.42
1:A:112:THR:CG2	1:A:124:GLY:HA3	2.46	0.42
1:A:161:GLY:CA	1:C:192:ILE:HG13	2.49	0.42
1:A:417:LEU:HD21	1:B:417:LEU:HD13	2.02	0.42
1:B:252:PHE:CZ	1:B:257:LEU:HD13	2.54	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:42:ARG:O	1:C:46:ARG:HG2	2.18	0.42
1:C:155:LYS:HG3	1:F:157:PHE:HE1	1.82	0.42
1:D:25:GLU:O	1:D:29:VAL:HG13	2.18	0.42
1:D:63:PHE:O	1:D:75:ILE:HG22	2.19	0.42
1:A:207:GLY:O	1:A:387:LYS:NZ	2.42	0.42
1:A:321:ILE:HA	1:A:343:ILE:O	2.19	0.42
1:B:26:ASP:HA	1:B:42:ARG:NH2	2.34	0.42
1:B:324:PRO:HD2	1:B:345:ALA:O	2.20	0.42
1:C:2:ASP:O	1:C:6:ASP:HB2	2.19	0.42
1:C:79:ARG:NH2	1:C:163:ASP:OD2	2.52	0.42
1:C:99:VAL:HG12	1:C:130:LYS:HA	2.02	0.42
1:C:110:LEU:HD12	1:C:110:LEU:HA	1.84	0.42
1:C:314:ILE:HA	1:C:317:VAL:HG23	2.00	0.42
1:E:5:ASP:HB3	1:E:332:THR:HG22	2.01	0.42
1:E:120:VAL:HG11	1:E:378:VAL:HG12	2.00	0.42
1:F:29:VAL:HG11	1:F:42:ARG:HH12	1.83	0.42
1:F:104:VAL:HG13	1:F:126:LYS:O	2.19	0.42
1:F:215:THR:O	1:F:219:VAL:HG23	2.20	0.42
1:A:211:ARG:NH2	3:A:602:NDP:H72N	2.17	0.42
1:A:371:LEU:HD23	1:A:371:LEU:HA	1.85	0.42
1:C:117:VAL:HG21	1:C:371:LEU:HD22	2.01	0.42
1:D:289:LYS:HE3	1:D:293:ASP:OD1	2.20	0.42
1:E:450:HIS:HE1	4:E:603:GTP:O2B	2.02	0.42
1:F:59:LEU:HD21	1:F:61:LEU:HD21	2.01	0.42
1:F:476:ASP:OD2	1:F:479:THR:HG23	2.19	0.42
1:A:59:LEU:HG	1:A:61:LEU:HD13	2.00	0.42
1:B:432:PRO:HB3	1:B:436:PHE:CD2	2.54	0.42
1:D:167:PRO:CD	1:D:200:GLY:HA3	2.50	0.42
1:E:273:VAL:HG12	1:E:301:ILE:HD13	2.01	0.42
1:E:358:LYS:O	1:E:362:GLU:HG2	2.19	0.42
1:E:401:TYR:O	1:E:405:SER:HB2	2.18	0.42
1:B:19:ARG:HG2	1:B:479:THR:HG21	2.02	0.42
1:B:89:CYS:HA	1:B:123:GLY:O	2.20	0.42
1:E:28:LEU:HD22	1:E:490:PHE:CD2	2.54	0.42
1:A:392:VAL:HG21	1:A:397:LEU:CD1	2.49	0.42
1:B:114:LYS:HE2	1:B:114:LYS:HB2	1.75	0.42
1:C:100:SER:H	1:C:103:GLU:HG2	1.84	0.42
1:D:346:GLU:HG2	1:D:351:PRO:HG2	2.02	0.42
1:E:443:ALA:HB2	1:F:401:TYR:CD2	2.55	0.42
1:F:373:LEU:HD12	1:F:373:LEU:HA	1.85	0.42
1:A:208:ILE:HG13	1:A:209:HIS:N	2.35	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:252:PHE:CE2	1:A:291:LEU:HD13	2.54	0.42
1:C:252:PHE:CZ	1:C:291:LEU:HD12	2.55	0.42
1:D:89:CYS:HA	1:D:123:GLY:O	2.20	0.42
1:E:89:CYS:O	1:E:163:ASP:HA	2.20	0.42
1:F:99:VAL:HG11	1:F:128:GLY:C	2.40	0.42
1:F:189:HIS:CD2	1:F:190:TYR:CD1	3.08	0.42
1:A:154:LYS:HD2	1:E:189:HIS:HB3	2.02	0.42
1:C:261:ARG:NH2	4:C:603:GTP:C8	2.88	0.42
1:C:264:HIS:HA	1:C:268:ALA:O	2.20	0.42
1:D:443:ALA:HB2	1:E:401:TYR:CE2	2.55	0.42
1:E:66:ARG:HD2	1:E:71:SER:O	2.19	0.42
1:E:175:GLU:CD	1:E:175:GLU:H	2.22	0.42
1:A:483:VAL:O	1:A:487:GLU:HB2	2.20	0.41
1:C:450:HIS:CE1	4:C:603:GTP:O2B	2.73	0.41
1:E:186:THR:OG1	1:E:187:ILE:N	2.49	0.41
1:E:216:GLY:HA2	1:E:219:VAL:HB	2.01	0.41
1:E:435:GLU:HB3	1:F:408:HIS:CD2	2.55	0.41
1:F:92:GLY:O	1:F:126:LYS:HD3	2.20	0.41
1:A:161:GLY:HA2	1:C:192:ILE:HG13	2.01	0.41
1:A:331:LEU:O	1:A:353:THR:HG23	2.20	0.41
1:A:420:LYS:HG2	1:A:421:PHE:CE2	2.55	0.41
1:B:322:LEU:HD23	1:B:344:ILE:HD12	2.00	0.41
1:B:432:PRO:HB3	1:B:436:PHE:HD2	1.85	0.41
1:C:126:LYS:NZ	2:C:601:GLU:N	2.68	0.41
1:C:420:LYS:HG2	1:C:421:PHE:HD2	1.80	0.41
1:D:95:TYR:HB3	1:D:133:PRO:CG	2.50	0.41
1:E:27:LYS:HE2	1:E:31:ASP:OD1	2.20	0.41
1:E:321:ILE:HG23	1:E:343:ILE:HB	2.02	0.41
1:F:113:TYR:CB	1:F:371:LEU:HD21	2.49	0.41
1:A:82:HIS:HD2	1:A:83:SER:HB2	1.85	0.41
1:B:79:ARG:HH11	1:B:163:ASP:CG	2.24	0.41
1:B:336:ALA:N	1:B:337:PRO:HD2	2.35	0.41
1:D:397:LEU:O	1:F:448:ILE:HD12	2.20	0.41
1:D:408:HIS:ND1	1:F:439:ARG:HD2	2.34	0.41
1:E:217:ARG:HB2	1:E:262:TYR:CE1	2.55	0.41
1:F:189:HIS:HD2	1:F:190:TYR:CE1	2.38	0.41
1:F:291:LEU:HD12	1:F:291:LEU:HA	1.84	0.41
1:A:34:THR:HG21	1:A:44:ARG:NH2	2.20	0.41
1:D:141:LEU:HD23	1:D:141:LEU:HA	1.81	0.41
1:E:26:ASP:OD1	1:E:42:ARG:NH2	2.49	0.41
1:E:339:VAL:H	1:E:363:ARG:HH22	1.68	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:44:ARG:HA	1:F:44:ARG:NH1	2.35	0.41
1:C:24:VAL:O	1:C:27:LYS:N	2.53	0.41
1:C:417:LEU:HD23	1:C:417:LEU:HA	1.72	0.41
1:D:65:ILE:HG13	1:D:144:ILE:CG1	2.51	0.41
1:D:364:ASN:HD22	1:D:364:ASN:HA	1.63	0.41
1:E:264:HIS:CD2	1:E:288:PRO:HD3	2.56	0.41
1:C:46:ARG:O	1:C:50:ARG:HB2	2.21	0.41
1:C:164:VAL:HA	1:C:197:CYS:O	2.20	0.41
1:D:100:SER:H	1:D:103:GLU:HB3	1.85	0.41
1:E:38:GLU:HG2	1:E:40:GLN:H	1.86	0.41
1:E:152:LEU:HA	1:E:152:LEU:HD23	1.67	0.41
1:E:199:THR:HA	1:E:384:GLU:OE1	2.20	0.41
1:E:344:ILE:HB	1:E:367:VAL:HG22	2.03	0.41
1:F:368:ILE:HB	1:F:373:LEU:HD22	2.03	0.41
1:A:95:TYR:CZ	1:A:145:THR:HG22	2.56	0.41
1:A:248:ALA:HB1	1:A:272:ALA:HB3	2.02	0.41
1:C:89:CYS:HB3	1:C:125:ALA:HB2	2.02	0.41
1:C:414:GLN:OE1	1:C:429:PRO:HA	2.19	0.41
1:E:158:ILE:HG12	1:E:159:GLY:H	1.86	0.41
1:F:146:ARG:HE	1:F:182:THR:HB	1.86	0.41
1:F:167:PRO:HB3	1:F:172:GLY:HA2	2.01	0.41
1:A:94:ARG:O	1:A:128:GLY:HA2	2.21	0.41
1:B:252:PHE:CE2	1:B:291:LEU:CD1	3.04	0.41
1:C:224:GLU:HA	1:C:227:ILE:HG22	2.03	0.41
1:C:271:VAL:CG1	1:C:283:PRO:HA	2.49	0.41
1:D:17:PHE:CE2	1:D:49:LEU:HD12	2.56	0.41
1:D:63:PHE:CD1	1:D:147:ARG:HG3	2.56	0.41
1:E:96:SER:O	1:E:99:VAL:HG12	2.20	0.41
1:E:304:PHE:CD1	1:E:305:PRO:HD2	2.56	0.41
1:A:199:THR:HG23	1:A:384:GLU:CD	2.41	0.41
1:A:295:LYS:O	1:A:299:GLY:N	2.51	0.41
1:A:339:VAL:HG11	1:A:344:ILE:HD11	2.03	0.41
1:A:477:LEU:HD23	1:A:477:LEU:HA	1.78	0.41
1:B:408:HIS:HB3	1:C:436:PHE:HB2	2.03	0.41
1:C:141:LEU:HD23	1:C:141:LEU:HA	1.80	0.41
1:C:382:TYR:CE1	1:C:386:LEU:HD13	2.55	0.41
1:D:211:ARG:NH2	2:D:601:GLU:HG2	2.35	0.41
1:D:448:ILE:HD12	1:E:397:LEU:O	2.21	0.41
1:E:93:ILE:HD13	1:E:148:PHE:CE2	2.56	0.41
1:F:380:VAL:HG22	1:F:380:VAL:H	1.66	0.41
1:F:446:LYS:HG3	1:F:450:HIS:CE1	2.55	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:477:LEU:HD23	1:F:477:LEU:HA	1.87	0.41
1:A:37:THR:O	1:A:40:GLN:NE2	2.40	0.41
1:A:431:VAL:O	1:C:412:SER:HB3	2.21	0.41
1:C:58:VAL:HG22	1:C:80:ALA:CB	2.51	0.41
1:C:222:GLY:HA2	1:C:372:TYR:OH	2.21	0.41
1:C:332:THR:HG22	1:C:353:THR:HG21	2.03	0.41
1:D:65:ILE:HD13	1:D:65:ILE:HA	1.86	0.41
1:D:236:LEU:HD12	1:D:236:LEU:HA	1.78	0.41
1:D:292:GLU:O	1:D:296:LEU:HD23	2.21	0.41
1:D:346:GLU:OE1	1:D:352:THR:HG23	2.20	0.41
1:E:363:ARG:HH11	1:E:363:ARG:HD3	1.74	0.41
1:A:211:ARG:HA	1:A:380:VAL:HG11	2.02	0.40
1:A:224:GLU:HB2	1:A:242:PHE:CE2	2.56	0.40
1:D:348:ALA:O	1:D:351:PRO:HD3	2.21	0.40
1:B:187:ILE:HD12	1:F:189:HIS:CE1	2.56	0.40
1:D:34:THR:OG1	1:D:36:GLU:OE1	2.26	0.40
1:E:296:LEU:HD23	1:E:296:LEU:HA	1.78	0.40
1:E:368:ILE:HG22	1:E:373:LEU:HG	2.02	0.40
1:F:37:THR:HG23	1:F:41:LYS:NZ	2.36	0.40
1:F:227:ILE:HD11	1:F:245:LYS:HG3	2.02	0.40
1:F:315:LEU:HD13	1:F:331:LEU:HD23	2.02	0.40
1:B:172:GLY:O	1:B:176:MET:HG2	2.21	0.40
1:B:409:LEU:HD21	1:C:409:LEU:CD2	2.52	0.40
1:D:42:ARG:O	1:D:46:ARG:HG3	2.21	0.40
1:D:55:CYS:HA	1:D:82:HIS:HA	2.03	0.40
1:E:68:ASP:OD2	1:E:140:GLU:HG2	2.20	0.40
1:E:82:HIS:HD2	1:E:112:THR:HG21	1.79	0.40
1:E:246:THR:O	1:E:320:ASP:HB2	2.21	0.40
1:F:264:HIS:ND1	1:F:288:PRO:HD3	2.35	0.40
1:A:8:ASN:HD22	1:A:11:LYS:CG	2.33	0.40
1:A:211:ARG:HH12	1:A:377:GLY:C	2.25	0.40
1:A:420:LYS:HD2	1:B:428:ILE:HA	2.03	0.40
1:B:90:LYS:HE2	1:B:164:VAL:HG12	2.03	0.40
1:B:263:LEU:CD1	1:B:323:ILE:HD11	2.51	0.40
1:C:169:MET:HE1	3:C:602:NDP:H8A	2.03	0.40
1:C:326:ALA:HB1	3:C:602:NDP:C8A	2.51	0.40
1:D:415:GLU:O	1:D:419:ARG:HB2	2.22	0.40
1:F:432:PRO:HB3	1:F:436:PHE:HD2	1.86	0.40
1:A:209:HIS:O	1:A:449:VAL:HG11	2.21	0.40
1:A:258:HIS:CD2	1:A:261:ARG:HD3	2.56	0.40
1:A:353:THR:HB	1:A:354:PRO:HD2	2.04	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:459:ARG:O	1:B:463:GLN:HG2	2.21	0.40
1:C:108:ALA:O	1:C:111:MET:HB2	2.21	0.40
1:C:448:ILE:HA	1:C:448:ILE:HD13	1.82	0.40
1:E:228:ASN:OD1	1:E:241:GLY:HA2	2.22	0.40
1:E:315:LEU:HD13	1:E:331:LEU:HD23	2.04	0.40
1:E:332:THR:C	1:E:356:ALA:HB2	2.42	0.40
1:F:168:ASP:CG	1:F:169:MET:H	2.25	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	493/582 (85%)	444 (90%)	40 (8%)	9 (2%)	8	37
1	B	493/582 (85%)	448 (91%)	41 (8%)	4 (1%)	19	57
1	C	493/582 (85%)	452 (92%)	31 (6%)	10 (2%)	7	34
1	D	493/582 (85%)	451 (92%)	39 (8%)	3 (1%)	25	64
1	E	493/582 (85%)	446 (90%)	39 (8%)	8 (2%)	9	40
1	F	499/582 (86%)	447 (90%)	42 (8%)	10 (2%)	7	34
All	All	2964/3492 (85%)	2688 (91%)	232 (8%)	44 (2%)	10	42

