



Full wwPDB X-ray Structure Validation Report ⓘ

Jun 3, 2020 – 07:38 am BST

PDB ID : 1R27
Title : Crystal Structure of NarGH complex
Authors : Jormakka, M.; Richardson, D.; Byrne, B.; Iwata, S.
Deposited on : 2003-09-26
Resolution : 2.00 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 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) : **NOT EXECUTED**
EDS : **NOT EXECUTED**
buster-report : 1.1.7 (2018)
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.11

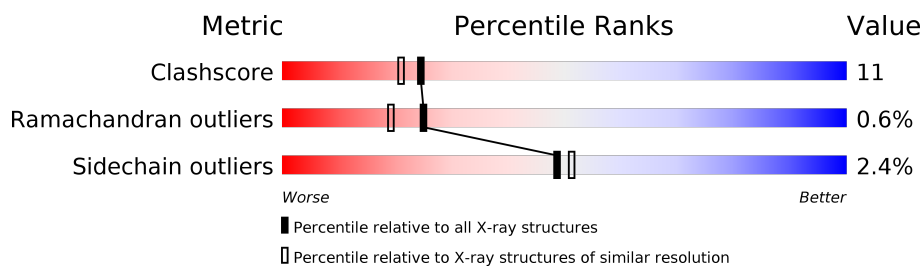
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.00 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))
Clashscore	141614	9178 (2.00-2.00)
Ramachandran outliers	138981	9054 (2.00-2.00)
Sidechain outliers	138945	9053 (2.00-2.00)

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 on the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$.

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	A	1246	
1	C	1246	
2	B	512	
2	D	512	

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
4	SF4	B	5800	-	-	X	-

2 Entry composition

There are 7 unique types of molecules in this entry. The entry contains 29331 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 Respiratory nitrate reductase 1 alpha chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	1218	Total	C	N	O	S	0	0	0
			9660	6100	1691	1821	48			
1	C	1218	Total	C	N	O	S	0	0	0
			9660	6100	1691	1821	48			

- Molecule 2 is a protein called Respiratory nitrate reductase 1 beta chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	465	Total	C	N	O	S	0	0	0
			3711	2354	640	687	30			
2	D	465	Total	C	N	O	S	0	0	0
			3711	2354	640	687	30			

- Molecule 3 is MOLYBDENUM ATOM (three-letter code: MO) (formula: Mo).

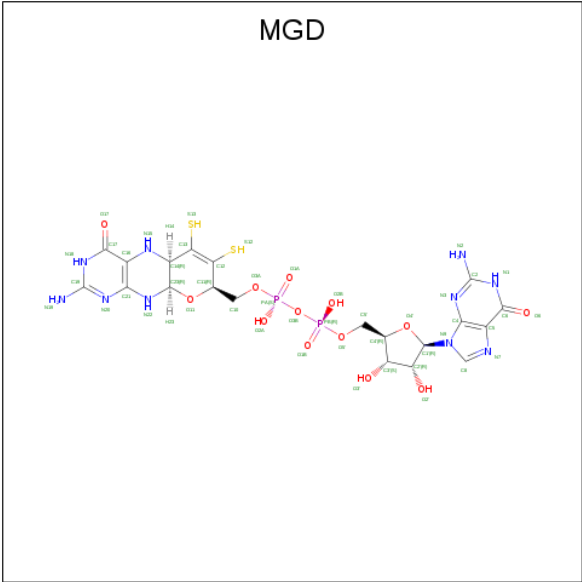
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	1	Total	Mo	0	0
			1	1		
3	C	1	Total	Mo	0	0
			1	1		

- Molecule 4 is IRON/SULFUR CLUSTER (three-letter code: SF4) (formula: Fe₄S₄).



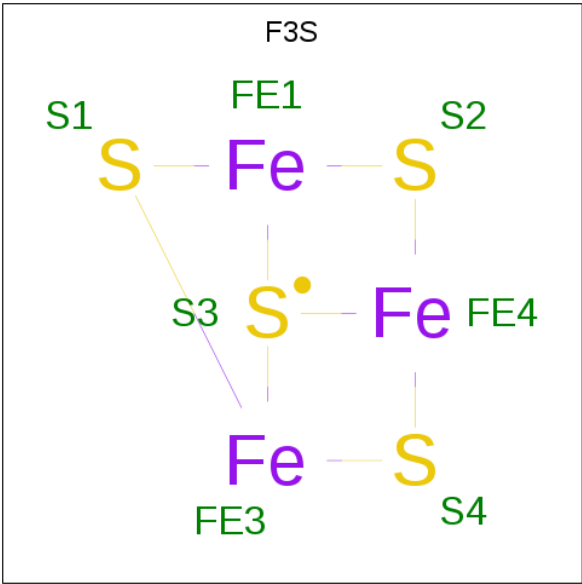
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	A	1	Total	Fe	S	0	0
			8	4	4		
4	B	1	Total	Fe	S	0	0
			8	4	4		
4	B	1	Total	Fe	S	0	0
			8	4	4		
4	B	1	Total	Fe	S	0	0
			8	4	4		
4	C	1	Total	Fe	S	0	0
			8	4	4		
4	D	1	Total	Fe	S	0	0
			8	4	4		
4	D	1	Total	Fe	S	0	0
			8	4	4		

- Molecule 5 is 2-AMINO-5,6-DIMERCAPTO-7-METHYL-3,7,8A,9-TETRAHYDRO-8-OXA-1,3,9,10-TETRAAZA-ANTHRACEN-4-ONE GUANOSINE DINUCLEOTIDE (three-letter code: MGD) (formula: $C_{20}H_{26}N_{10}O_{13}P_2S_2$).



Mol	Chain	Residues	Atoms						ZeroOcc	AltConf
5	A	1	Total	C	N	O	P	S	0	0
			47	20	10	13	2	2		
5	A	1	Total	C	N	O	P	S	0	0
			47	20	10	13	2	2		
5	C	1	Total	C	N	O	P	S	0	0
			47	20	10	13	2	2		
5	C	1	Total	C	N	O	P	S	0	0
			47	20	10	13	2	2		

- Molecule 6 is FE3-S4 CLUSTER (three-letter code: F3S) (formula: Fe₃S₄).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
6	B	1	Total	Fe	S	0	0
			7	3	4		
6	D	1	Total	Fe	S	0	0
			7	3	4		

- Molecule 7 is water.

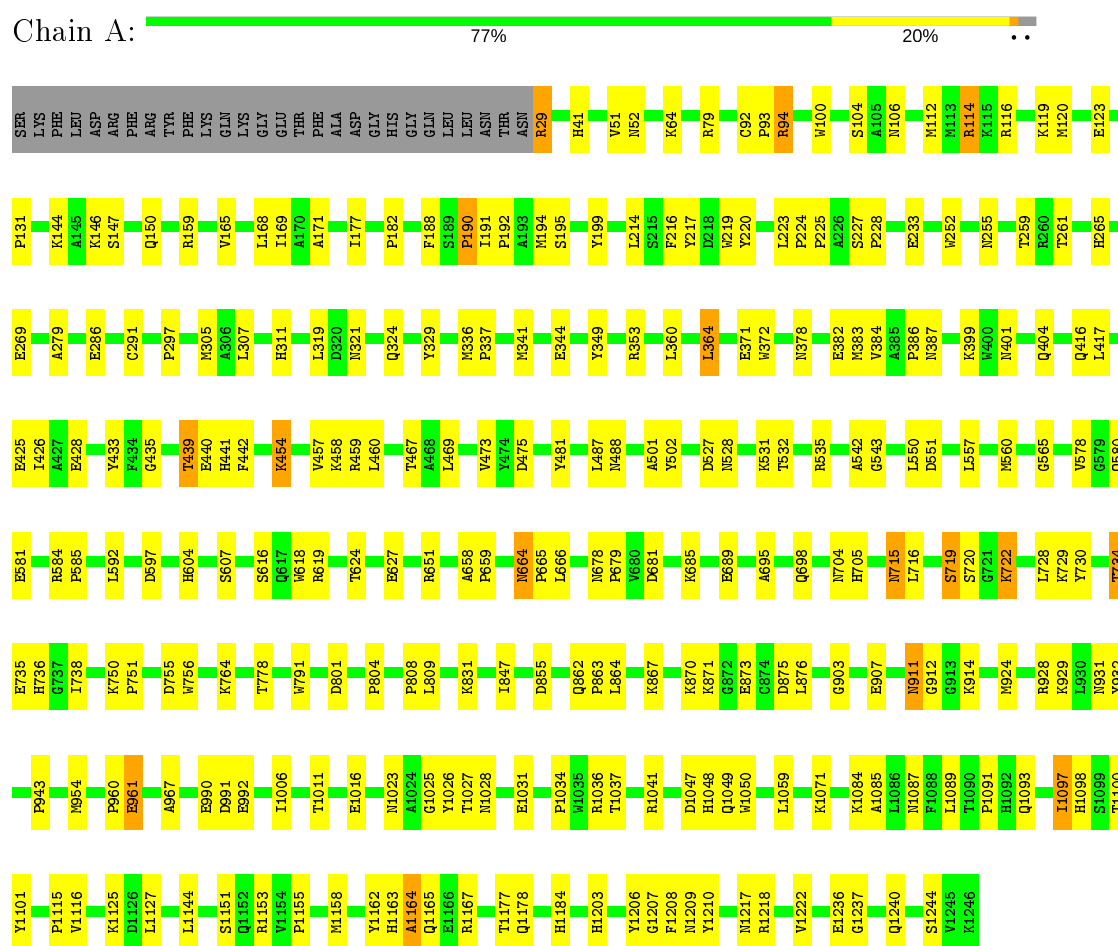
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	A	815	Total	O	0	0
			815	815		
7	B	376	Total	O	0	0
			376	376		
7	C	784	Total	O	0	0
			784	784		
7	D	346	Total	O	0	0
			346	346		

3 Residue-property plots

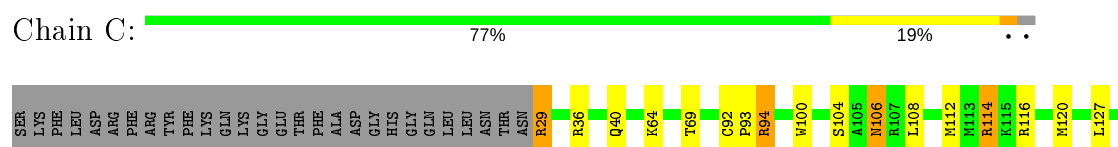
These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry. Residues are color-coded according 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. 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.