All (44) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	38	GLU
1	A	39	GLU
1	A	371	LEU
1	B	37	THR
1	B	38	GLU

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Mol	Chain	Res	Type
1	E	38	GLU
1	F	36	GLU
1	F	38	GLU
1	B	34	THR
1	C	36	GLU
1	C	299	GLY
1	C	433	THR
1	D	36	GLU
1	D	38	GLU
1	D	422	GLY
1	F	3	ARG
1	F	396	ARG
1	F	496	ALA
1	C	306	LYS
1	A	32	LEU
1	A	396	ARG
1	C	2	ASP
1	C	305	PRO
1	E	31	ASP
1	E	39	GLU
1	E	210	GLY
1	F	371	LEU
1	F	498	VAL
1	A	476	ASP
1	B	371	LEU
1	C	19	ARG
1	C	340	LYS
1	C	422	GLY
1	E	32	LEU
1	E	422	GLY
1	F	422	GLY
1	A	377	GLY
1	E	305	PRO
1	F	391	HIS
1	A	422	GLY
1	C	282	ASN
1	E	378	VAL
1	F	165	PRO
1	A	99	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	413/471 (88%)	396 (96%)	17 (4%)	30	67
1	B	413/471 (88%)	395 (96%)	18 (4%)	28	65
1	C	413/471 (88%)	400 (97%)	13 (3%)	40	75
1	D	413/471 (88%)	397 (96%)	16 (4%)	32	69
1	E	413/471 (88%)	396 (96%)	17 (4%)	30	67
1	F	417/471 (88%)	399 (96%)	18 (4%)	29	66
All	All	2482/2826 (88%)	2383 (96%)	99 (4%)	31	68

All (99) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	9	PHE
1	A	26	ASP
1	A	44	ARG
1	A	61	LEU
1	A	79	ARG
1	A	134	LYS
1	A	162	VAL
1	A	205	GLN
1	A	234	SER
1	A	291	LEU
1	A	305	PRO
1	A	306	LYS
1	A	363	ARG
1	A	371	LEU
1	A	373	LEU
1	A	405	SER
1	A	462	ARG
1	B	9	PHE
1	B	19	ARG
1	B	31	ASP
1	B	35	ARG
1	B	78	TYR

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Mol	Chain	Res	Type
1	B	112	THR
1	B	162	VAL
1	B	168	ASP
1	B	175	GLU
1	B	182	THR
1	B	244	ASP
1	B	365	ILE
1	B	386	LEU
1	B	393	SER
1	B	397	LEU
1	B	403	ARG
1	B	405	SER
1	B	421	PHE
1	C	3	ARG
1	C	9	PHE
1	C	42	ARG
1	C	44	ARG
1	C	46	ARG
1	C	66	ARG
1	C	78	TYR
1	C	130	LYS
1	C	306	LYS
1	C	358	LYS
1	C	371	LEU
1	C	410	LEU
1	C	423	LYS
1	D	3	ARG
1	D	9	PHE
1	D	44	ARG
1	D	78	TYR
1	D	175	GLU
1	D	182	THR
1	D	238	MET
1	D	291	LEU
1	D	296	LEU
1	D	308	LYS
1	D	313	SER
1	D	364	ASN
1	D	386	LEU
1	D	423	LYS
1	D	458	GLU
1	D	494	ASN

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Mol	Chain	Res	Type
1	E	9	PHE
1	E	19	ARG
1	E	31	ASP
1	E	42	ARG
1	E	44	ARG
1	E	49	LEU
1	E	93	ILE
1	E	107	LEU
1	E	306	LYS
1	E	313	SER
1	E	340	LYS
1	E	363	ARG
1	E	405	SER
1	E	410	LEU
1	E	463	GLN
1	E	492	VAL
1	E	495	GLU
1	F	9	PHE
1	F	22	SER
1	F	96	SER
1	F	100	SER
1	F	107	LEU
1	F	205	GLN
1	F	217	ARG
1	F	239	THR
1	F	321	ILE
1	F	340	LYS
1	F	363	ARG
1	F	364	ASN
1	F	378	VAL
1	F	386	LEU
1	F	405	SER
1	F	424	HIS
1	F	466	ARG
1	F	487	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (11) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	8	ASN
1	A	82	HIS
1	A	205	GLN

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Mol	Chain	Res	Type
1	A	258	HIS
1	B	258	HIS
1	C	43	ASN
1	D	364	ASN
1	E	82	HIS
1	F	82	HIS
1	F	139	ASN
1	F	484	ASN

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 monosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 30 ligands modelled in this entry, 12 are monoatomic - leaving 18 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$
2	GLU	E	601	-	8,9,9	1.06	1 (12%)	10,11,11	1.15	1 (10%)
2	GLU	C	601	-	8,9,9	1.02	1 (12%)	10,11,11	1.39	2 (20%)
3	NDP	B	602	-	45,52,52	2.26	7 (15%)	53,80,80	1.66	11 (20%)
4	GTP	C	603	5	26,34,34	1.05	1 (3%)	32,54,54	1.45	4 (12%)
3	NDP	C	602	-	45,52,52	2.61	8 (17%)	53,80,80	1.65	10 (18%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	GLU	D	601	-	8,9,9	1.07	0	10,11,11	1.02	0
4	GTP	D	603	5	26,34,34	1.06	1 (3%)	32,54,54	1.49	5 (15%)
4	GTP	F	604	5	26,34,34	1.24	1 (3%)	32,54,54	1.42	8 (25%)
2	GLU	F	602	-	8,9,9	0.83	0	10,11,11	1.70	3 (30%)
2	GLU	B	601	-	8,9,9	1.05	1 (12%)	10,11,11	1.21	1 (10%)
4	GTP	B	603	5	26,34,34	1.19	1 (3%)	32,54,54	1.50	8 (25%)
3	NDP	F	603	-	45,52,52	2.33	8 (17%)	53,80,80	1.66	10 (18%)
4	GTP	E	603	5	26,34,34	1.16	1 (3%)	32,54,54	1.55	7 (21%)
3	NDP	A	602	-	45,52,52	2.40	8 (17%)	53,80,80	1.67	10 (18%)
3	NDP	D	602	-	45,52,52	2.55	11 (24%)	53,80,80	1.76	13 (24%)
2	GLU	A	601	-	8,9,9	0.95	0	10,11,11	1.49	2 (20%)
4	GTP	A	603	5	26,34,34	1.47	3 (11%)	32,54,54	1.88	10 (31%)
3	NDP	E	602	-	45,52,52	2.37	7 (15%)	53,80,80	1.73	14 (26%)

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	GLU	E	601	-	-	0/9/9/9	-
2	GLU	C	601	-	-	3/9/9/9	-
3	NDP	B	602	-	-	4/30/77/77	0/5/5/5
4	GTP	C	603	5	-	1/18/38/38	0/3/3/3
3	NDP	C	602	-	-	6/30/77/77	0/5/5/5
2	GLU	D	601	-	-	4/9/9/9	-
4	GTP	D	603	5	-	0/18/38/38	0/3/3/3
4	GTP	F	604	5	-	2/18/38/38	0/3/3/3
2	GLU	F	602	-	-	3/9/9/9	-
2	GLU	B	601	-	-	6/9/9/9	-
4	GTP	B	603	5	-	3/18/38/38	0/3/3/3
3	NDP	F	603	-	-	10/30/77/77	0/5/5/5
4	GTP	E	603	5	-	3/18/38/38	0/3/3/3
3	NDP	A	602	-	-	14/30/77/77	0/5/5/5
3	NDP	D	602	-	-	5/30/77/77	0/5/5/5
2	GLU	A	601	-	-	3/9/9/9	-
4	GTP	A	603	5	-	1/18/38/38	0/3/3/3

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	NDP	E	602	-	-	6/30/77/77	0/5/5/5

All (60) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	C	602	NDP	P2B-O2B	14.14	1.86	1.59
3	D	602	NDP	P2B-O2B	13.04	1.83	1.59
3	F	603	NDP	P2B-O2B	12.90	1.83	1.59
3	A	602	NDP	P2B-O2B	12.51	1.82	1.59
3	E	602	NDP	P2B-O2B	12.32	1.82	1.59
3	B	602	NDP	P2B-O2B	12.07	1.82	1.59
4	A	603	GTP	C5-C6	-5.34	1.36	1.47
3	F	603	NDP	PN-O5D	4.49	1.77	1.59
3	C	602	NDP	PN-O5D	4.41	1.77	1.59
3	D	602	NDP	O4B-C1B	4.39	1.47	1.41
4	F	604	GTP	C5-C6	-4.18	1.38	1.47
3	B	602	NDP	PN-O5D	4.03	1.75	1.59
4	E	603	GTP	C5-C6	-4.01	1.39	1.47
3	D	602	NDP	C7N-C3N	-3.94	1.40	1.48
4	B	603	GTP	C5-C6	-3.94	1.39	1.47
3	A	602	NDP	PN-O5D	3.88	1.75	1.59
3	A	602	NDP	C7N-C3N	-3.85	1.40	1.48
3	E	602	NDP	PN-O5D	3.82	1.74	1.59
3	C	602	NDP	O4B-C1B	3.67	1.46	1.41
3	A	602	NDP	O2B-C2B	-3.64	1.30	1.44
4	C	603	GTP	C5-C6	-3.40	1.40	1.47
4	D	603	GTP	C5-C6	-3.24	1.40	1.47
3	E	602	NDP	O2B-C2B	-3.22	1.32	1.44
3	F	603	NDP	O2B-C2B	-3.19	1.32	1.44
3	B	602	NDP	O2B-C2B	-3.14	1.32	1.44
3	D	602	NDP	PN-O5D	3.11	1.71	1.59
3	D	602	NDP	C3B-C2B	3.10	1.59	1.52
3	E	602	NDP	C4A-N3A	2.99	1.39	1.35
3	D	602	NDP	O2B-C2B	-2.99	1.33	1.44
3	E	602	NDP	C2A-N1A	2.89	1.39	1.33
3	C	602	NDP	O2B-C2B	-2.83	1.33	1.44
3	B	602	NDP	O3D-C3D	-2.71	1.36	1.43
3	A	602	NDP	C4A-N3A	2.70	1.39	1.35
3	C	602	NDP	C7N-C3N	-2.70	1.42	1.48
3	C	602	NDP	O5D-C5D	-2.69	1.34	1.44
3	F	603	NDP	C5B-C4B	2.66	1.59	1.51
3	D	602	NDP	O5D-C5D	-2.58	1.34	1.44

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	602	NDP	C5B-C4B	2.57	1.59	1.51
3	E	602	NDP	O4B-C4B	-2.57	1.39	1.45
3	D	602	NDP	O3D-C3D	-2.48	1.37	1.43
3	B	602	NDP	C4A-N3A	2.32	1.38	1.35
3	D	602	NDP	C4N-C3N	-2.24	1.45	1.49
3	D	602	NDP	PA-O5B	2.23	1.68	1.59
2	E	601	GLU	OXT-C	-2.20	1.23	1.30
3	F	603	NDP	C7N-C3N	-2.17	1.44	1.48
3	B	602	NDP	C4N-C3N	-2.15	1.45	1.49
3	C	602	NDP	PA-O5B	2.15	1.68	1.59
3	B	602	NDP	C7N-C3N	-2.12	1.44	1.48
3	A	602	NDP	C2A-N1A	2.11	1.37	1.33
3	F	603	NDP	PA-O5B	2.11	1.67	1.59
3	A	602	NDP	O2D-C2D	-2.09	1.38	1.43
3	C	602	NDP	C2A-N1A	2.09	1.37	1.33
3	F	603	NDP	C3B-C2B	2.08	1.57	1.52
4	A	603	GTP	C6-N1	2.07	1.41	1.37
3	E	602	NDP	O5D-C5D	-2.06	1.36	1.44
3	D	602	NDP	C2A-N1A	2.05	1.37	1.33
3	F	603	NDP	O5D-C5D	-2.03	1.37	1.44
2	B	601	GLU	OXT-C	-2.02	1.23	1.30
2	C	601	GLU	OXT-C	-2.02	1.23	1.30
4	A	603	GTP	C2'-C1'	-2.00	1.50	1.53