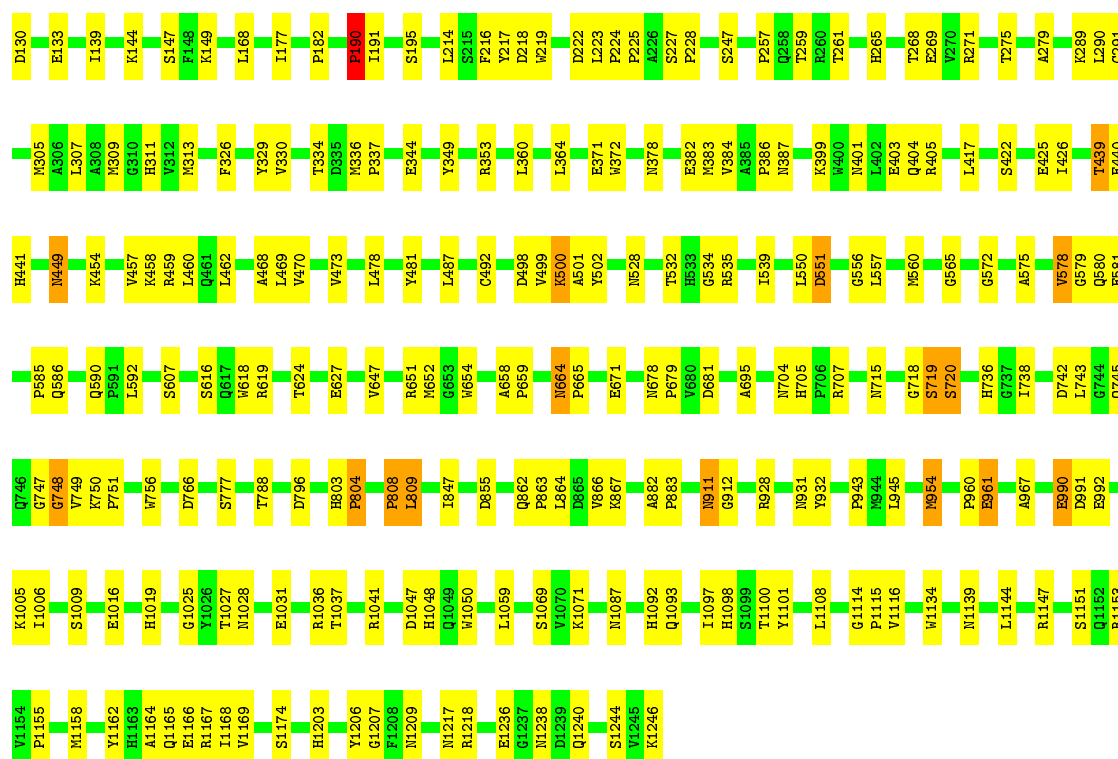
Note EDS was not executed.

- Molecule 1: Respiratory nitrate reductase 1 alpha chain



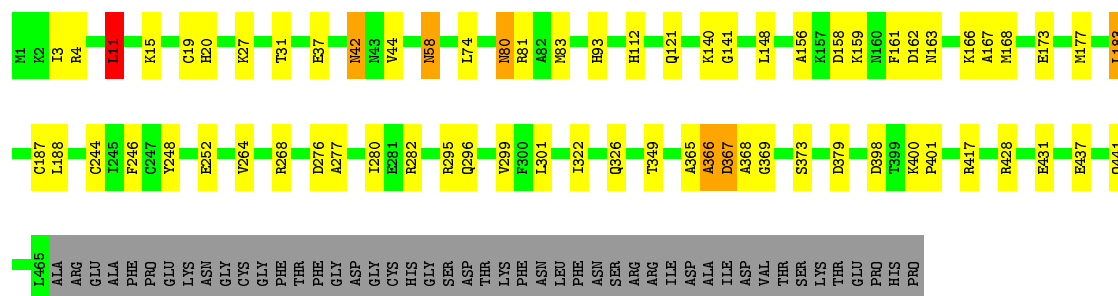
- Molecule 1: Respiratory nitrate reductase 1 alpha chain





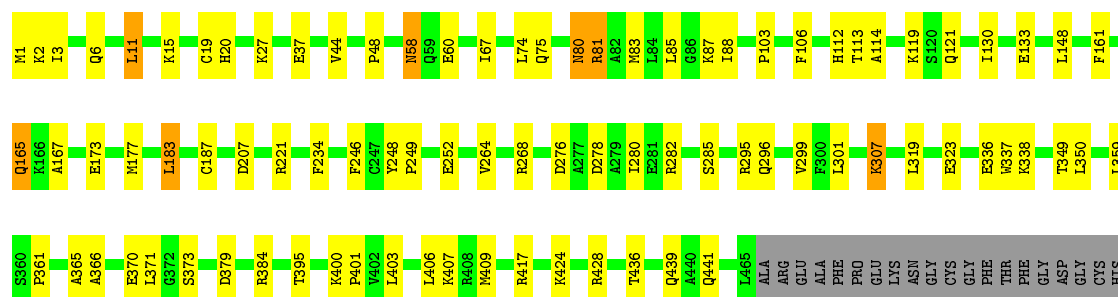
• Molecule 2: Respiratory nitrate reductase 1 beta chain

Chain B: 78% 12% 9%



• Molecule 2: Respiratory nitrate reductase 1 beta chain

Chain D: 74% 16% 9%



GLY
SER
ASP
THR
LYS
PHE
ASN
LEU
PHE
ASN
SER
ARG
ARG
ILE
ASP
ALA
ILE
ASP
VAL
THR
SER
LYS
THR
GLU
PRO
HIS
PRO

4 Data and refinement statistics

Xtriage (Phenix) and EDS were not executed - this section is therefore incomplete.

Property	Value	Source
Space group	I 2 2 2	Depositor
Cell constants a, b, c, α , β , γ	127.40 Å 298.30 Å 296.85 Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	39.86 – 2.00	Depositor
% Data completeness (in resolution range)	88.2 (39.86-2.00)	Depositor
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
Refinement program	CNS 1.1	Depositor
R, R_{free}	0.204 , 0.230	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	29331	wwPDB-VP
Average B, all atoms (Å ²)	32.0	wwPDB-VP

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: SF4, F3S, MO, MGD

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	0.32	0/9914	0.62	2/13462 (0.0%)
1	C	0.32	0/9914	0.61	2/13462 (0.0%)
2	B	0.32	0/3800	0.61	1/5145 (0.0%)
2	D	0.32	0/3800	0.60	0/5145
All	All	0.32	0/27428	0.61	5/37214 (0.0%)

There are no bond length outliers.

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	809	LEU	N-CA-C	-5.66	95.73	111.00
2	B	11	LEU	CA-CB-CG	5.41	127.75	115.30
1	A	1097	ILE	N-CA-C	-5.38	96.47	111.00
1	C	990	GLU	N-CA-C	-5.36	96.54	111.00
1	C	809	LEU	N-CA-C	-5.13	97.15	111.00

There are no chirality outliers.

There are no planarity outliers.

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	9660	0	9330	239	0
1	C	9660	0	9330	227	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	B	3711	0	3659	57	0
2	D	3711	0	3659	74	0
3	A	1	0	0	0	0
3	C	1	0	0	0	0
4	A	8	0	0	0	0
4	B	24	0	0	2	0
4	C	8	0	0	0	0
4	D	24	0	0	1	0
5	A	94	0	44	6	0
5	C	94	0	44	7	0
6	B	7	0	0	0	0
6	D	7	0	0	0	0
7	A	815	0	0	39	0
7	B	376	0	0	8	0
7	C	784	0	0	26	0
7	D	346	0	0	9	0
All	All	29331	0	26066	577	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 11.

All (577) 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:1098:HIS:O	1:A:1164:ALA:HB1	1.50	1.11
1:A:454:LYS:HD3	1:A:487:LEU:HB3	1.40	1.00
1:C:990:GLU:O	1:C:991:ASP:HB2	1.66	0.96
1:C:106:ASN:HD22	2:D:112:HIS:HE1	1.17	0.93
1:A:1164:ALA:HA	7:A:6567:HOH:O	1.69	0.92
1:C:945:LEU:HD21	1:C:954:MET:HE2	1.50	0.91
1:A:457:VAL:HG11	1:A:469:LEU:HB3	1.54	0.90
1:A:439:THR:HG23	1:A:441:HIS:H	1.34	0.90
1:C:961:GLU:HG2	1:C:1006:ILE:HB	1.54	0.88
1:A:862:GLN:HE22	1:A:867:LYS:H	1.23	0.86
1:C:862:GLN:HE22	1:C:867:LYS:H	1.19	0.86
1:C:439:THR:HG22	1:C:441:HIS:H	1.42	0.85
1:C:112:MET:HG3	7:D:8136:HOH:O	1.75	0.85
1:A:990:GLU:O	1:A:991:ASP:HB2	1.76	0.84
1:A:106:ASN:HD22	2:B:112:HIS:HE1	1.23	0.84
1:C:532:THR:HB	1:C:535:ARG:NH1	1.93	0.83
1:A:592:LEU:HD13	1:A:954:MET:CE	2.11	0.81