All (119) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	602	NDP	PN-O3-PA	-6.54	110.39	132.83
3	D	602	NDP	PN-O3-PA	-6.49	110.54	132.83
3	C	602	NDP	PN-O3-PA	-6.28	111.27	132.83
3	F	603	NDP	PN-O3-PA	-6.05	112.07	132.83
3	E	602	NDP	PN-O3-PA	-6.02	112.16	132.83
3	B	602	NDP	PN-O3-PA	-5.59	113.63	132.83
4	A	603	GTP	O6-C6-C5	-4.53	115.53	124.37
4	A	603	GTP	O6-C6-N1	4.35	125.78	120.65
4	D	603	GTP	PB-O3B-PG	-4.15	118.57	132.83
4	C	603	GTP	PB-O3B-PG	-3.86	119.59	132.83
4	E	603	GTP	PB-O3B-PG	-3.75	119.95	132.83
4	A	603	GTP	N2-C2-N1	3.67	124.52	116.71
4	A	603	GTP	PB-O3B-PG	-3.47	120.92	132.83
2	F	602	GLU	CG-CB-CA	3.45	121.89	113.84
4	C	603	GTP	C8-N7-C5	3.42	109.51	102.99

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	F	603	NDP	O2B-P2B-O1X	-3.31	96.61	109.39
4	D	603	GTP	C5-C6-N1	3.31	119.80	113.95
3	E	602	NDP	O5D-PN-O1N	-3.30	96.16	109.07
3	E	602	NDP	O7N-C7N-C3N	3.23	126.98	120.90
4	B	603	GTP	C8-N7-C5	3.20	109.08	102.99
3	F	603	NDP	C2A-N1A-C6A	-3.18	113.31	118.75
4	D	603	GTP	C8-N7-C5	3.17	109.02	102.99
3	A	602	NDP	O2B-P2B-O1X	-3.16	97.19	109.39
4	B	603	GTP	PB-O3B-PG	-3.15	122.01	132.83
4	E	603	GTP	C8-N7-C5	3.13	108.96	102.99
3	A	602	NDP	O5D-PN-O1N	-3.12	96.89	109.07
3	D	602	NDP	PN-O5D-C5D	-3.08	103.59	121.68
3	D	602	NDP	O2B-P2B-O1X	-3.05	97.63	109.39
3	F	603	NDP	O5D-PN-O1N	-3.04	97.20	109.07
3	B	602	NDP	O2B-P2B-O1X	-3.03	97.68	109.39
4	C	603	GTP	C5-C6-N1	3.00	119.26	113.95
4	E	603	GTP	C5-C6-N1	3.00	119.25	113.95
2	A	601	GLU	OXT-C-O	-2.99	117.29	124.09
4	F	604	GTP	C5-C6-N1	2.93	119.13	113.95
3	D	602	NDP	C3N-C2N-N1N	-2.86	119.01	123.10
3	B	602	NDP	O5D-PN-O1N	-2.86	97.89	109.07
4	F	604	GTP	PB-O3B-PG	-2.86	123.03	132.83
4	B	603	GTP	C5-C6-N1	2.84	118.97	113.95
3	C	602	NDP	O2B-P2B-O1X	-2.82	98.49	109.39
4	C	603	GTP	C2-N1-C6	-2.82	119.90	125.10
3	D	602	NDP	C3B-C2B-C1B	-2.81	97.60	102.89
3	C	602	NDP	O5D-PN-O1N	-2.77	98.24	109.07
2	A	601	GLU	OXT-C-CA	2.76	122.80	113.38
3	E	602	NDP	O3X-P2B-O2X	2.76	118.19	107.64
3	B	602	NDP	O7N-C7N-C3N	2.76	126.09	120.90
3	D	602	NDP	O7N-C7N-C3N	2.73	126.04	120.90
4	F	604	GTP	PA-O3A-PB	-2.72	123.49	132.83
3	C	602	NDP	C2A-N1A-C6A	-2.71	114.11	118.75
3	B	602	NDP	PN-O5D-C5D	-2.70	105.84	121.68
3	D	602	NDP	O2N-PN-O1N	2.69	125.52	112.24
4	A	603	GTP	C5-C6-N1	2.69	118.69	113.95
3	E	602	NDP	O2B-P2B-O1X	-2.68	99.06	109.39
3	B	602	NDP	C3B-C2B-C1B	-2.67	97.87	102.89
3	D	602	NDP	C2A-N1A-C6A	-2.66	114.20	118.75
3	D	602	NDP	O5D-PN-O1N	-2.65	98.70	109.07
4	D	603	GTP	C2-N1-C6	-2.65	120.23	125.10
4	B	603	GTP	C2-N1-C6	-2.63	120.25	125.10

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	B	602	NDP	O3X-P2B-O2X	2.63	117.70	107.64
3	E	602	NDP	C3B-C2B-C1B	-2.61	97.97	102.89
4	F	604	GTP	C8-N7-C5	2.61	107.96	102.99
2	C	601	GLU	OXT-C-O	-2.59	118.22	124.09
3	C	602	NDP	O3X-P2B-O2X	2.59	117.52	107.64
3	A	602	NDP	O3X-P2B-O2X	2.58	117.49	107.64
3	B	602	NDP	PA-O5B-C5B	-2.58	106.57	121.68
3	A	602	NDP	PN-O5D-C5D	-2.57	106.59	121.68
3	F	603	NDP	O7N-C7N-C3N	2.55	125.71	120.90
4	A	603	GTP	N1-C2-N3	-2.54	118.57	123.32
3	F	603	NDP	O3X-P2B-O2X	2.52	117.26	107.64
3	D	602	NDP	O3X-P2B-O2X	2.52	117.26	107.64
3	C	602	NDP	PN-O5D-C5D	-2.48	107.15	121.68
3	B	602	NDP	O2N-PN-O1N	2.47	124.46	112.24
4	E	603	GTP	C2-N1-C6	-2.47	120.56	125.10
3	E	602	NDP	PA-O5B-C5B	-2.45	107.30	121.68
3	A	602	NDP	PA-O5B-C5B	-2.44	107.38	121.68
2	E	601	GLU	OXT-C-O	-2.43	118.58	124.09
4	D	603	GTP	O6-C6-N1	-2.41	117.81	120.65
3	C	602	NDP	PA-O5B-C5B	-2.39	107.67	121.68
3	A	602	NDP	O7N-C7N-C3N	2.39	125.39	120.90
4	A	603	GTP	C8-N7-C5	2.39	107.53	102.99
2	C	601	GLU	OXT-C-CA	2.38	121.49	113.38
4	F	604	GTP	C2-N1-C6	-2.35	120.76	125.10
3	F	603	NDP	O2N-PN-O1N	2.34	123.80	112.24
3	D	602	NDP	C3N-C7N-N7N	-2.31	113.57	117.67
3	E	602	NDP	O3X-P2B-O2B	-2.29	95.74	105.99
4	F	604	GTP	O6-C6-C5	-2.28	119.93	124.37
3	C	602	NDP	O2N-PN-O1N	2.27	123.45	112.24
4	B	603	GTP	N2-C2-N1	2.25	121.49	116.71
4	E	603	GTP	PA-O3A-PB	-2.24	125.14	132.83
3	E	602	NDP	C5D-C4D-C3D	-2.23	106.83	115.18
4	E	603	GTP	O3G-PG-O3B	2.22	112.07	104.64
2	F	602	GLU	OXT-C-O	-2.21	119.06	124.09
4	A	603	GTP	C2-N1-C6	-2.20	121.04	125.10
3	A	602	NDP	C3N-C2N-N1N	-2.19	119.97	123.10
4	B	603	GTP	O2G-PG-O3B	2.18	111.95	104.64
2	B	601	GLU	OXT-C-O	-2.17	119.16	124.09
3	E	602	NDP	C2A-N1A-C6A	-2.16	115.06	118.75
4	A	603	GTP	O3'-C3'-C2'	-2.16	104.85	111.82
3	B	602	NDP	C2A-N1A-C6A	-2.13	115.10	118.75
4	F	604	GTP	O3'-C3'-C2'	-2.12	104.95	111.82

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	F	603	NDP	C3B-C2B-C1B	-2.12	98.90	102.89
3	E	602	NDP	C5B-C4B-C3B	-2.11	107.28	115.18
3	D	602	NDP	C5D-C4D-C3D	-2.09	107.35	115.18
4	B	603	GTP	O6-C6-C5	-2.09	120.30	124.37
4	A	603	GTP	O3'-C3'-C4'	-2.08	105.03	111.05
3	C	602	NDP	O4B-C4B-C3B	2.08	109.23	105.11
4	F	604	GTP	N2-C2-N1	2.08	121.14	116.71
3	B	602	NDP	C3N-C2N-N1N	-2.07	120.14	123.10
3	A	602	NDP	C3N-C7N-N7N	-2.07	113.99	117.67
3	F	603	NDP	C5D-C4D-C3D	-2.06	107.46	115.18
3	D	602	NDP	PA-O5B-C5B	-2.05	109.64	121.68
3	C	602	NDP	C3B-C2B-C1B	-2.05	99.03	102.89
4	B	603	GTP	O3'-C3'-C4'	-2.05	105.12	111.05
3	F	603	NDP	C3N-C2N-N1N	-2.05	120.17	123.10
2	F	602	GLU	CB-CA-C	2.05	115.17	110.30
3	A	602	NDP	C2A-N1A-C6A	-2.03	115.28	118.75
3	E	602	NDP	O2N-PN-O1N	2.02	122.24	112.24
3	E	602	NDP	PN-O5D-C5D	-2.02	109.85	121.68
3	E	602	NDP	O4B-C4B-C3B	2.01	109.08	105.11
4	E	603	GTP	N2-C2-N1	2.00	120.98	116.71

There are no chirality outliers.

All (74) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	602	NDP	C5B-O5B-PA-O1A
3	A	602	NDP	C5B-O5B-PA-O3
3	A	602	NDP	C5D-O5D-PN-O3
3	A	602	NDP	O4D-C4D-C5D-O5D
3	C	602	NDP	C5B-O5B-PA-O3
3	E	602	NDP	C2N-C3N-C7N-O7N
4	F	604	GTP	PB-O3B-PG-O3G
3	A	602	NDP	C3D-C4D-C5D-O5D
3	D	602	NDP	O4D-C4D-C5D-O5D
3	E	602	NDP	O4D-C4D-C5D-O5D
3	A	602	NDP	O4B-C4B-C5B-O5B
3	A	602	NDP	C3B-C4B-C5B-O5B
3	B	602	NDP	O4B-C4B-C5B-O5B
3	E	602	NDP	C3D-C4D-C5D-O5D
3	F	603	NDP	O4B-C4B-C5B-O5B
3	F	603	NDP	C3B-C4B-C5B-O5B
3	D	602	NDP	C3D-C4D-C5D-O5D

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Mol	Chain	Res	Type	Atoms
4	F	604	GTP	PB-O3A-PA-O1A
2	B	601	GLU	O-C-CA-N
3	F	603	NDP	C2D-C1D-N1N-C6N
4	B	603	GTP	PB-O3A-PA-O5'
3	D	602	NDP	O4B-C4B-C5B-O5B
3	F	603	NDP	O4D-C4D-C5D-O5D
3	A	602	NDP	C2B-O2B-P2B-O2X
3	A	602	NDP	PN-O3-PA-O1A
3	D	602	NDP	O4D-C1D-N1N-C6N
3	A	602	NDP	C5B-O5B-PA-O2A
3	A	602	NDP	C5D-O5D-PN-O1N
3	A	602	NDP	C5D-O5D-PN-O2N
3	C	602	NDP	C5B-O5B-PA-O1A
3	C	602	NDP	C5B-O5B-PA-O2A
3	E	602	NDP	C2N-C3N-C7N-N7N
2	A	601	GLU	N-CA-CB-CG
2	B	601	GLU	N-CA-CB-CG
2	D	601	GLU	N-CA-CB-CG
3	E	602	NDP	O4D-C1D-N1N-C6N
3	F	603	NDP	O4D-C1D-N1N-C6N
4	A	603	GTP	PB-O3B-PG-O1G
3	A	602	NDP	O4D-C1D-N1N-C6N
3	B	602	NDP	O4D-C1D-N1N-C6N
4	B	603	GTP	PA-O3A-PB-O1B
3	A	602	NDP	C2D-C1D-N1N-C6N
3	C	602	NDP	O4D-C1D-N1N-C6N
2	F	602	GLU	OE2-CD-CG-CB
2	C	601	GLU	OE2-CD-CG-CB
3	B	602	NDP	C2D-C1D-N1N-C6N
3	C	602	NDP	C2D-C1D-N1N-C6N
3	B	602	NDP	C3B-C4B-C5B-O5B
2	C	601	GLU	OE1-CD-CG-CB
2	B	601	GLU	O-C-CA-CB
3	F	603	NDP	C2D-C1D-N1N-C2N
2	F	602	GLU	OE1-CD-CG-CB
2	F	602	GLU	O-C-CA-N
2	B	601	GLU	OXT-C-CA-N
3	F	603	NDP	PN-O3-PA-O2A
2	A	601	GLU	OE2-CD-CG-CB
4	E	603	GTP	O4'-C4'-C5'-O5'
2	D	601	GLU	OE2-CD-CG-CB
2	B	601	GLU	OXT-C-CA-CB

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Mol	Chain	Res	Type	Atoms
3	F	603	NDP	O4D-C1D-N1N-C2N
2	A	601	GLU	OE1-CD-CG-CB
3	C	602	NDP	O4B-C4B-C5B-O5B
2	B	601	GLU	C-CA-CB-CG
2	D	601	GLU	C-CA-CB-CG
4	E	603	GTP	PB-O3B-PG-O2G
2	D	601	GLU	OE1-CD-CG-CB
3	D	602	NDP	C3B-C4B-C5B-O5B
4	B	603	GTP	PG-O3B-PB-O2B
3	F	603	NDP	C5B-O5B-PA-O1A
4	C	603	GTP	C5'-O5'-PA-O2A
4	E	603	GTP	C5'-O5'-PA-O1A
3	E	602	NDP	O4B-C4B-C5B-O5B
3	F	603	NDP	C3D-C4D-C5D-O5D
2	C	601	GLU	N-CA-CB-CG