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:454:LYS:HD3	1:A:487:LEU:CB	2.10	0.81
1:C:705:HIS:CE1	1:C:707:ARG:HH12	1.99	0.80
2:D:165:GLN:H	2:D:165:GLN:CD	1.81	0.79
1:C:592:LEU:HD13	1:C:954:MET:CE	2.13	0.78
2:D:307:LYS:HE2	2:D:307:LYS:HA	1.65	0.78
1:C:378:ASN:ND2	1:C:382:GLU:HB2	1.99	0.78
1:A:592:LEU:HB2	1:A:954:MET:CE	2.14	0.78
1:C:1217:ASN:HD21	1:C:1218:ARG:HE	1.28	0.77
1:A:1098:HIS:C	1:A:1164:ALA:HB1	2.05	0.76
1:A:1163:HIS:O	1:A:1164:ALA:CB	2.33	0.76
1:C:592:LEU:HD13	1:C:954:MET:HE1	1.67	0.75
1:A:1151:SER:OG	1:A:1153:ARG:HG2	1.87	0.75
1:C:457:VAL:HG11	1:C:469:LEU:HB3	1.66	0.74
1:A:592:LEU:HB2	1:A:954:MET:HE3	1.70	0.74
1:A:216:PHE:H	1:A:1209:ASN:HD21	1.34	0.74
1:A:106:ASN:ND2	2:B:112:HIS:HE1	1.86	0.74
1:C:106:ASN:ND2	2:D:112:HIS:HE1	1.86	0.74
1:A:255:ASN:HB2	7:A:6615:HOH:O	1.87	0.73
1:C:114:ARG:HD3	7:C:7919:HOH:O	1.89	0.73
1:A:227:SER:HB3	1:A:228:PRO:HD3	1.70	0.73
1:A:1098:HIS:O	1:A:1164:ALA:CB	2.34	0.73
1:C:139:ILE:HD11	7:C:8591:HOH:O	1.89	0.73
1:C:557:LEU:HA	1:C:560:MET:HE3	1.71	0.72
1:A:1116:VAL:H	1:A:1165:GLN:HE22	1.37	0.72
1:A:1217:ASN:HD21	1:A:1218:ARG:HE	1.33	0.72
1:C:1006:ILE:HD12	1:C:1016:GLU:HG3	1.72	0.71
1:C:855:ASP:OD1	1:C:1036:ARG:HD2	1.90	0.71
1:C:404:GLN:HE22	1:C:1041:ARG:HH22	1.36	0.71
1:A:1163:HIS:O	1:A:1164:ALA:HB3	1.91	0.70
1:C:378:ASN:HD21	1:C:382:GLU:HB2	1.53	0.70
2:D:11:LEU:HD13	2:D:268:ARG:HG2	1.72	0.70
1:A:116:ARG:HD2	1:A:120:MET:HE2	1.74	0.69
1:C:736:HIS:HD2	1:C:738:ILE:H	1.39	0.69
1:C:1116:VAL:H	1:C:1165:GLN:HE22	1.40	0.69
2:D:3:ILE:HD12	2:D:301:LEU:HD12	1.74	0.69
2:B:27:LYS:HE3	2:B:31:THR:OG1	1.93	0.69
1:A:651:ARG:CZ	1:A:870:LYS:HD3	2.22	0.69
1:A:1025:GLY:HA2	1:A:1028:ASN:HD22	1.58	0.68
1:C:383:MET:HE1	1:C:460:LEU:HD13	1.74	0.68
1:C:387:ASN:HD21	1:C:399:LYS:HE3	1.57	0.68
1:A:1006:ILE:HD12	1:A:1016:GLU:HG3	1.75	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:282:ARG:HG3	2:B:295:ARG:HH22	1.59	0.67
2:D:296:GLN:O	2:D:299:VAL:HG22	1.95	0.67
2:B:400:LYS:HB2	2:B:400:LYS:NZ	2.09	0.67
7:A:6542:HOH:O	2:D:428:ARG:HB2	1.93	0.67
1:A:404:GLN:HE22	1:A:1041:ARG:HH22	1.42	0.66
1:C:144:LYS:O	1:C:147:SER:HB3	1.94	0.66
1:C:190:PRO:HB2	1:C:191:ILE:HD12	1.77	0.66
1:C:191:ILE:H	1:C:191:ILE:HD12	1.61	0.66
2:B:373:SER:O	2:B:428:ARG:NH2	2.29	0.65
1:C:1244:SER:OG	1:C:1246:LYS:HE3	1.95	0.65
1:C:616:SER:HB3	1:C:619:ARG:HD3	1.77	0.65
1:A:79:ARG:CZ	7:A:6576:HOH:O	2.43	0.65
1:C:227:SER:HB3	1:C:228:PRO:HD3	1.79	0.65
1:C:439:THR:CG2	1:C:441:HIS:H	2.07	0.65
1:A:265:HIS:HD2	1:A:269:GLU:OE1	1.81	0.64
1:C:353:ARG:CZ	1:C:864:LEU:HD22	2.27	0.64
1:A:664:ASN:C	1:A:664:ASN:HD22	2.00	0.63
1:A:592:LEU:HD13	1:A:954:MET:HE2	1.80	0.63
1:A:664:ASN:ND2	1:A:666:LEU:H	1.97	0.63
1:C:454:LYS:HD2	7:C:8414:HOH:O	1.98	0.63
1:A:855:ASP:OD1	1:A:1036:ARG:HD2	1.98	0.63
1:A:378:ASN:HD21	1:A:382:GLU:HB2	1.64	0.62
1:A:592:LEU:HD13	1:A:954:MET:HE1	1.80	0.62
1:A:1162:TYR:HE1	7:A:6577:HOH:O	1.80	0.62
1:C:961:GLU:HB3	7:C:7809:HOH:O	1.98	0.62
2:D:400:LYS:HB3	2:D:401:PRO:HD3	1.81	0.62
1:A:29:ARG:HG3	7:A:6150:HOH:O	1.99	0.62
1:C:945:LEU:CD2	1:C:954:MET:HE2	2.25	0.62
1:A:191:ILE:HD13	1:A:216:PHE:CE1	2.35	0.62
1:A:750:LYS:HD2	1:A:756:TRP:CG	2.35	0.62
1:C:216:PHE:H	1:C:1209:ASN:HD21	1.46	0.62
2:D:133:GLU:HG2	7:D:8129:HOH:O	1.99	0.62
1:A:1236:GLU:HG2	7:A:6619:HOH:O	1.99	0.62
1:C:191:ILE:HD12	1:C:191:ILE:N	2.14	0.62
1:C:750:LYS:HD2	1:C:756:TRP:CG	2.35	0.62
2:D:15:LYS:HE2	7:D:7864:HOH:O	1.99	0.61
2:D:80:ASN:ND2	2:D:83:MET:H	1.98	0.61
1:A:220:TYR:HE1	1:A:720:SER:HG	1.48	0.61
2:D:173:GLU:H	2:D:173:GLU:CD	2.04	0.61
1:A:459:ARG:HD3	7:D:8138:HOH:O	1.99	0.61
2:B:365:ALA:O	2:B:366:ALA:HB3	2.00	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:705:HIS:NE2	1:C:707:ARG:NH1	2.49	0.61
1:A:92:CYS:SG	1:A:94:ARG:HD2	2.41	0.61
1:C:265:HIS:HD2	1:C:269:GLU:OE1	1.82	0.61
1:C:337:PRO:HG3	1:C:417:LEU:HD23	1.82	0.61
1:A:454:LYS:HB3	1:A:487:LEU:CD1	2.31	0.61
1:C:426:ILE:HD13	1:C:487:LEU:HD13	1.83	0.61
1:C:747:GLY:O	1:C:748:GLY:O	2.18	0.60
1:A:928:ARG:HG2	1:A:943:PRO:HG3	1.83	0.60
1:C:108:LEU:HD22	7:C:8586:HOH:O	2.00	0.60
2:D:319:LEU:O	2:D:323:GLU:HG3	2.02	0.60
1:A:871:LYS:HE2	1:A:873:GLU:OE2	2.02	0.59
1:C:329:TYR:CE2	1:C:565:GLY:HA2	2.36	0.59
1:C:578:VAL:HG23	1:C:579:GLY:H	1.67	0.59
1:C:1151:SER:OG	1:C:1153:ARG:HG2	2.02	0.59
7:C:8546:HOH:O	2:D:409:MET:HE3	2.02	0.59
2:D:58:ASN:HD21	2:D:60:GLU:HB2	1.68	0.59
1:A:722:LYS:H	1:A:722:LYS:HD2	1.66	0.59
1:A:1098:HIS:C	1:A:1164:ALA:CB	2.70	0.59
1:A:144:LYS:O	1:A:147:SER:HB3	2.03	0.59
2:B:173:GLU:H	2:B:173:GLU:CD	2.06	0.59
2:D:365:ALA:O	2:D:366:ALA:HB3	2.03	0.59
1:A:1116:VAL:H	1:A:1165:GLN:NE2	2.00	0.59
1:A:716:LEU:HA	1:A:720:SER:HB3	1.84	0.59
1:C:1025:GLY:HA2	1:C:1028:ASN:HD22	1.68	0.58
1:C:307:LEU:HD21	1:C:1059:LEU:HG	1.85	0.58
1:C:557:LEU:HA	1:C:560:MET:CE	2.33	0.58
2:D:20:HIS:CE1	2:D:44:VAL:HB	2.38	0.58
2:B:296:GLN:O	2:B:299:VAL:HG22	2.02	0.58
1:A:457:VAL:CG1	1:A:469:LEU:HB3	2.31	0.58
1:A:399:LYS:HE2	7:A:6265:HOH:O	2.03	0.58
2:B:80:ASN:ND2	2:B:83:MET:H	2.01	0.58
1:A:371:GLU:N	1:A:371:GLU:OE1	2.30	0.58
1:C:705:HIS:CE1	1:C:707:ARG:NH1	2.71	0.58
1:A:532:THR:HB	1:A:535:ARG:NH1	2.19	0.58
1:A:1093:GLN:HE21	1:A:1164:ALA:HB3	1.68	0.58
1:A:550:LEU:H	1:A:550:LEU:HD23	1.69	0.58
1:C:647:VAL:O	1:C:651:ARG:HG3	2.04	0.58
1:C:1240:GLN:HG3	7:C:8147:HOH:O	2.03	0.58
1:C:862:GLN:HE22	1:C:867:LYS:N	1.97	0.58
1:A:592:LEU:HB2	1:A:954:MET:HE1	1.84	0.57
2:D:67:ILE:HD12	2:D:67:ILE:O	2.04	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:931:ASN:O	1:A:932:TYR:HB2	2.04	0.57
1:C:449:ASN:HD22	1:C:449:ASN:N	2.01	0.57
1:A:1098:HIS:CE1	5:A:5802:MGD:S13	2.97	0.57
1:A:439:THR:CG2	1:A:441:HIS:H	2.13	0.57
1:A:114:ARG:HD3	7:A:5918:HOH:O	2.04	0.57
1:C:931:ASN:O	1:C:932:TYR:HB2	2.04	0.57
1:A:216:PHE:H	1:A:1209:ASN:ND2	2.03	0.57
1:C:92:CYS:HB2	1:C:93:PRO:HD2	1.86	0.57
1:A:557:LEU:HA	1:A:560:MET:HE3	1.86	0.56
1:A:225:PRO:HB2	7:A:6096:HOH:O	2.04	0.56
1:A:378:ASN:ND2	1:A:382:GLU:HB2	2.20	0.56
1:A:961:GLU:OE1	1:A:961:GLU:N	2.31	0.56
1:A:736:HIS:HD2	1:A:738:ILE:H	1.53	0.56
2:B:248:TYR:O	2:B:252:GLU:HG3	2.04	0.56
1:C:130:ASP:HB3	1:C:133:GLU:HG2	1.87	0.56
1:C:223:LEU:O	1:C:225:PRO:HD3	2.05	0.56
1:C:225:PRO:HB2	7:C:8543:HOH:O	2.04	0.56
1:C:279:ALA:HB2	1:C:291:CYS:SG	2.45	0.56
1:A:584:ARG:O	1:A:961:GLU:OE2	2.23	0.56
1:C:592:LEU:HD13	1:C:954:MET:HE3	1.86	0.56
1:A:616:SER:HB3	1:A:619:ARG:HD3	1.87	0.56
1:C:460:LEU:HD11	1:C:470:VAL:HG21	1.88	0.56
1:A:1093:GLN:HE21	1:A:1164:ALA:CB	2.19	0.55
2:B:3:ILE:HD12	2:B:301:LEU:CD1	2.35	0.55
1:C:92:CYS:SG	1:C:94:ARG:HD2	2.45	0.55
2:D:336:GLU:HG2	2:D:337:TRP:CD1	2.40	0.55
1:C:336:MET:HA	1:C:473:VAL:HB	1.88	0.55
2:D:3:ILE:HD12	2:D:301:LEU:CD1	2.36	0.55
1:A:353:ARG:HA	1:A:1047:ASP:HB2	1.86	0.55
1:C:652:MET:HE1	1:C:654:TRP:CZ2	2.41	0.55
1:C:1167:ARG:HD3	2:D:121:GLN:HE22	1.69	0.55
1:A:371:GLU:HG2	1:A:372:TRP:CD1	2.42	0.55
1:A:624:THR:O	1:A:627:GLU:HG2	2.06	0.55
1:C:344:GLU:HG3	1:C:349:TYR:CE1	2.42	0.55
1:A:425:GLU:OE1	1:A:459:ARG:NE	2.40	0.55
1:A:454:LYS:HB3	1:A:487:LEU:HD12	1.88	0.55
1:C:130:ASP:HB3	1:C:133:GLU:CG	2.36	0.55
1:A:191:ILE:HG23	1:A:580:GLN:O	2.07	0.54
2:B:20:HIS:CE1	2:B:44:VAL:HB	2.42	0.54
1:C:679:PRO:HB3	1:C:847:ILE:HD11	1.89	0.54
2:B:365:ALA:O	2:B:366:ALA:CB	2.56	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:1069:SER:O	1:C:1139:ASN:HB2	2.08	0.54
1:C:550:LEU:H	1:C:550:LEU:HD23	1.73	0.54
1:A:383:MET:HE3	1:A:460:LEU:HD21	1.89	0.54
1:C:106:ASN:ND2	2:D:112:HIS:CE1	2.74	0.54
1:C:422:SER:O	1:C:458:LYS:HE2	2.07	0.54
1:A:679:PRO:HB3	1:A:847:ILE:HD11	1.89	0.54
2:B:19:CYS:O	2:B:20:HIS:HB2	2.07	0.54
1:A:383:MET:HE3	1:A:460:LEU:CD2	2.38	0.54
1:A:51:VAL:HB	1:A:791:TRP:CH2	2.42	0.54
2:D:248:TYR:O	2:D:252:GLU:HG3	2.08	0.54
1:A:428:GLU:HB3	7:A:6540:HOH:O	2.08	0.54
1:A:439:THR:HG22	1:A:442:PHE:HD1	1.72	0.54
1:A:907:GLU:HG3	1:A:924:MET:HG3	1.89	0.54
2:D:282:ARG:HG2	2:D:295:ARG:HH22	1.72	0.53
2:D:58:ASN:HD22	2:D:58:ASN:C	2.09	0.53
1:A:664:ASN:HD22	1:A:666:LEU:H	1.56	0.53
2:D:280:ILE:HG23	2:D:350:LEU:HD22	1.88	0.53
1:C:1115:PRO:HA	1:C:1165:GLN:NE2	2.23	0.53
1:C:551:ASP:N	1:C:551:ASP:OD2	2.42	0.53
1:A:321:ASN:HB3	7:A:6288:HOH:O	2.06	0.53
2:B:159:LYS:HE2	2:B:162:ASP:OD2	2.08	0.53
1:C:796:ASP:HB3	1:C:809:LEU:HD13	1.89	0.53
1:A:116:ARG:HD2	1:A:120:MET:CE	2.39	0.53
1:A:439:THR:HG21	7:A:6392:HOH:O	2.09	0.53
1:C:1098:HIS:C	1:C:1164:ALA:HB3	2.28	0.53
1:C:961:GLU:HG2	1:C:961:GLU:O	2.08	0.53
1:C:551:ASP:HB3	7:C:8543:HOH:O	2.09	0.52
2:D:80:ASN:C	2:D:80:ASN:HD22	2.12	0.52
2:D:85:LEU:HD23	2:D:88:ILE:HD11	1.90	0.52
1:C:311:HIS:HD2	1:C:481:TYR:O	1.92	0.52
1:A:94:ARG:HD3	1:A:1097:ILE:HD11	1.90	0.52
1:C:454:LYS:HG3	1:C:487:LEU:HD12	1.92	0.52
1:C:928:ARG:HG2	1:C:943:PRO:HG3	1.91	0.52
1:C:1144:LEU:C	1:C:1144:LEU:HD12	2.30	0.52
1:A:557:LEU:HA	1:A:560:MET:CE	2.39	0.52
2:B:74:LEU:HD12	7:B:5944:HOH:O	2.10	0.52
1:C:457:VAL:CG1	1:C:469:LEU:HB3	2.37	0.52
1:A:265:HIS:HE1	7:A:5813:HOH:O	1.92	0.52
1:A:165:VAL:O	1:A:169:ILE:HG13	2.10	0.52
2:B:80:ASN:C	2:B:80:ASN:HD22	2.13	0.52
1:C:664:ASN:C	1:C:664:ASN:HD22	2.12	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:D:83:MET:O	2:D:87:LYS:HG3	2.10	0.51
1:A:454:LYS:HE3	1:A:488:ASN:H	1.75	0.51
1:A:428:GLU:HG2	7:A:6056:HOH:O	2.10	0.51
2:B:27:LYS:CE	2:B:31:THR:OG1	2.59	0.51
1:A:454:LYS:CD	1:A:487:LEU:HB3	2.27	0.51
1:C:257:PRO:HG3	1:C:290:LEU:HD12	1.93	0.51
1:C:862:GLN:NE2	1:C:866:VAL:HA	2.25	0.51
1:A:146:LYS:HE3	1:A:150:GLN:OE1	2.10	0.51
1:C:911:ASN:ND2	1:C:912:GLY:H	2.08	0.51
1:C:1097:ILE:O	1:C:1098:HIS:HB2	2.11	0.51
1:C:578:VAL:HG23	1:C:579:GLY:N	2.26	0.51
1:C:326:PHE:O	1:C:330:VAL:HG22	2.11	0.51
2:D:74:LEU:HG	2:D:285:SER:HB3	1.93	0.51
1:A:1048:HIS:CD2	1:A:1050:TRP:H	2.29	0.51
1:A:384:VAL:O	1:A:386:PRO:HD3	2.11	0.51
1:C:190:PRO:HB2	1:C:191:ILE:CD1	2.39	0.51
1:A:168:LEU:C	1:A:168:LEU:HD23	2.32	0.50
2:B:400:LYS:HB3	2:B:401:PRO:HD3	1.92	0.50
1:A:112:MET:HE2	1:A:159:ARG:HA	1.93	0.50
1:A:217:TYR:H	1:A:1209:ASN:ND2	2.10	0.50
1:A:550:LEU:N	1:A:550:LEU:HD23	2.26	0.50
1:C:191:ILE:O	1:C:191:ILE:HG22	2.10	0.50
1:C:216:PHE:H	1:C:1209:ASN:ND2	2.08	0.50
2:D:395:THR:HG21	2:D:401:PRO:HB2	1.93	0.50
1:A:311:HIS:HD2	1:A:481:TYR:O	1.94	0.50
1:A:467:THR:HG21	7:D:8138:HOH:O	2.10	0.50
1:C:1100:THR:O	1:C:1101:TYR:HB2	2.12	0.50
1:C:371:GLU:HG2	1:C:372:TRP:CD1	2.47	0.50
1:C:498:ASP:OD2	1:C:500:LYS:HD3	2.11	0.50
1:A:1240:GLN:HG3	7:A:6608:HOH:O	2.12	0.50
2:B:93:HIS:HD2	7:B:5930:HOH:O	1.95	0.50
1:C:1217:ASN:ND2	1:C:1218:ARG:HE	2.02	0.50
1:C:803:HIS:HB2	1:C:804:PRO:HD2	1.94	0.50
2:D:1:MET:HB2	2:D:276:ASP:OD1	2.11	0.50
7:A:6103:HOH:O	2:D:424:LYS:HE2	2.12	0.50
1:A:1178:GLN:HG3	7:A:6574:HOH:O	2.12	0.50
1:C:528:ASN:HD22	2:D:417:ARG:NH2	2.10	0.50
1:A:1125:LYS:NZ	1:A:1125:LYS:HB2	2.27	0.49
1:A:92:CYS:HB2	1:A:93:PRO:HD2	1.94	0.49
1:C:330:VAL:HA	1:C:334:THR:HG23	1.93	0.49
1:A:146:LYS:O	1:A:150:GLN:HG3	2.12	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:870:LYS:HE3	7:A:6267:HOH:O	2.11	0.49
1:A:79:ARG:NE	7:A:6576:HOH:O	2.45	0.49
1:C:1027:THR:O	1:C:1031:GLU:HB2	2.10	0.49
1:C:749:VAL:HG13	1:C:749:VAL:O	2.11	0.49
1:A:255:ASN:CB	7:A:6615:HOH:O	2.52	0.49
1:A:457:VAL:CG1	1:A:458:LYS:N	2.74	0.49
1:A:719:SER:HB3	7:A:5995:HOH:O	2.11	0.49
1:C:36:ARG:O	1:C:40:GLN:HG3	2.11	0.49
1:C:528:ASN:HD22	2:D:417:ARG:HH22	1.59	0.49
1:A:960:PRO:HG2	1:A:961:GLU:OE1	2.12	0.49
1:A:1167:ARG:HD3	2:B:121:GLN:HE22	1.77	0.49
1:C:678:ASN:ND2	1:C:681:ASP:OD2	2.44	0.49
1:C:882:ALA:HB1	1:C:883:PRO:HD2	1.93	0.49
1:C:94:ARG:HD3	1:C:1097:ILE:HD11	1.95	0.49
1:C:457:VAL:CG1	1:C:458:LYS:N	2.75	0.49
1:A:119:LYS:O	1:A:123:GLU:HG3	2.12	0.49
2:B:246:PHE:HA	4:B:5800:SF4:S1	2.53	0.49
1:C:29:ARG:HD3	7:C:8196:HOH:O	2.12	0.49
1:C:384:VAL:O	1:C:386:PRO:HD3	2.13	0.49
1:A:106:ASN:HD22	2:B:112:HIS:CE1	2.15	0.49
1:A:29:ARG:HB3	7:A:6191:HOH:O	2.13	0.49
1:A:261:THR:HG22	2:B:264:VAL:HG11	1.94	0.49
2:D:67:ILE:HD12	2:D:67:ILE:C	2.33	0.49
1:A:131:PRO:HB2	1:A:171:ALA:HB2	1.95	0.48
1:A:341:MET:HE3	7:A:6427:HOH:O	2.13	0.48
2:B:156:ALA:HB1	2:B:166:LYS:HD2	1.95	0.48
2:B:400:LYS:HB2	2:B:400:LYS:HZ3	1.77	0.48
1:C:1116:VAL:H	1:C:1165:GLN:NE2	2.10	0.48
1:A:94:ARG:HB3	1:A:1101:TYR:CD2	2.48	0.48
1:C:862:GLN:NE2	1:C:867:LYS:H	2.00	0.48
1:A:542:ALA:HB3	5:A:5802:MGD:O3B	2.13	0.48
1:C:387:ASN:ND2	1:C:399:LYS:HE3	2.25	0.48
2:B:4:ARG:HG3	2:B:277:ALA:HB2	1.95	0.48
1:C:961:GLU:CG	1:C:1006:ILE:HB	2.37	0.48
1:A:1206:TYR:CG	1:A:1207:GLY:N	2.82	0.48
1:A:383:MET:HE1	1:A:460:LEU:HD11	1.96	0.48
1:C:550:LEU:N	1:C:550:LEU:HD23	2.29	0.48
1:C:1167:ARG:CD	2:D:121:GLN:HE22	2.27	0.48
2:D:2:LYS:HE3	7:D:8148:HOH:O	2.14	0.48
1:A:214:LEU:HB3	1:A:607:SER:OG	2.13	0.48
1:A:52:ASN:CG	1:A:191:ILE:HG13	2.34	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:383:MET:HE1	1:A:460:LEU:CD1	2.43	0.48
1:C:1206:TYR:CG	1:C:1207:GLY:N	2.81	0.48
1:C:265:HIS:HE1	7:C:7811:HOH:O	1.97	0.48
1:C:353:ARG:NE	1:C:864:LEU:HD22	2.28	0.48
2:B:168:MET:HE3	7:B:6005:HOH:O	2.13	0.48
2:B:11:LEU:HD13	2:B:268:ARG:HG2	1.96	0.48
1:C:305:MET:O	1:C:309:MET:HG3	2.13	0.48
1:C:457:VAL:HG12	1:C:458:LYS:N	2.29	0.48
1:A:191:ILE:HG21	1:A:580:GLN:HB3	1.96	0.48
1:A:279:ALA:HB2	1:A:291:CYS:SG	2.54	0.48
1:C:1093:GLN:HB3	1:C:1162:TYR:HB3	1.96	0.48
7:C:8546:HOH:O	2:D:409:MET:HG2	2.14	0.47
1:A:116:ARG:NH1	1:A:147:SER:OG	2.47	0.47
2:B:322:ILE:O	2:B:326:GLN:HG3	2.14	0.47
1:C:652:MET:CE	1:C:866:VAL:HG13	2.44	0.47
1:C:1037:THR:HA	1:C:1203:HIS:HB3	1.96	0.47
1:A:29:ARG:HB2	7:B:5940:HOH:O	2.14	0.47
1:C:265:HIS:CD2	1:C:269:GLU:OE1	2.66	0.47
1:A:1155:PRO:HG2	1:A:1158:MET:HG2	1.97	0.47
1:A:715:ASN:HD21	1:A:778:THR:H	1.61	0.47
1:C:309:MET:O	1:C:313:MET:HG3	2.14	0.47
1:C:439:THR:HB	7:C:7966:HOH:O	2.14	0.47
1:A:1144:LEU:C	1:A:1144:LEU:HD12	2.35	0.47
1:A:383:MET:CE	1:A:460:LEU:HD11	2.44	0.47
2:D:1:MET:SD	2:D:3:ILE:HD11	2.53	0.47
2:B:437:GLU:O	2:B:441:GLN:HG3	2.15	0.47
1:C:1071:LYS:HB3	7:C:8289:HOH:O	2.15	0.47
1:C:454:LYS:HD3	1:C:487:LEU:HB3	1.96	0.47
1:A:1115:PRO:HA	1:A:1165:GLN:NE2	2.30	0.47
1:A:592:LEU:CD1	1:A:954:MET:HE1	2.43	0.47
1:A:191:ILE:O	1:A:194:MET:HG2	2.15	0.47
1:A:341:MET:HE1	1:A:353:ARG:CZ	2.45	0.47
1:A:502:TYR:CD1	1:A:502:TYR:N	2.80	0.47
2:D:2:LYS:HG2	7:D:8123:HOH:O	2.15	0.47
1:A:457:VAL:HG12	1:A:458:LYS:N	2.29	0.46
1:A:1011:THR:HB	7:A:6566:HOH:O	2.14	0.46
1:A:112:MET:CE	1:A:159:ARG:HA	2.45	0.46
1:C:426:ILE:HG21	1:C:454:LYS:CE	2.45	0.46
1:C:671:GLU:HG2	7:C:8553:HOH:O	2.15	0.46
1:A:618:TRP:CZ3	1:A:751:PRO:HG2	2.50	0.46
1:C:268:THR:HA	1:C:271:ARG:HD3	1.98	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:618:TRP:CZ3	1:C:751:PRO:HG2	2.50	0.46
2:D:221:ARG:HD3	2:D:234:PHE:CD1	2.51	0.46
1:A:1100:THR:O	1:A:1101:TYR:HB2	2.15	0.46
1:C:149:LYS:CE	7:C:8591:HOH:O	2.63	0.46
1:C:426:ILE:HG21	1:C:454:LYS:HE3	1.97	0.46
2:D:441:GLN:HG2	7:D:7948:HOH:O	2.16	0.46
1:A:1084:LYS:HB2	1:A:1127:LEU:HD21	1.98	0.46
1:C:1006:ILE:HD12	1:C:1016:GLU:CG	2.43	0.46
1:C:585:PRO:HB3	1:C:961:GLU:OE1	2.15	0.46
1:A:1049:GLN:HG2	7:A:6121:HOH:O	2.14	0.46
2:B:187:CYS:HB3	2:B:349:THR:O	2.16	0.46
1:A:106:ASN:ND2	2:B:112:HIS:CE1	2.76	0.46
2:B:148:LEU:HG	2:B:177:MET:HE1	1.98	0.46
1:C:624:THR:O	1:C:627:GLU:HG2	2.15	0.46
2:D:67:ILE:HD11	2:D:75:GLN:HB3	1.98	0.46
1:A:337:PRO:HG3	1:A:417:LEU:HD23	1.98	0.46
1:A:705:HIS:CD2	1:A:764:LYS:HB3	2.50	0.46
1:A:960:PRO:O	1:A:967:ALA:HB2	2.15	0.46
1:C:664:ASN:HD22	1:C:665:PRO:N	2.14	0.46
1:C:585:PRO:HD3	1:C:961:GLU:OE2	2.16	0.46
2:B:81:ARG:HG2	2:B:81:ARG:HH11	1.79	0.45
1:A:685:LYS:O	1:A:689:GLU:HG2	2.16	0.45
1:A:914:LYS:HE2	1:A:1011:THR:O	2.16	0.45
1:A:585:PRO:HA	1:A:961:GLU:CD	2.37	0.45
1:C:1092:HIS:ND1	5:C:7802:MGD:N15	2.61	0.45
1:C:218:ASP:N	1:C:218:ASP:OD1	2.50	0.45
1:C:383:MET:HE1	1:C:460:LEU:CD1	2.42	0.45
2:D:81:ARG:HG2	2:D:81:ARG:HH11	1.81	0.45
2:B:398:ASP:O	2:B:401:PRO:HD2	2.16	0.45
1:C:1236:GLU:HA	1:C:1236:GLU:OE2	2.17	0.45
1:C:736:HIS:CD2	1:C:738:ILE:H	2.27	0.45
2:D:19:CYS:O	2:D:20:HIS:HB2	2.15	0.45
1:A:487:LEU:HD11	7:A:6595:HOH:O	2.14	0.45
1:C:1174:SER:HB2	7:C:8542:HOH:O	2.16	0.45
1:C:257:PRO:HG3	1:C:290:LEU:CD1	2.47	0.45
1:A:219:TRP:HB2	1:A:607:SER:HB2	1.98	0.45
1:C:1098:HIS:CE1	5:C:7802:MGD:S13	3.10	0.45
1:C:665:PRO:HG3	7:C:7835:HOH:O	2.16	0.45
1:C:387:ASN:HD21	1:C:399:LYS:CE	2.27	0.45
1:C:425:GLU:OE1	1:C:459:ARG:NH2	2.50	0.45
1:C:658:ALA:HA	1:C:659:PRO:C	2.36	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:527:ASP:OD2	1:A:531:LYS:HE2	2.17	0.45
1:C:528:ASN:ND2	2:D:417:ARG:HH22	2.14	0.45
1:A:862:GLN:HE22	1:A:867:LYS:N	2.02	0.45
1:C:116:ARG:HG3	1:C:120:MET:CE	2.46	0.45