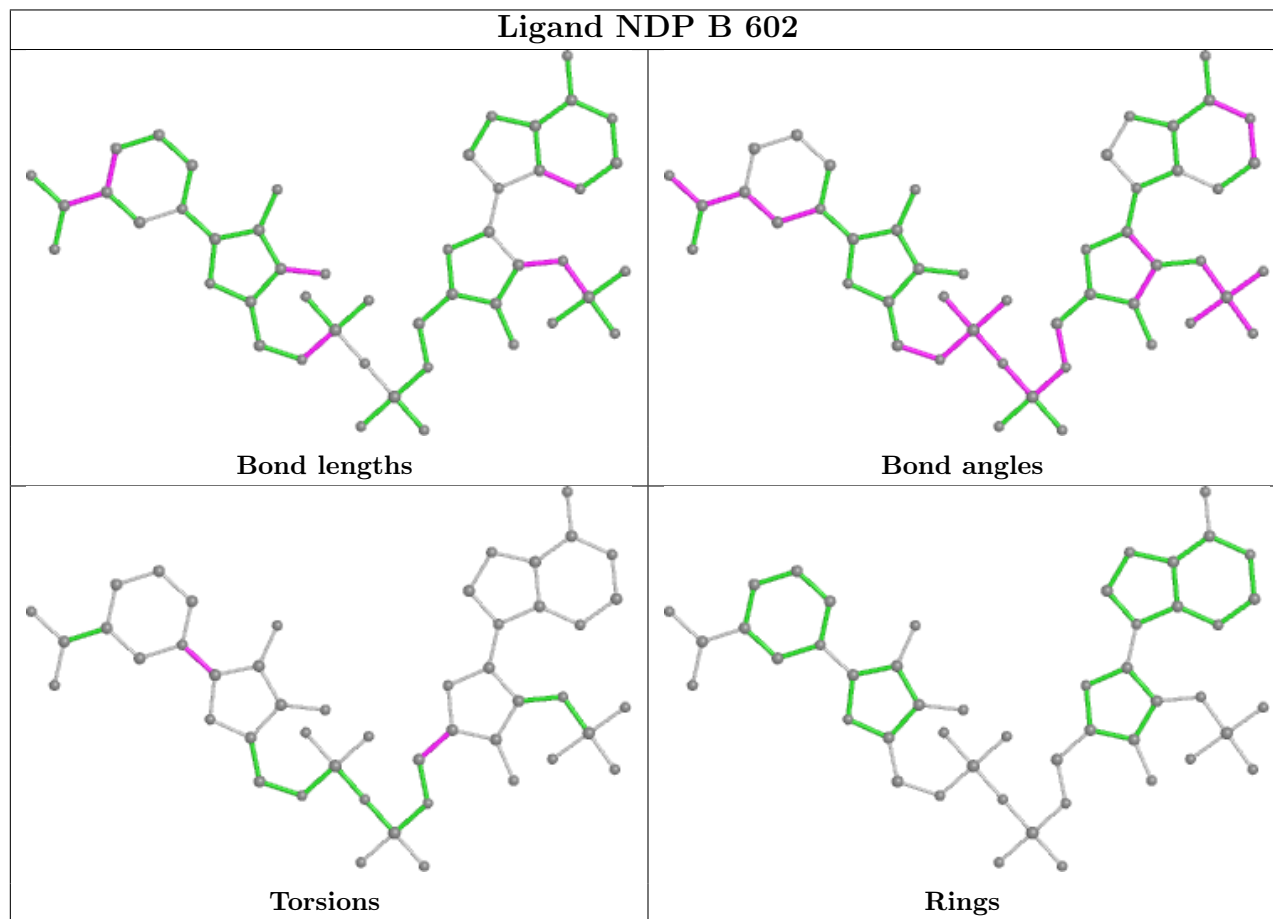
There are no ring outliers.

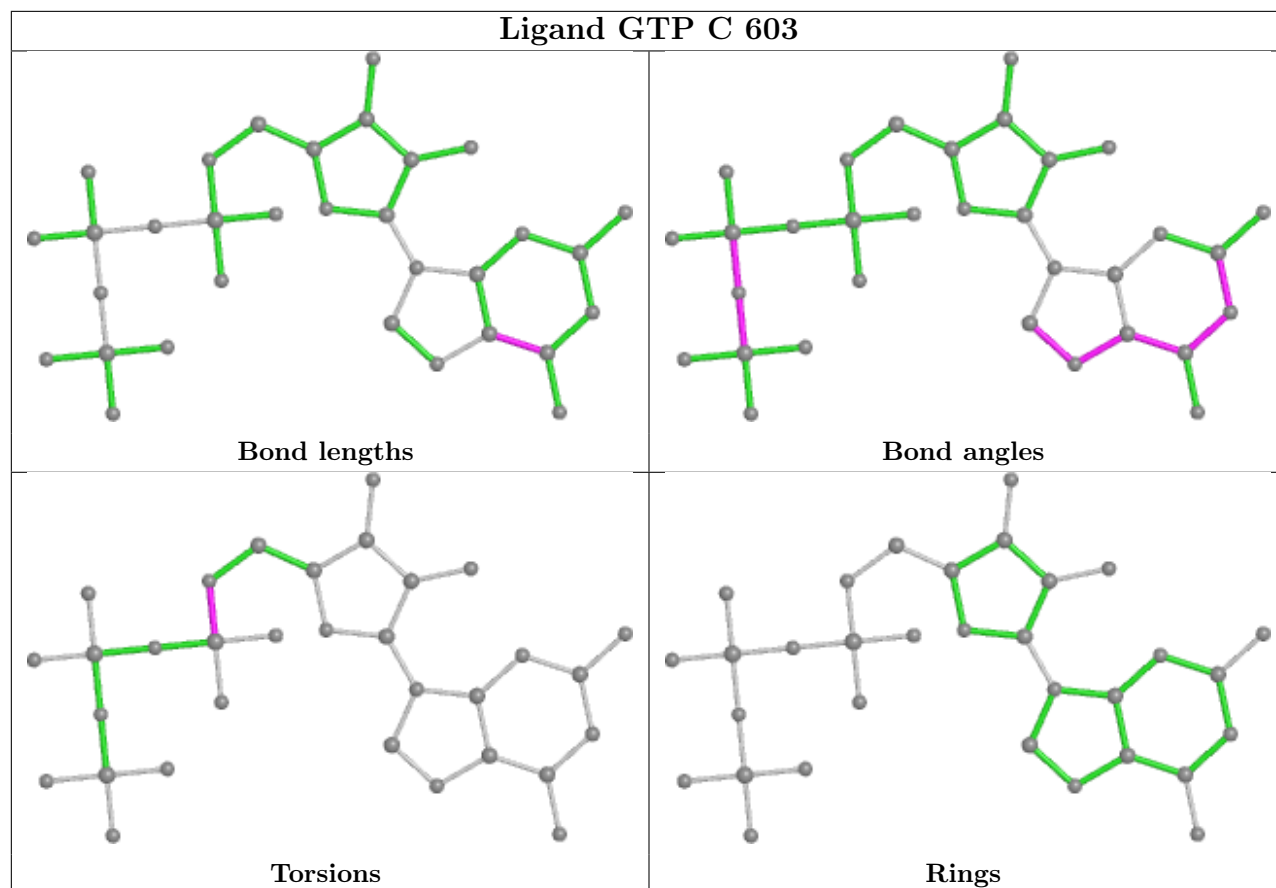
15 monomers are involved in 42 short contacts:

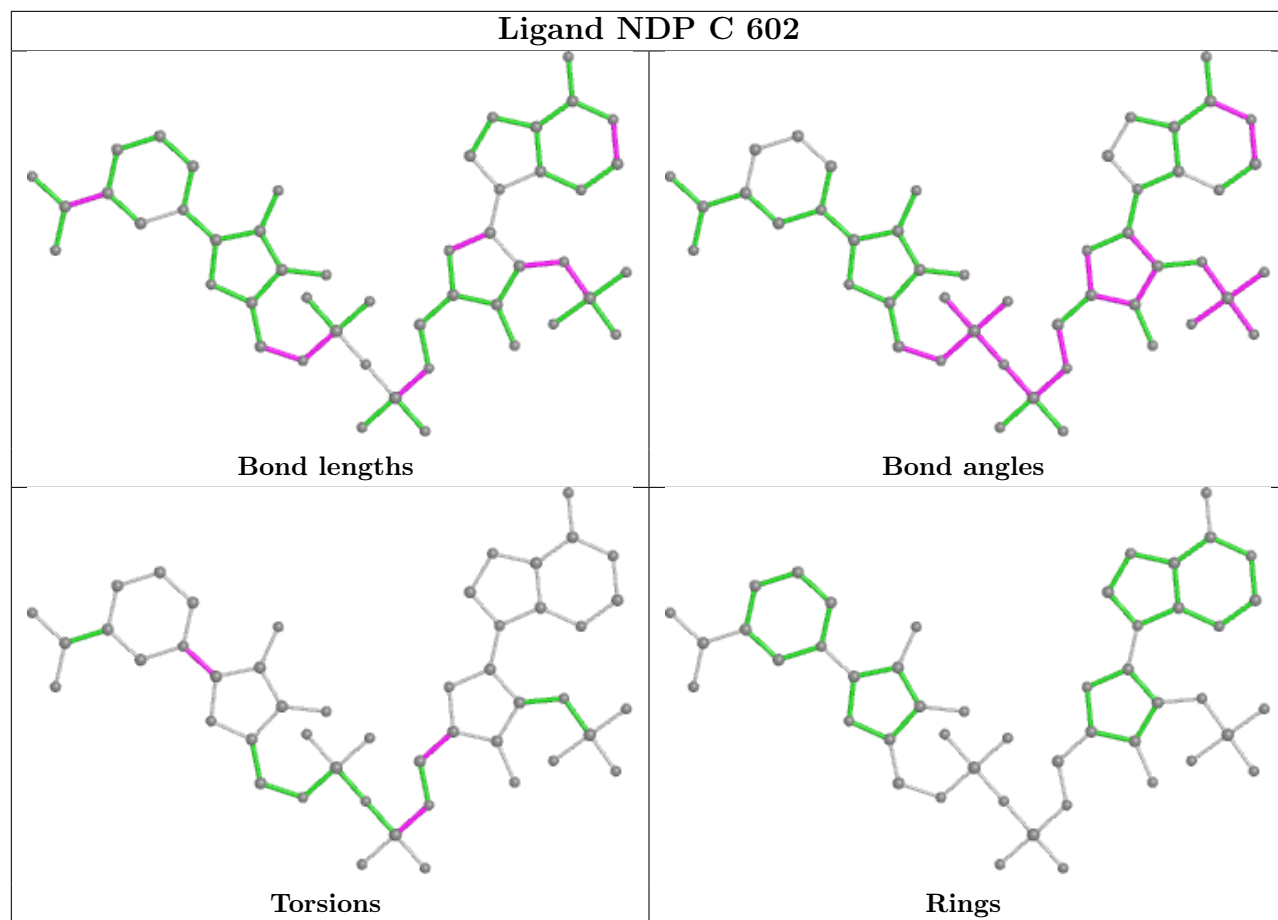
Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	E	601	GLU	1	0
2	C	601	GLU	4	0
3	B	602	NDP	4	0
4	C	603	GTP	3	0
3	C	602	NDP	5	0
2	D	601	GLU	2	0
4	D	603	GTP	2	0
2	F	602	GLU	3	0
2	B	601	GLU	1	0
4	B	603	GTP	2	0
3	F	603	NDP	4	0
4	E	603	GTP	2	0
3	A	602	NDP	6	0
2	A	601	GLU	5	0
3	E	602	NDP	4	0

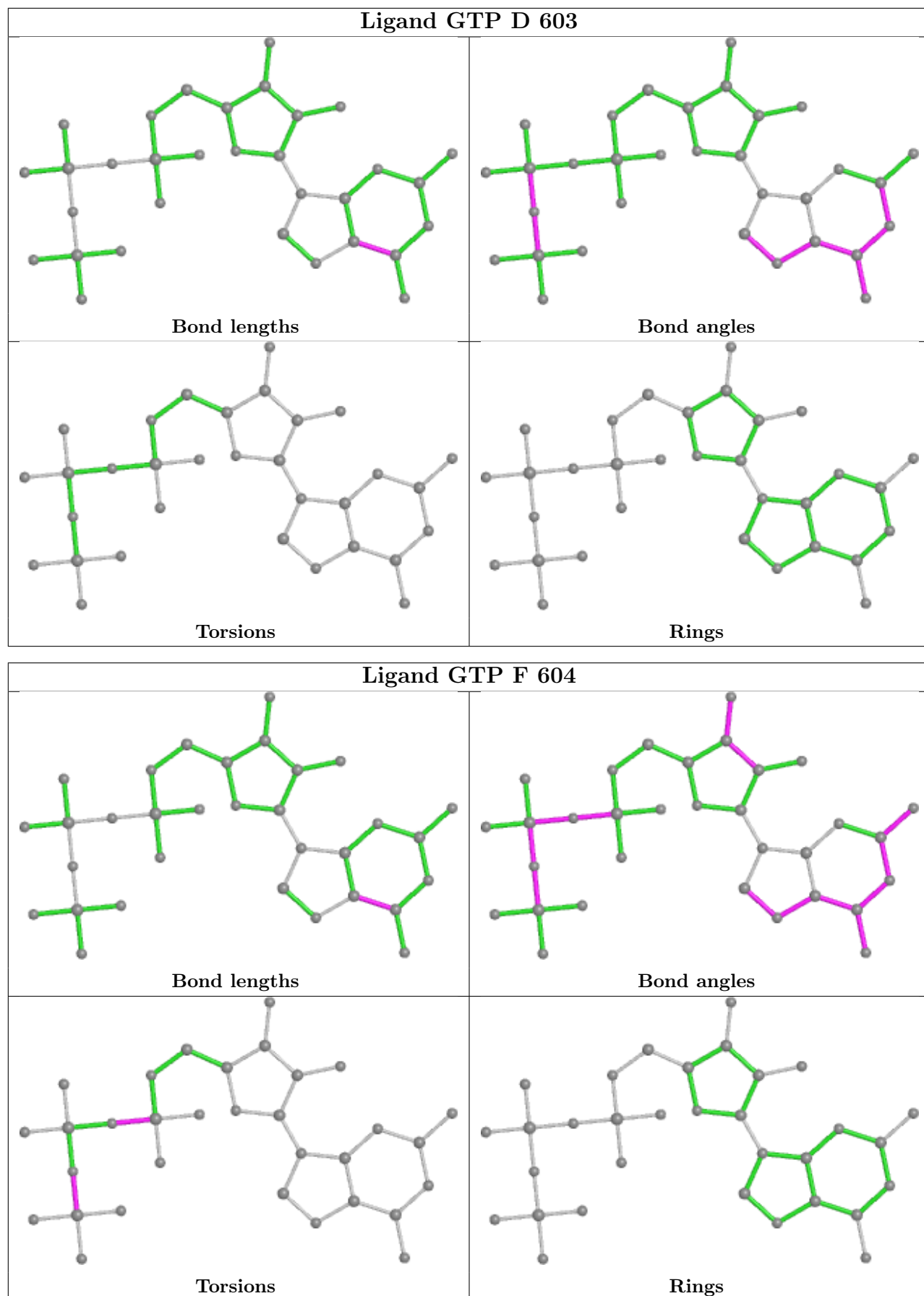
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included.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

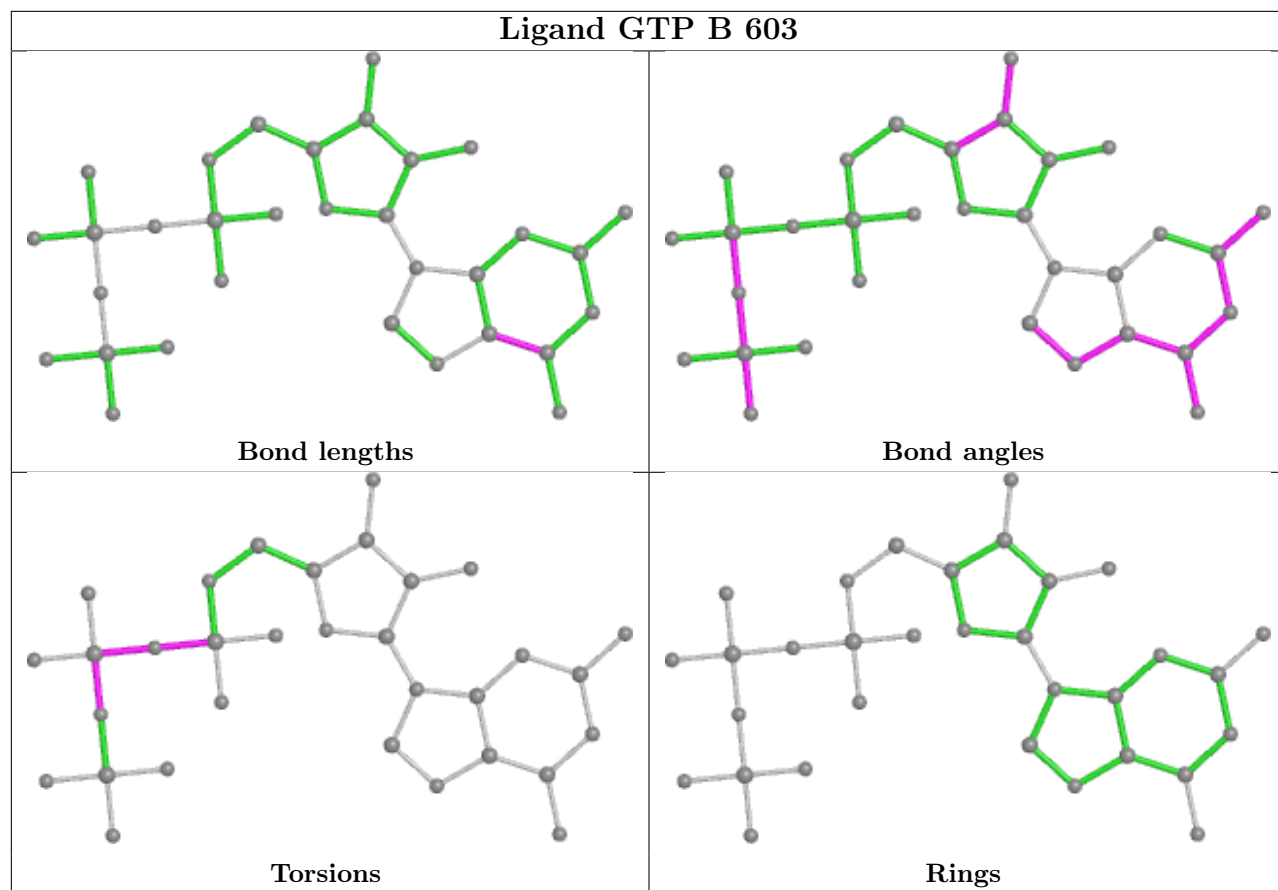
highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified 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.