1:C:718:GLY:O	1:C:719:SER:HB2	2.17	0.45
2:D:103:PRO:HG2	2:D:130:ILE:HG12	1.99	0.45
2:D:373:SER:O	2:D:428:ARG:NH2	2.50	0.45
1:A:433:TYR:CZ	1:A:435:GLY:HA3	2.52	0.45
1:A:52:ASN:HB3	7:A:6580:HOH:O	2.16	0.45
2:B:58:ASN:HD22	2:B:58:ASN:C	2.19	0.45
1:C:353:ARG:HA	1:C:1047:ASP:HB2	1.99	0.45
2:D:187:CYS:HB3	2:D:349:THR:O	2.17	0.45
2:D:359:LEU:HD23	2:D:406:LEU:HD22	1.99	0.45
1:A:664:ASN:HD22	1:A:665:PRO:N	2.14	0.44
1:C:217:TYR:CZ	1:C:581:GLU:HG3	2.51	0.44
1:C:191:ILE:HG23	1:C:580:GLN:O	2.17	0.44
2:D:436:THR:OG1	2:D:439:GLN:HG3	2.16	0.44
2:B:140:LYS:HG3	2:B:141:GLY:N	2.32	0.44
2:B:27:LYS:HE2	2:B:31:THR:O	2.17	0.44
1:C:177:ILE:HG23	1:C:182:PRO:HG3	1.99	0.44
1:C:29:ARG:HA	7:C:8549:HOH:O	2.17	0.44
1:C:652:MET:HE3	1:C:866:VAL:HG13	2.00	0.44
1:A:551:ASP:HA	7:A:6096:HOH:O	2.16	0.44
1:A:664:ASN:ND2	1:A:664:ASN:C	2.71	0.44
1:C:289:LYS:O	1:C:289:LYS:HD3	2.17	0.44
1:C:268:THR:HG22	1:C:290:LEU:HD22	2.00	0.44
2:D:67:ILE:HG13	2:D:75:GLN:O	2.17	0.44
1:A:177:ILE:HG23	1:A:182:PRO:HG3	2.00	0.44
1:A:372:TRP:CE2	1:A:863:PRO:HB3	2.53	0.44
1:A:454:LYS:HB3	1:A:487:LEU:HD13	1.97	0.44
1:C:1134:TRP:CE3	1:C:1147:ARG:HG3	2.52	0.44
1:C:114:ARG:NH2	7:C:7851:HOH:O	2.40	0.44
1:A:550:LEU:H	1:A:550:LEU:CD2	2.30	0.44
1:A:698:GLN:HG2	1:A:755:ASP:OD2	2.18	0.44
2:D:246:PHE:HA	4:D:7800:SF4:S1	2.58	0.44
1:A:1207:GLY:HA3	1:A:1210:TYR:HB3	2.00	0.44
1:A:217:TYR:CZ	1:A:581:GLU:HG3	2.53	0.44
1:C:556:GLY:HA2	1:C:1059:LEU:CD2	2.48	0.44
1:C:960:PRO:O	1:C:967:ALA:HB2	2.18	0.44
1:A:1091:PRO:HB2	7:A:6577:HOH:O	2.18	0.44
1:A:734:THR:HG23	1:A:735:GLU:O	2.17	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:597:ASP:O	1:A:903:GLY:HA3	2.17	0.44
1:A:928:ARG:CG	1:A:943:PRO:HG3	2.46	0.44
1:C:454:LYS:HE2	1:C:487:LEU:HD13	2.00	0.44
2:D:361:PRO:HD2	2:D:384:ARG:HD3	2.00	0.44
1:A:1236:GLU:HG3	1:A:1237:GLY:N	2.33	0.43
1:A:307:LEU:HD21	1:A:1059:LEU:HG	1.99	0.43
1:A:399:LYS:HG3	7:A:6330:HOH:O	2.18	0.43
1:A:543:GLY:HA3	5:A:5802:MGD:H5'2	1.99	0.43
2:B:15:LYS:HE2	7:B:6163:HOH:O	2.18	0.43
1:C:261:THR:HG22	2:D:264:VAL:HG11	2.00	0.43
1:C:405:ARG:HD3	7:C:8544:HOH:O	2.18	0.43
1:A:1098:HIS:ND1	5:A:5801:MGD:H102	2.33	0.43
1:C:1048:HIS:CD2	1:C:1050:TRP:H	2.36	0.43
1:C:217:TYR:H	1:C:1209:ASN:ND2	2.17	0.43
1:C:329:TYR:CD2	1:C:565:GLY:HA2	2.53	0.43
1:A:233:GLU:OE1	1:A:1036:ARG:NH2	2.49	0.43
1:A:1093:GLN:HB3	1:A:1162:TYR:HB3	2.01	0.43
1:A:750:LYS:HD3	7:A:6597:HOH:O	2.18	0.43
1:C:1005:LYS:HB3	1:C:1005:LYS:HE2	1.87	0.43
1:C:399:LYS:HE2	7:C:8217:HOH:O	2.16	0.43
1:C:454:LYS:CE	1:C:487:LEU:HB3	2.49	0.43
1:A:911:ASN:ND2	1:A:912:GLY:H	2.16	0.43
1:A:528:ASN:HD22	2:B:417:ARG:HH22	1.66	0.43
1:A:1048:HIS:HD2	1:A:1050:TRP:HB2	1.83	0.43
1:A:1084:LYS:CB	1:A:1127:LEU:HD21	2.49	0.43
1:A:168:LEU:O	1:A:168:LEU:HD23	2.17	0.43
1:A:383:MET:CE	1:A:460:LEU:CD1	2.97	0.43
2:B:83:MET:HE3	7:B:5923:HOH:O	2.19	0.43
2:D:165:GLN:N	2:D:165:GLN:CD	2.60	0.43
2:D:1:MET:HA	2:D:278:ASP:OD2	2.18	0.43
1:C:219:TRP:HB2	1:C:607:SER:HB2	2.00	0.43
1:C:578:VAL:HB	5:C:7802:MGD:S12	2.59	0.43
2:D:80:ASN:HD22	2:D:83:MET:H	1.64	0.43
1:A:1208:PHE:O	1:A:1209:ASN:HB2	2.19	0.43
2:B:188:LEU:HB3	2:B:280:ILE:HD13	1.99	0.43
1:C:1168:ILE:HG13	1:C:1169:VAL:HG23	2.00	0.43
1:C:550:LEU:H	1:C:550:LEU:CD2	2.31	0.43
2:D:371:LEU:HD12	2:D:371:LEU:N	2.33	0.43
1:A:1037:THR:HA	1:A:1203:HIS:HB3	2.01	0.43
1:A:259:THR:HA	5:A:5802:MGD:N20	2.34	0.43
1:A:658:ALA:HA	1:A:659:PRO:C	2.39	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:353:ARG:CZ	1:A:864:LEU:HD22	2.49	0.43
1:C:1019:HIS:HD2	7:C:8193:HOH:O	2.01	0.43
1:C:222:ASP:HB3	1:C:578:VAL:HG21	1.99	0.43
1:C:360:LEU:HD12	1:C:364:LEU:HD13	2.01	0.43
1:C:695:ALA:HB1	1:C:704:ASN:HB3	2.00	0.43
1:A:286:GLU:HA	7:A:6543:HOH:O	2.19	0.43
1:C:1155:PRO:HG2	1:C:1158:MET:HG2	1.99	0.43
1:C:168:LEU:HD23	1:C:168:LEU:C	2.39	0.43
1:C:535:ARG:NH1	7:C:8505:HOH:O	2.51	0.43
2:D:48:PRO:HD2	2:D:148:LEU:HD21	2.01	0.43
1:A:604:HIS:HB3	1:A:1208:PHE:CD1	2.54	0.43
2:D:6:GLN:HG3	2:D:207:ASP:O	2.18	0.43
1:A:1027:THR:O	1:A:1031:GLU:HB2	2.19	0.42
1:A:252:TRP:CZ3	1:A:557:LEU:HD22	2.54	0.42
2:B:431:GLU:HG2	7:B:6148:HOH:O	2.19	0.42
1:C:492:CYS:O	1:C:500:LYS:HG2	2.19	0.42
1:A:41:HIS:HA	1:A:64:LYS:HG2	2.01	0.42
2:B:42:ASN:HB2	4:B:5800:SF4:S2	2.59	0.42
1:C:401:ASN:OD1	1:C:403:GLU:HG3	2.18	0.42
1:A:1098:HIS:NE2	5:A:5802:MGD:S13	2.92	0.42
1:A:192:PRO:HB3	1:A:199:TYR:CG	2.54	0.42
1:A:223:LEU:O	1:A:225:PRO:HD3	2.19	0.42
2:B:156:ALA:C	2:B:158:ASP:H	2.21	0.42
1:C:100:TRP:O	1:C:104:SER:HB3	2.19	0.42
1:C:214:LEU:HB3	1:C:607:SER:OG	2.19	0.42
1:C:720:SER:HB2	5:C:7801:MGD:O3A	2.19	0.42
1:C:1153:ARG:HD2	2:D:177:MET:CE	2.50	0.42
1:A:875:ASP:OD1	1:A:876:LEU:N	2.52	0.42
1:C:1114:GLY:O	1:C:1116:VAL:HG13	2.20	0.42
1:A:360:LEU:HD12	1:A:364:LEU:HD13	2.01	0.42
1:C:225:PRO:O	1:C:228:PRO:HD2	2.19	0.42
1:C:1098:HIS:CE1	5:C:7801:MGD:S12	3.12	0.42
1:C:439:THR:HG23	1:C:440:GLU:N	2.35	0.42
2:D:365:ALA:O	2:D:366:ALA:CB	2.68	0.42
1:A:426:ILE:HG21	1:A:454:LYS:HG2	2.02	0.42
1:A:501:ALA:HB3	7:A:6248:HOH:O	2.19	0.42
2:B:183:LEU:HD23	2:B:183:LEU:N	2.35	0.42
2:D:183:LEU:HD23	2:D:183:LEU:N	2.34	0.42
1:A:401:ASN:HA	1:A:1034:PRO:HD3	2.02	0.42
2:B:276:ASP:HB3	7:B:6160:HOH:O	2.20	0.42
2:B:3:ILE:HD12	2:B:301:LEU:HD11	2.01	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:64:LYS:HB3	1:C:69:THR:HG21	2.02	0.42
1:C:1098:HIS:ND1	5:C:7801:MGD:H102	2.35	0.42
1:C:862:GLN:HE22	1:C:866:VAL:HA	1.85	0.42
1:A:831:LYS:HE2	7:A:6372:HOH:O	2.19	0.42
1:C:556:GLY:HA2	1:C:1059:LEU:HD22	2.02	0.42
1:A:1089:LEU:HD12	1:A:1158:MET:CE	2.49	0.41
1:C:94:ARG:HB3	1:C:1101:TYR:CD2	2.55	0.41
1:C:217:TYR:CE1	1:C:223:LEU:HA	2.55	0.41
2:D:248:TYR:N	2:D:249:PRO:CD	2.83	0.41
1:C:94:ARG:H	1:C:94:ARG:HD2	1.85	0.41
1:A:1071:LYS:HE2	1:A:1071:LYS:HB3	1.81	0.41
1:A:1091:PRO:O	1:A:1162:TYR:HA	2.20	0.41
1:A:191:ILE:CG2	1:A:580:GLN:HB3	2.51	0.41
2:B:373:SER:HB2	2:B:379:ASP:OD1	2.21	0.41
1:C:1048:HIS:HD2	1:C:1050:TRP:HB2	1.84	0.41
1:C:945:LEU:HD11	1:C:954:MET:HE1	2.03	0.41
1:C:539:ILE:HA	1:C:575:ALA:HB3	2.01	0.41
2:D:3:ILE:CD1	2:D:301:LEU:CD1	2.98	0.41
2:B:400:LYS:HB2	2:B:400:LYS:HZ2	1.84	0.41
1:C:462:LEU:HD11	1:C:468:ALA:HB2	2.02	0.41
1:C:499:VAL:HG12	1:C:499:VAL:O	2.20	0.41
1:C:586:GLN:O	1:C:590:GLN:HG3	2.20	0.41
2:D:113:THR:O	2:D:114:ALA:C	2.58	0.41
2:D:119:LYS:HD3	2:D:119:LYS:HA	1.85	0.41
1:A:439:THR:HG23	1:A:440:GLU:N	2.36	0.41
1:A:329:TYR:CE2	1:A:565:GLY:HA2	2.55	0.41
1:A:528:ASN:ND2	2:B:417:ARG:HH22	2.18	0.41
2:B:80:ASN:HD21	2:B:83:MET:H	1.69	0.41
1:C:191:ILE:CD1	1:C:191:ILE:N	2.82	0.41
1:C:247:SER:C	1:C:275:THR:HG23	2.41	0.41
1:C:449:ASN:HD22	1:C:449:ASN:H	1.68	0.41
1:A:992:GLU:HG2	7:A:6579:HOH:O	2.21	0.41
2:D:338:LYS:HE2	7:D:8149:HOH:O	2.21	0.41
1:A:297:PRO:HG3	1:A:305:MET:HE1	2.03	0.41
1:A:695:ALA:HB1	1:A:704:ASN:HB3	2.02	0.41
1:A:750:LYS:HB3	1:A:751:PRO:CD	2.51	0.41
1:A:929:LYS:HD2	7:A:6622:HOH:O	2.19	0.41
1:A:1023:ASN:O	1:A:1026:TYR:HB2	2.21	0.41
1:A:1098:HIS:HA	1:A:1164:ALA:HB2	2.03	0.41
1:A:728:LEU:HB3	1:A:734:THR:HG22	2.03	0.41
1:C:259:THR:HA	5:C:7802:MGD:N20	2.35	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:336:MET:HA	1:A:473:VAL:HB	2.03	0.41
1:A:344:GLU:HG3	1:A:349:TYR:CE1	2.56	0.41
2:B:162:ASP:O	2:B:163:ASN:HB2	2.21	0.41
1:C:777:SER:OG	1:C:1166:GLU:HG2	2.21	0.41
1:C:449:ASN:ND2	1:C:449:ASN:N	2.69	0.41
1:A:1085:ALA:HA	1:A:1222:VAL:O	2.21	0.40
1:A:1177:THR:O	1:A:1178:GLN:HB2	2.21	0.40
1:A:992:GLU:HB3	7:A:6375:HOH:O	2.21	0.40
1:C:454:LYS:HE2	1:C:487:LEU:HB3	2.04	0.40
1:C:1108:LEU:HD13	2:D:106:PHE:CE2	2.57	0.40
2:D:403:LEU:O	2:D:407:LYS:HB2	2.22	0.40
1:A:100:TRP:O	1:A:104:SER:HB3	2.21	0.40
1:A:220:TYR:HE1	1:A:720:SER:OG	2.01	0.40
1:A:619:ARG:NH1	7:A:6573:HOH:O	2.54	0.40
1:A:729:LYS:HD3	1:A:730:TYR:CE1	2.56	0.40
1:A:1167:ARG:CD	2:B:121:GLN:HE22	2.34	0.40
1:C:535:ARG:NE	7:C:8540:HOH:O	2.47	0.40
1:C:766:ASP:HA	7:C:8591:HOH:O	2.21	0.40
2:B:367:ASP:O	2:B:369:GLY:N	2.55	0.40
1:C:743:LEU:C	1:C:745:GLN:H	2.24	0.40
1:A:216:PHE:CD1	1:A:217:TYR:N	2.89	0.40
1:A:188:PHE:HE2	1:A:220:TYR:HH	1.69	0.40
1:A:585:PRO:HA	1:A:961:GLU:CG	2.51	0.40
1:A:678:ASN:ND2	1:A:681:ASP:OD2	2.53	0.40
1:C:534:GLY:O	1:C:572:GLY:HA3	2.22	0.40
1:C:372:TRP:CE2	1:C:863:PRO:HB3	2.56	0.40
2:D:373:SER:HB2	2:D:379:ASP:OD1	2.21	0.40

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	1216/1246 (98%)	1150 (95%)	59 (5%)	7 (1%)	25	19
1	C	1216/1246 (98%)	1144 (94%)	62 (5%)	10 (1%)	19	13
2	B	463/512 (90%)	450 (97%)	10 (2%)	3 (1%)	25	19
2	D	463/512 (90%)	448 (97%)	14 (3%)	1 (0%)	47	44
All	All	3358/3516 (96%)	3192 (95%)	145 (4%)	21 (1%)	25	19

All (21) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	1164	ALA
1	A	1244	SER
1	C	748	GLY
1	A	578	VAL
1	A	719	SER
2	B	368	ALA
1	C	501	ALA
1	C	578	VAL
1	C	719	SER
1	C	742	ASP
2	B	167	ALA
2	B	366	ALA
2	D	167	ALA
1	C	195	SER
1	C	502	TYR
1	A	195	SER
1	A	224	PRO
1	C	808	PRO
1	A	190	PRO
1	C	190	PRO
1	C	224	PRO

5.3.2 Protein sidechains ⓘ

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	1019/1043 (98%)	996 (98%)	23 (2%)	50	53
1	C	1019/1043 (98%)	995 (98%)	24 (2%)	49	51
2	B	400/439 (91%)	391 (98%)	9 (2%)	50	53
2	D	400/439 (91%)	389 (97%)	11 (3%)	43	44
All	All	2838/2964 (96%)	2771 (98%)	67 (2%)	49	51