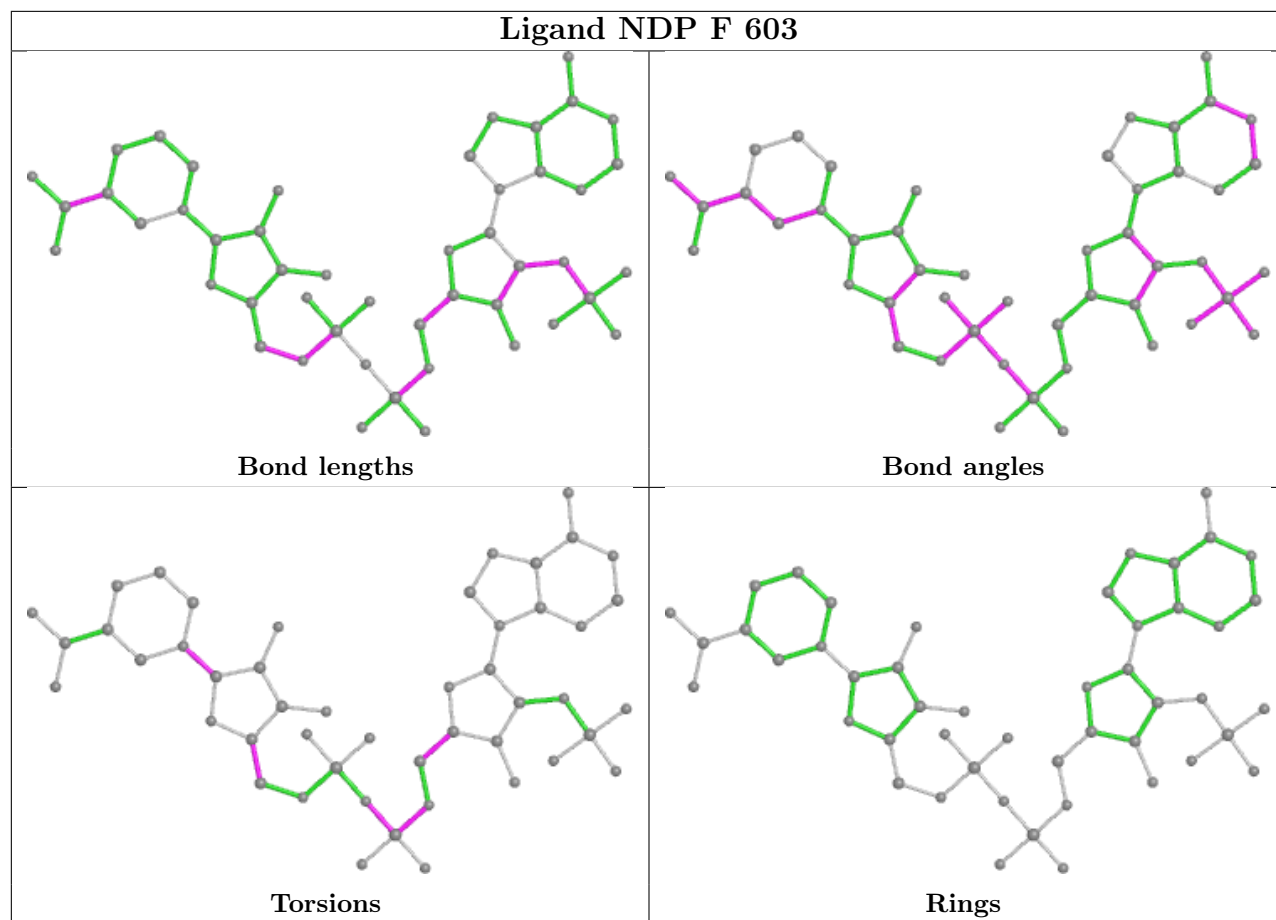


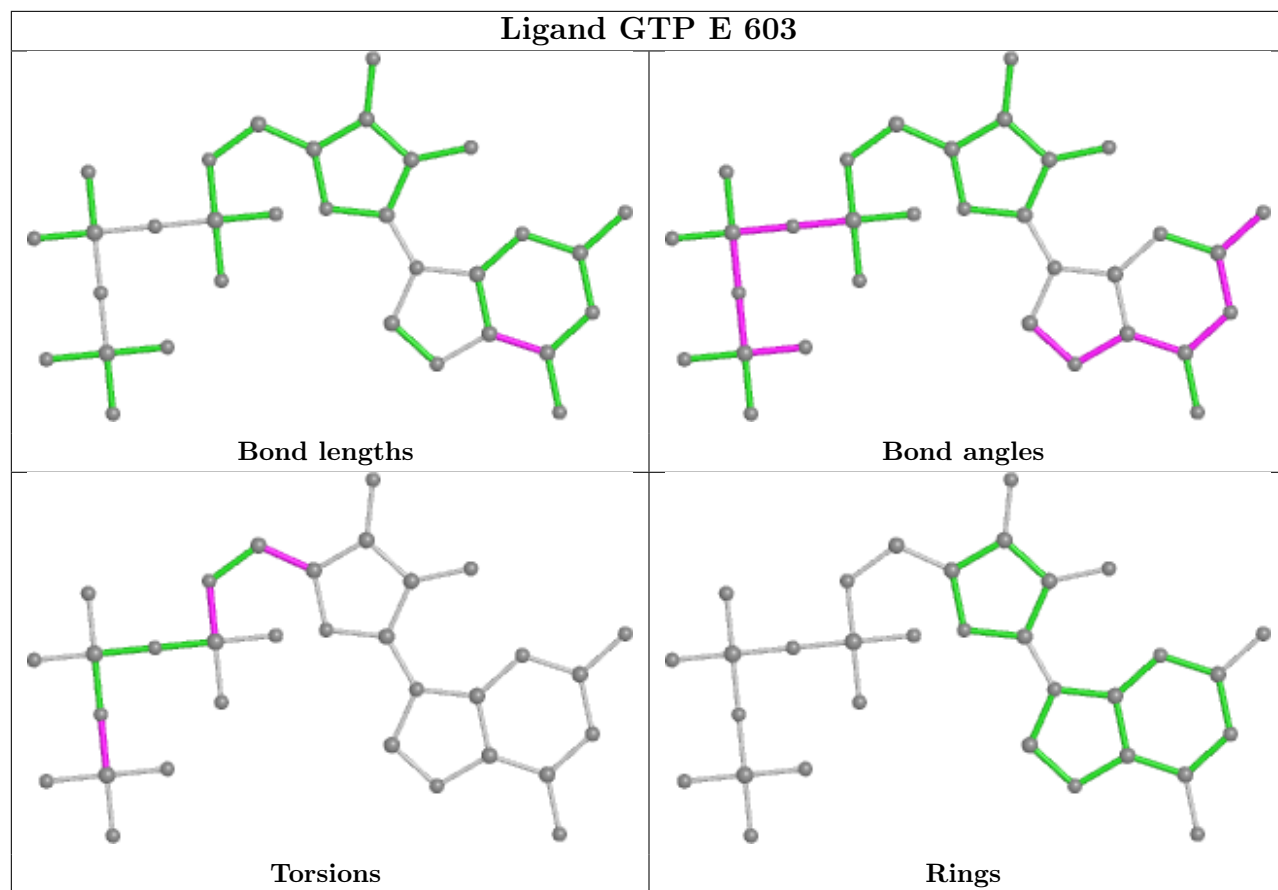


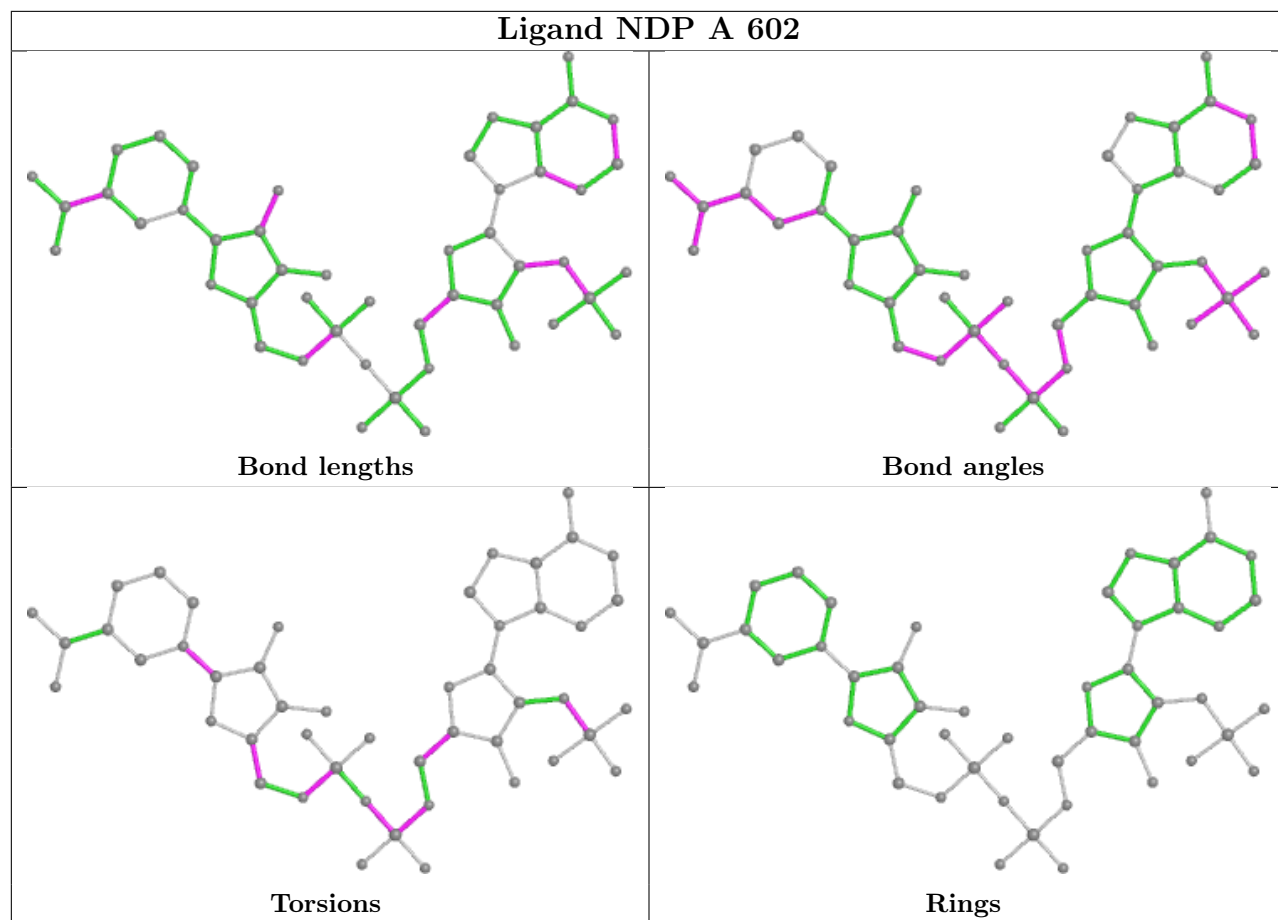


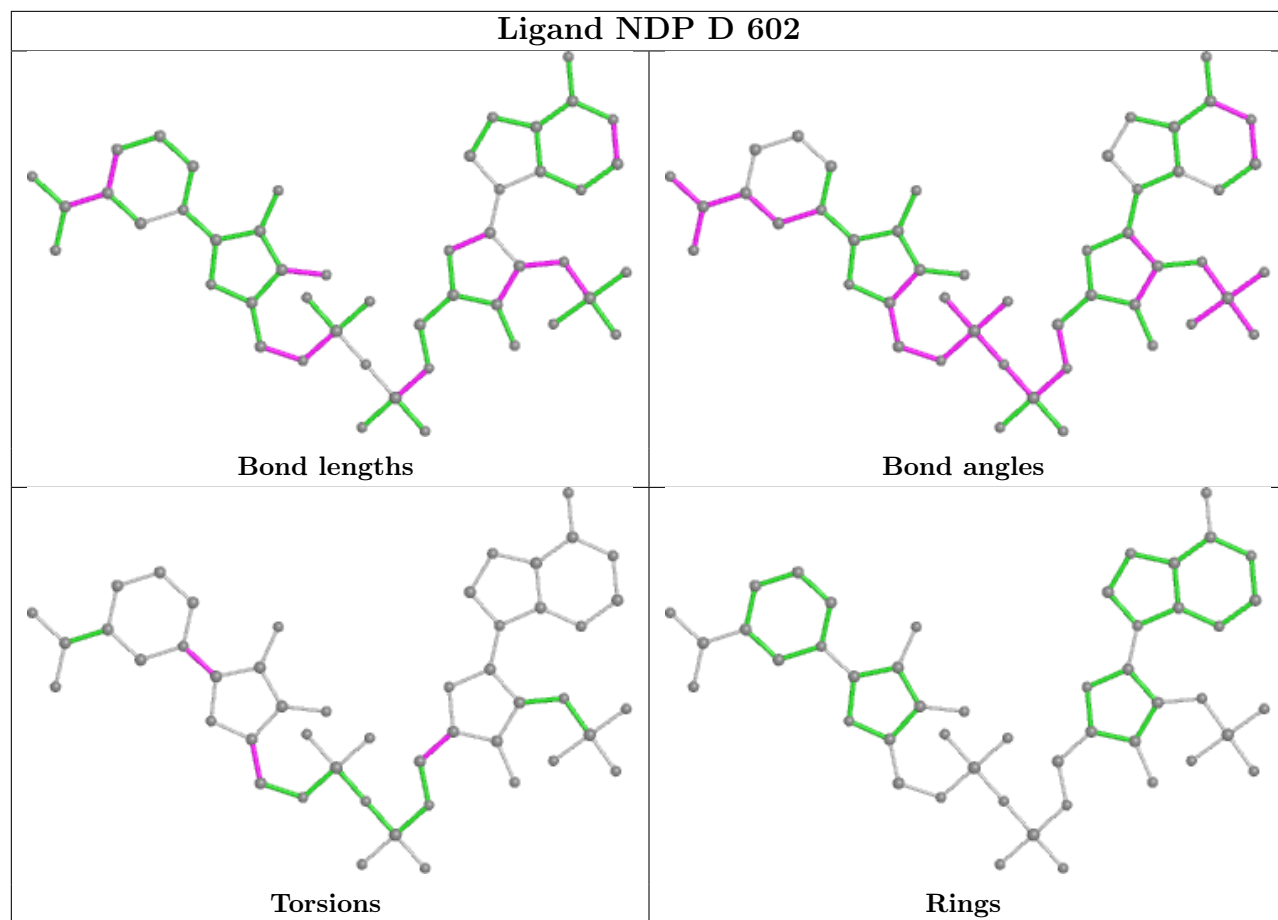


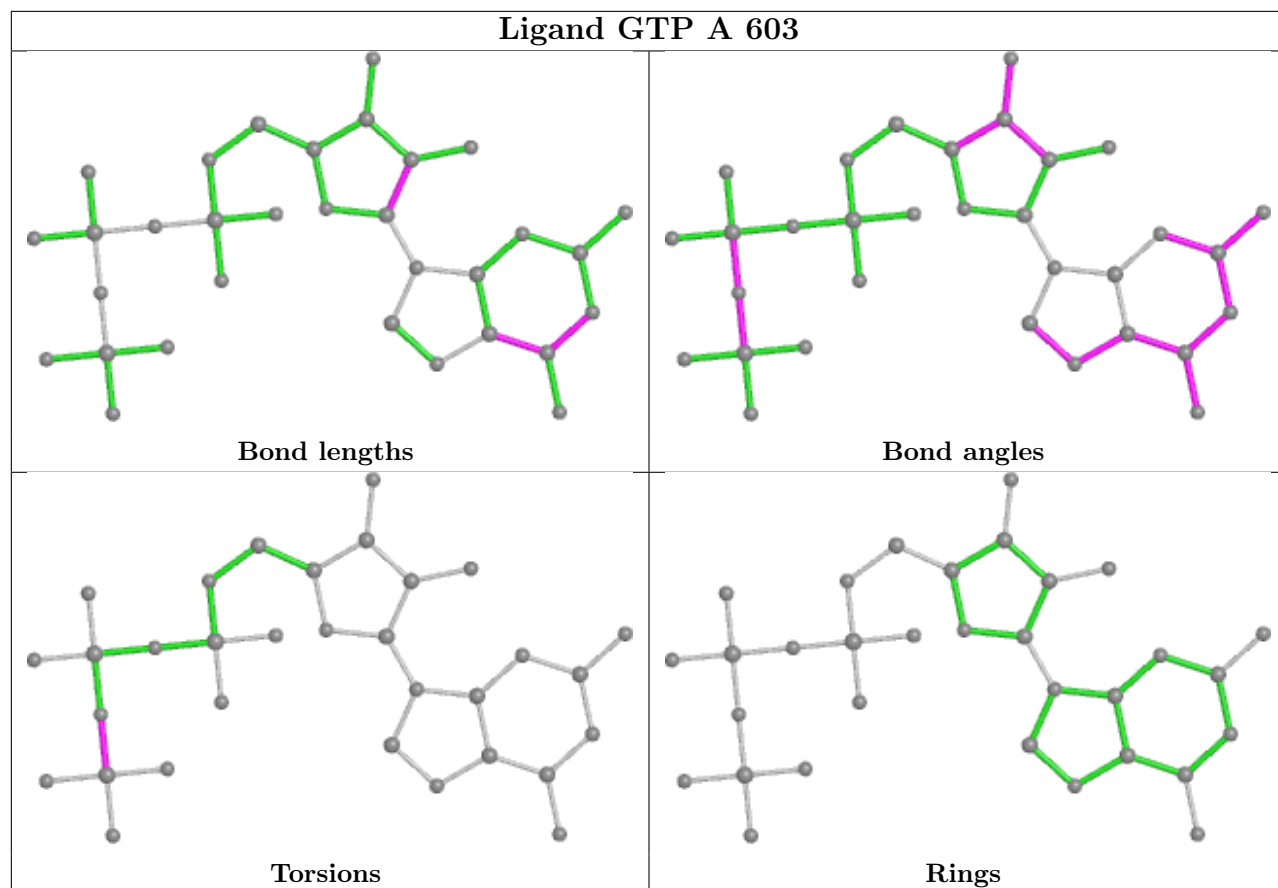


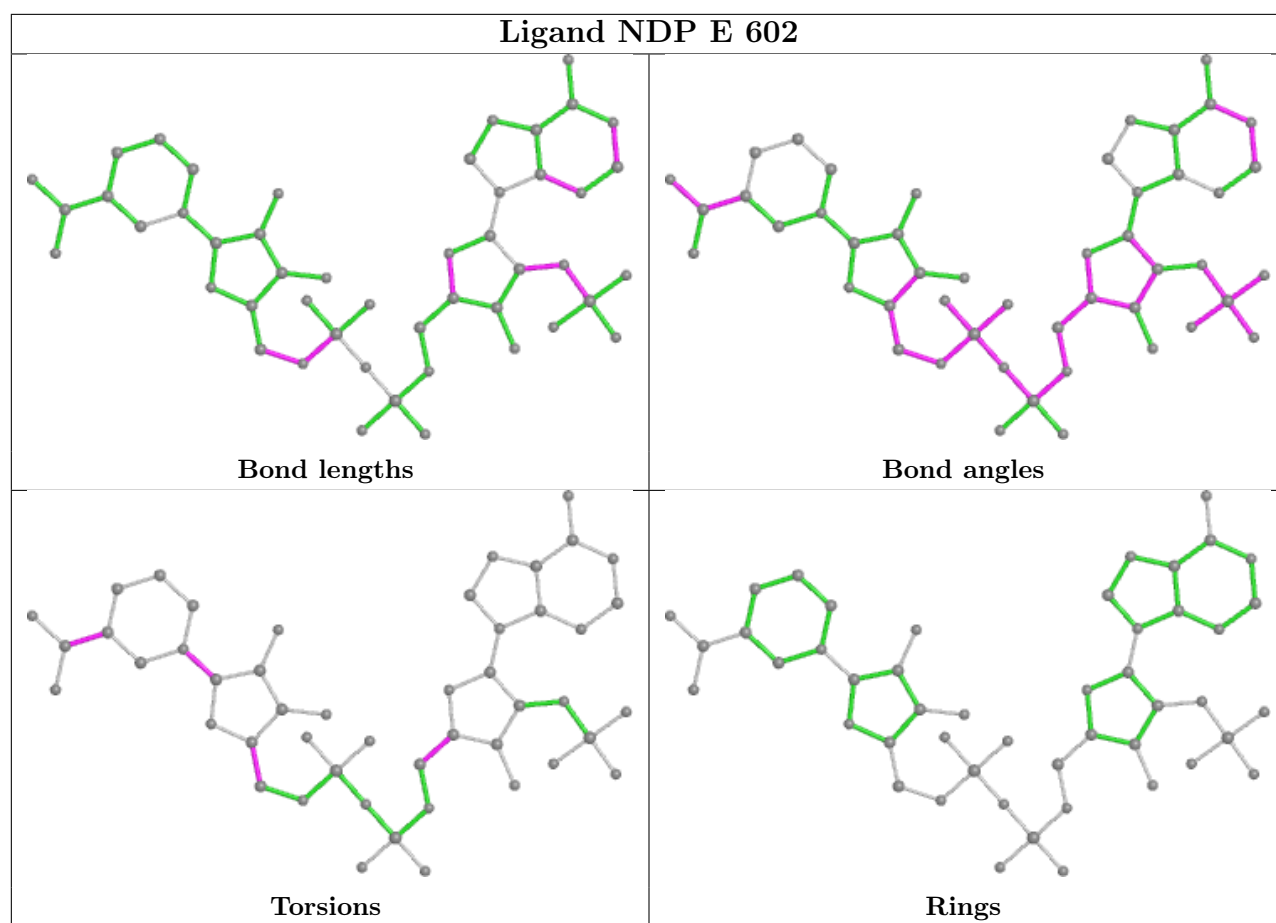












5.7 Other polymers [i](#)

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, 95th percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q< 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	A	495/582 (85%)	-0.26	5 (1%) 82 59	14, 29, 57, 111	0
1	B	495/582 (85%)	-0.26	7 (1%) 75 49	14, 33, 65, 112	0
1	C	495/582 (85%)	-0.15	13 (2%) 56 27	15, 38, 70, 114	0
1	D	495/582 (85%)	-0.28	4 (0%) 86 65	11, 29, 64, 108	0
1	E	495/582 (85%)	-0.27	8 (1%) 72 44	13, 29, 62, 107	0
1	F	501/582 (86%)	-0.40	5 (0%) 82 59	12, 26, 59, 106	0
All	All	2976/3492 (85%)	-0.27	42 (1%) 75 49	11, 30, 66, 114	0

All (42) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	2	ASP	6.6
1	E	424	HIS	4.8
1	C	4	GLU	4.8
1	C	3	ARG	4.5
1	A	1	ALA	4.2
1	E	425	GLY	3.9
1	A	3	ARG	3.8
1	F	498	VAL	3.7
1	E	3	ARG	3.5
1	B	1	ALA	3.5
1	B	424	HIS	3.3
1	B	3	ARG	3.3
1	B	425	GLY	3.2
1	A	424	HIS	3.1
1	F	1	ALA	3.1
1	A	2	ASP	3.0
1	C	33	LYS	2.9
1	F	497	GLY	2.9
1	C	334	SER	2.8

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Mol	Chain	Res	Type	RSRZ
1	D	424	HIS	2.8
1	F	429	PRO	2.8
1	C	339	VAL	2.8
1	D	2	ASP	2.7
1	C	32	LEU	2.7
1	C	1	ALA	2.7
1	E	1	ALA	2.6
1	C	303	GLY	2.6
1	E	2	ASP	2.6
1	B	39	GLU	2.5
1	C	364	ASN	2.5
1	E	72	TRP	2.5
1	C	268	ALA	2.4
1	D	281	TRP	2.4
1	A	21	ALA	2.3
1	C	329	LYS	2.3
1	F	496	ALA	2.3
1	C	2	ASP	2.2
1	D	31	ASP	2.2
1	E	426	GLY	2.2
1	C	36	GLU	2.1
1	E	427	THR	2.1
1	B	297	GLN	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](#)

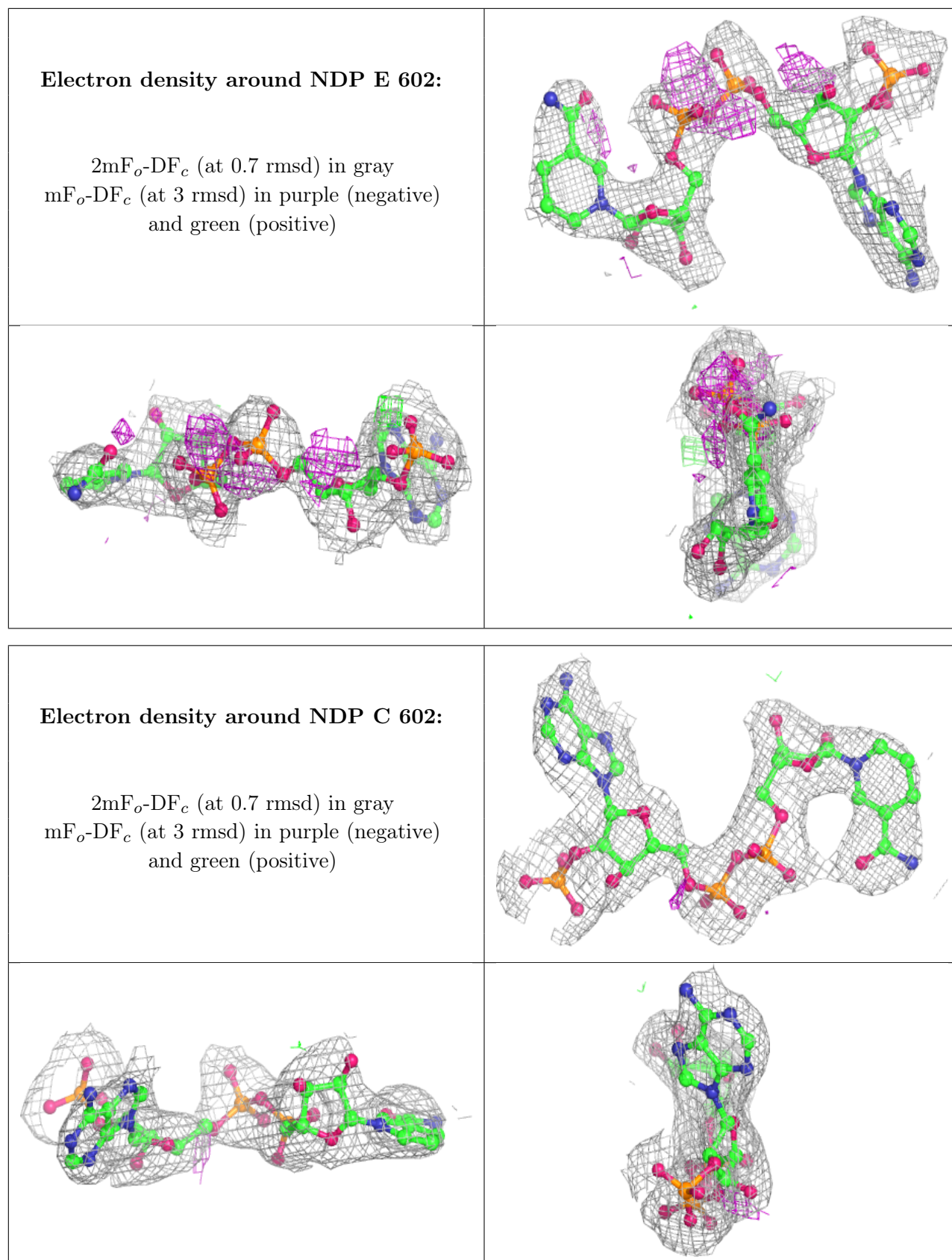
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists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

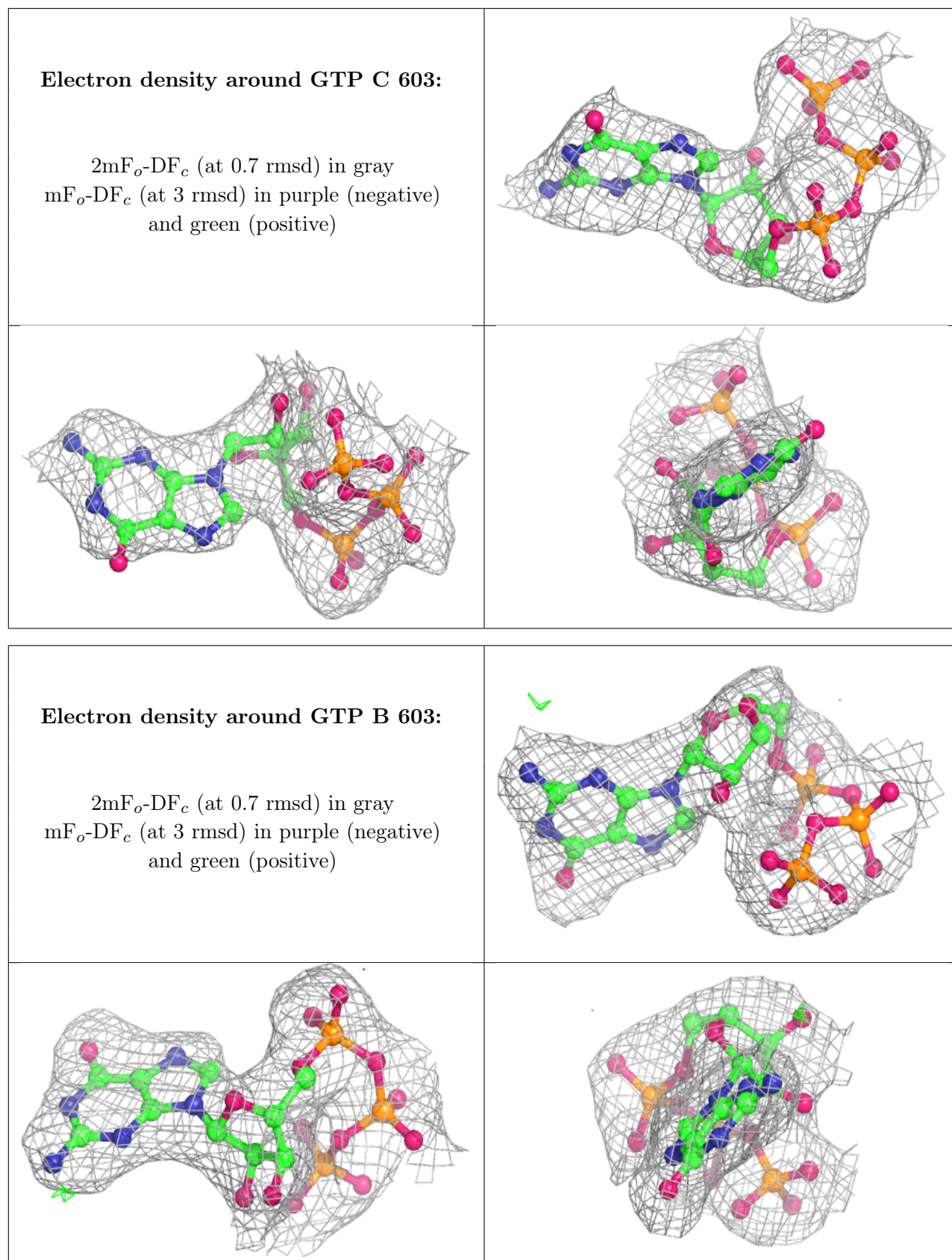
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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
5	ZN	D	604	1/1	0.89	0.08	70,70,70,70	0
5	ZN	B	604	1/1	0.90	0.09	71,71,71,71	0
5	ZN	C	604	1/1	0.91	0.07	62,62,62,62	0
2	GLU	A	601	10/10	0.94	0.15	17,24,27,30	0
2	GLU	E	601	10/10	0.94	0.20	22,31,36,36	0
3	NDP	E	602	48/48	0.94	0.16	22,34,46,54	0
5	ZN	F	601	1/1	0.94	0.05	61,61,61,61	0
2	GLU	B	601	10/10	0.95	0.19	22,27,34,35	0
3	NDP	C	602	48/48	0.95	0.16	26,42,58,62	0
2	GLU	D	601	10/10	0.95	0.19	20,24,26,29	0
4	GTP	C	603	32/32	0.95	0.14	28,41,56,64	0
4	GTP	B	603	32/32	0.96	0.13	27,35,43,47	0
3	NDP	A	602	48/48	0.96	0.17	17,25,32,37	0
4	GTP	E	603	32/32	0.96	0.14	15,21,31,36	0
5	ZN	A	604	1/1	0.96	0.09	57,57,57,57	0
2	GLU	C	601	10/10	0.96	0.16	25,31,36,36	0
2	GLU	F	602	10/10	0.96	0.17	14,20,22,23	0
3	NDP	F	603	48/48	0.96	0.16	13,20,30,33	0
4	GTP	A	603	32/32	0.96	0.15	22,28,34,38	0
5	ZN	A	605	1/1	0.97	0.09	28,28,28,28	0
4	GTP	D	603	32/32	0.97	0.13	19,28,36,37	0
5	ZN	B	605	1/1	0.97	0.13	38,38,38,38	0
3	NDP	D	602	48/48	0.97	0.14	16,25,34,44	0
4	GTP	F	604	32/32	0.97	0.12	17,22,30,35	0
5	ZN	D	605	1/1	0.97	0.13	34,34,34,34	0
5	ZN	E	605	1/1	0.97	0.07	27,27,27,27	0
3	NDP	B	602	48/48	0.97	0.16	23,29,36,40	0
5	ZN	C	605	1/1	0.98	0.16	37,37,37,37	0
5	ZN	F	605	1/1	0.98	0.11	22,22,22,22	0
5	ZN	E	604	1/1	0.99	0.06	58,58,58,58	0

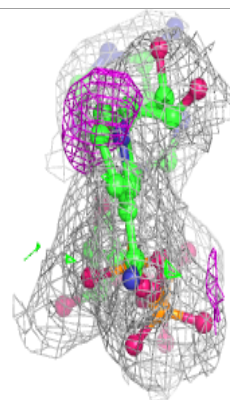
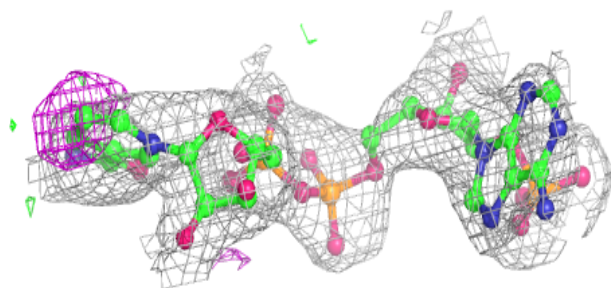
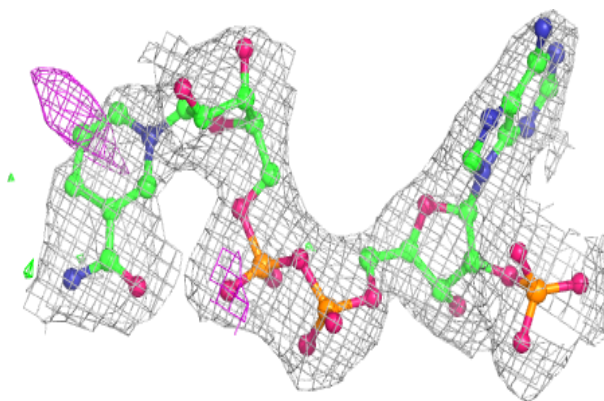
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation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



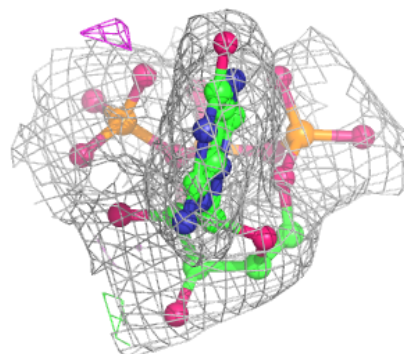
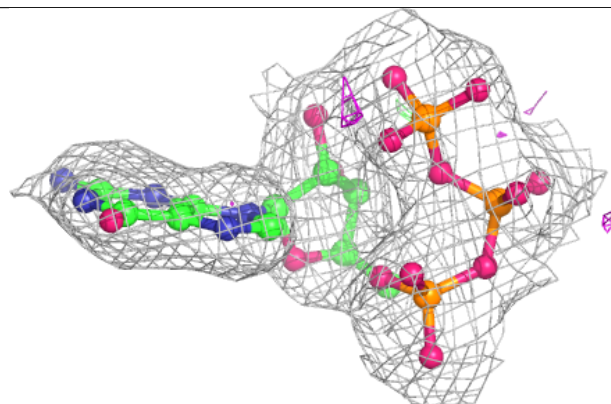
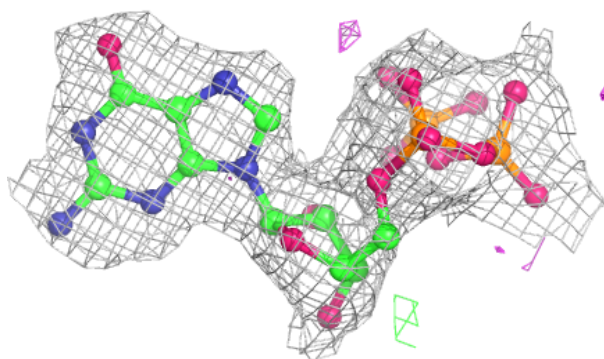


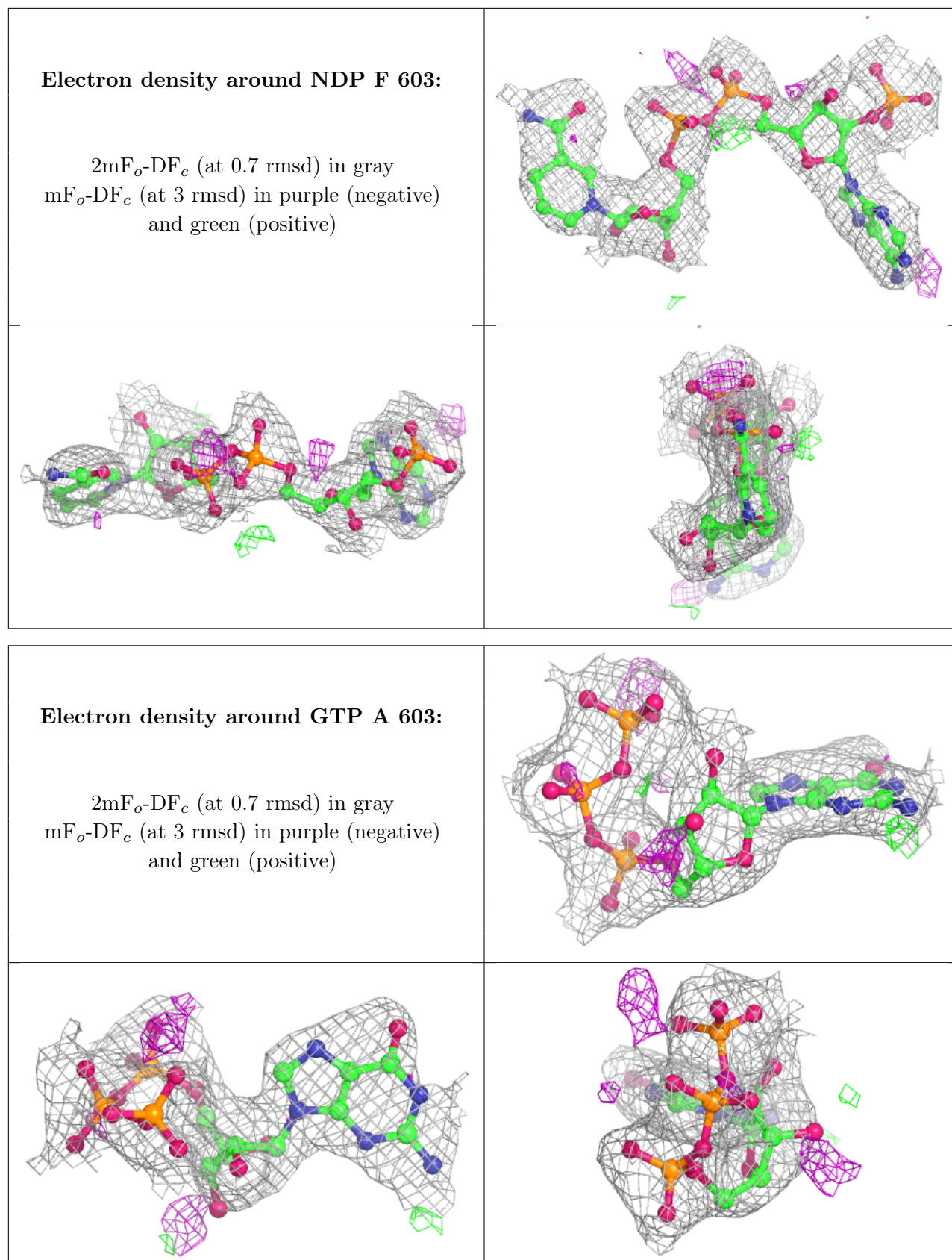
Electron density around NDP A 602:

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

**Electron density around GTP E 603:**

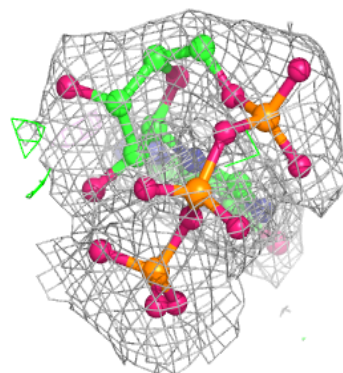
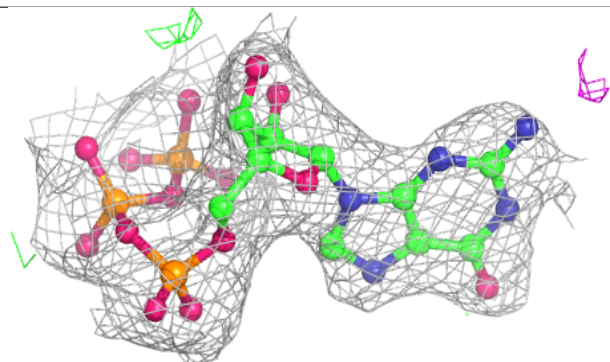
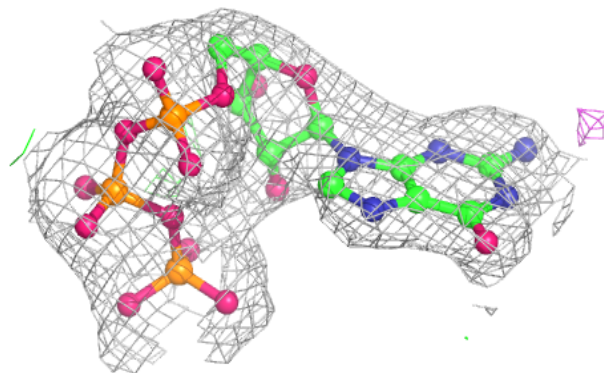
$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



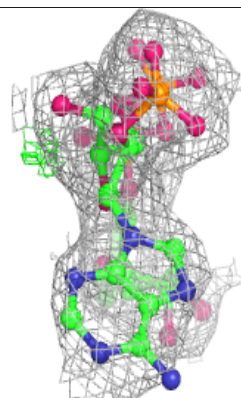
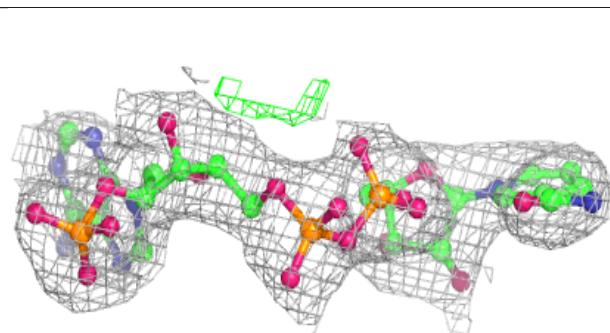
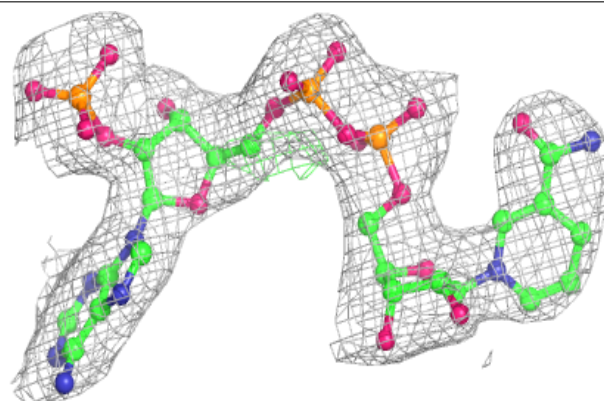


Electron density around GTP D 603:

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

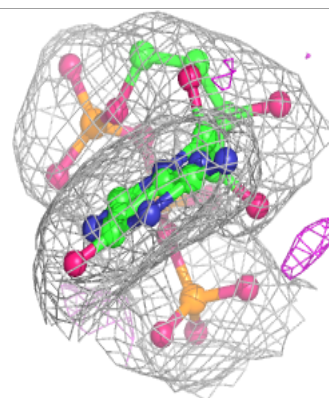
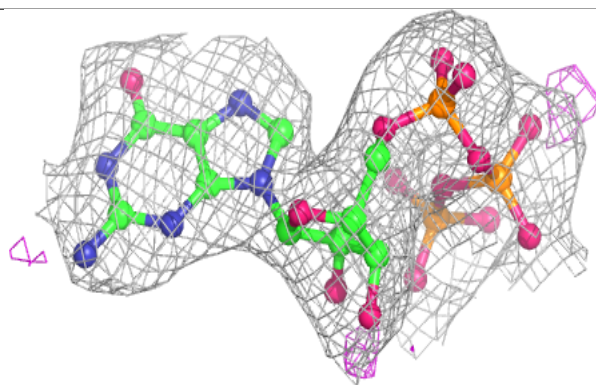
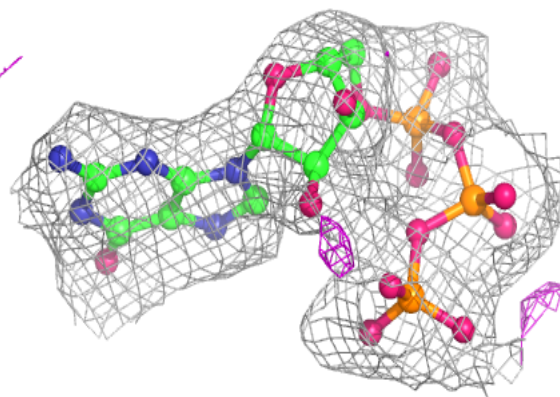
**Electron density around NDP D 602:**

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

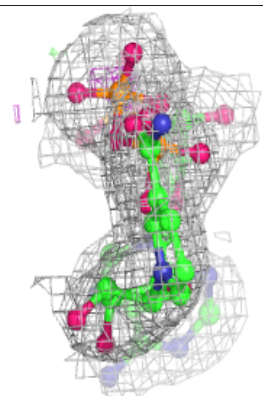
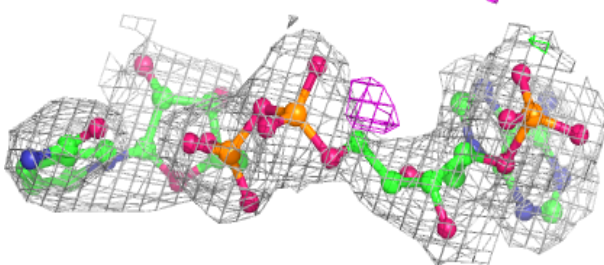
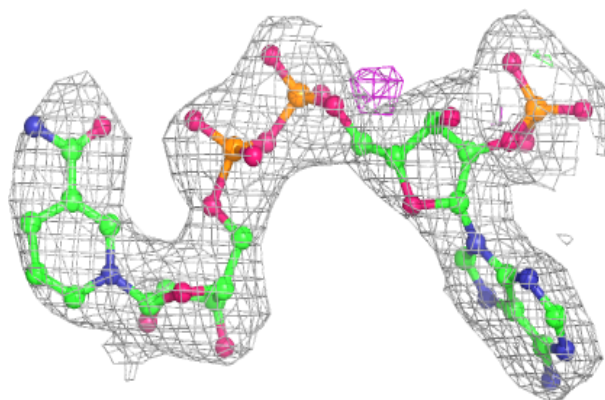


Electron density around GTP F 604:

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

**Electron density around NDP B 602:**

$2mF_o-DF_c$ (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.