All (67) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	29	ARG
1	A	94	ARG
1	A	114	ARG
1	A	190	PRO
1	A	319	LEU
1	A	324	GLN
1	A	364	LEU
1	A	387	ASN
1	A	416	GLN
1	A	439	THR
1	A	454	LYS
1	A	475	ASP
1	A	664	ASN
1	A	715	ASN
1	A	722	LYS
1	A	734	THR
1	A	801	ASP
1	A	804	PRO
1	A	808	PRO
1	A	911	ASN
1	A	961	GLU
1	A	1087	ASN
1	A	1184	HIS
2	B	11	LEU
2	B	37	GLU
2	B	42	ASN
2	B	58	ASN
2	B	80	ASN
2	B	161	PHE
2	B	183	LEU
2	B	244	CYS
2	B	367	ASP
1	C	29	ARG

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Mol	Chain	Res	Type
1	C	94	ARG
1	C	106	ASN
1	C	114	ARG
1	C	127	LEU
1	C	190	PRO
1	C	439	THR
1	C	449	ASN
1	C	478	LEU
1	C	500	LYS
1	C	551	ASP
1	C	664	ASN
1	C	715	ASN
1	C	720	SER
1	C	788	THR
1	C	804	PRO
1	C	808	PRO
1	C	911	ASN
1	C	954	MET
1	C	961	GLU
1	C	992	GLU
1	C	1009	SER
1	C	1087	ASN
1	C	1238	ASN
2	D	11	LEU
2	D	27	LYS
2	D	37	GLU
2	D	58	ASN
2	D	80	ASN
2	D	81	ARG
2	D	161	PHE
2	D	165	GLN
2	D	183	LEU
2	D	307	LYS
2	D	370	GLU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (77) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	106	ASN
1	A	173	ASN
1	A	179	ASN
1	A	265	HIS

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Mol	Chain	Res	Type
1	A	311	HIS
1	A	366	GLN
1	A	387	ASN
1	A	404	GLN
1	A	517	GLN
1	A	528	ASN
1	A	590	GLN
1	A	604	HIS
1	A	646	ASN
1	A	664	ASN
1	A	708	ASN
1	A	715	ASN
1	A	736	HIS
1	A	862	GLN
1	A	911	ASN
1	A	921	GLN
1	A	942	GLN
1	A	984	HIS
1	A	1028	ASN
1	A	1030	HIS
1	A	1048	HIS
1	A	1093	GLN
1	A	1141	ASN
1	A	1165	GLN
1	A	1209	ASN
1	A	1217	ASN
2	B	58	ASN
2	B	80	ASN
2	B	93	HIS
2	B	112	HIS
2	B	121	GLN
2	B	143	ASN
2	B	160	ASN
2	B	174	ASN
1	C	65	ASN
1	C	106	ASN
1	C	128	HIS
1	C	173	ASN
1	C	265	HIS
1	C	311	HIS
1	C	366	GLN
1	C	369	ASN

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Mol	Chain	Res	Type
1	C	387	ASN
1	C	404	GLN
1	C	449	ASN
1	C	517	GLN
1	C	528	ASN
1	C	604	HIS
1	C	646	ASN
1	C	664	ASN
1	C	708	ASN
1	C	715	ASN
1	C	736	HIS
1	C	862	GLN
1	C	911	ASN
1	C	921	GLN
1	C	984	HIS
1	C	1028	ASN
1	C	1030	HIS
1	C	1048	HIS
1	C	1141	ASN
1	C	1165	GLN
1	C	1209	ASN
1	C	1217	ASN
1	C	1229	ASN
2	D	58	ASN
2	D	80	ASN
2	D	112	HIS
2	D	121	GLN
2	D	143	ASN
2	D	160	ASN
2	D	165	GLN
2	D	174	ASN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no carbohydrates in this entry.

5.6 Ligand geometry [i](#)

Of 16 ligands modelled in this entry, 2 are monoatomic - leaving 14 for Mogul analysis.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
4	SF4	D	7805	2	0,12,12	0.00	-	-		
6	F3S	B	5808	2	0,9,9	0.00	-	-		
5	MGD	A	5801	3	41,52,52	2.66	14 (34%)	43,81,81	2.56	14 (32%)
4	SF4	A	5807	1	0,12,12	0.00	-	-		
4	SF4	D	7806	2	0,12,12	0.00	-	-		
4	SF4	B	5800	2	0,12,12	0.00	-	-		
5	MGD	C	7801	3	41,52,52	2.56	13 (31%)	43,81,81	2.49	14 (32%)
4	SF4	C	7807	1	0,12,12	0.00	-	-		
6	F3S	D	7808	2	0,9,9	0.00	-	-		
5	MGD	A	5802	3	41,52,52	2.39	10 (24%)	43,81,81	2.90	16 (37%)
4	SF4	B	5806	2	0,12,12	0.00	-	-		
4	SF4	D	7800	2	0,12,12	0.00	-	-		
5	MGD	C	7802	3	41,52,52	2.40	12 (29%)	43,81,81	2.95	14 (32%)
4	SF4	B	5805	2	0,12,12	0.00	-	-		

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
4	SF4	D	7805	2	-	-	0/6/5/5
6	F3S	B	5808	2	-	-	0/3/3/3
5	MGD	A	5801	3	-	6/18/66/66	0/6/6/6
4	SF4	A	5807	1	-	-	0/6/5/5
4	SF4	D	7806	2	-	-	0/6/5/5

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
4	SF4	B	5800	2	-	-	0/6/5/5
5	MGD	C	7801	3	-	6/18/66/66	0/6/6/6
4	SF4	C	7807	1	-	-	0/6/5/5
6	F3S	D	7808	2	-	-	0/3/3/3
5	MGD	A	5802	3	-	5/18/66/66	0/6/6/6
4	SF4	B	5806	2	-	-	0/6/5/5
4	SF4	D	7800	2	-	-	0/6/5/5
5	MGD	C	7802	3	-	5/18/66/66	0/6/6/6
4	SF4	B	5805	2	-	-	0/6/5/5

All (49) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	C	7801	MGD	O11-C11	7.26	1.53	1.43
5	C	7802	MGD	C14-N15	7.21	1.55	1.45
5	A	5801	MGD	O11-C11	7.16	1.53	1.43
5	A	5802	MGD	C14-N15	6.49	1.54	1.45
5	C	7802	MGD	C17-N18	6.39	1.44	1.33
5	A	5802	MGD	C17-N18	6.37	1.44	1.33
5	C	7801	MGD	C17-N18	6.08	1.43	1.33
5	A	5801	MGD	C17-N18	6.03	1.43	1.33
5	A	5802	MGD	C6-N1	5.83	1.43	1.33
5	A	5802	MGD	C16-N15	5.82	1.49	1.38
5	C	7802	MGD	C16-N15	5.78	1.49	1.38
5	A	5801	MGD	C6-N1	5.60	1.42	1.33
5	C	7801	MGD	C6-N1	5.34	1.42	1.33
5	C	7802	MGD	C6-N1	5.30	1.42	1.33
5	A	5801	MGD	O11-C23	4.81	1.50	1.43
5	A	5801	MGD	C23-N22	4.44	1.53	1.44
5	A	5802	MGD	O11-C11	4.33	1.49	1.43
5	A	5801	MGD	C23-C14	4.26	1.57	1.53
5	C	7801	MGD	C23-N22	3.97	1.52	1.44
5	C	7802	MGD	O11-C11	3.95	1.49	1.43
5	C	7801	MGD	O11-C23	3.90	1.49	1.43
5	C	7801	MGD	C23-C14	3.89	1.56	1.53
5	A	5801	MGD	C14-N15	3.87	1.50	1.45
5	C	7801	MGD	C16-N15	3.85	1.45	1.38
5	A	5801	MGD	C16-N15	3.77	1.45	1.38
5	A	5801	MGD	C21-N20	3.67	1.41	1.34
5	C	7801	MGD	C21-N20	3.66	1.41	1.34
5	A	5802	MGD	C2-N1	3.60	1.41	1.35
5	A	5801	MGD	C2-N1	3.50	1.41	1.35

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	C	7801	MGD	C2-N1	3.47	1.41	1.35
5	C	7801	MGD	C14-N15	3.44	1.50	1.45
5	C	7802	MGD	C2-N1	3.37	1.41	1.35
5	A	5802	MGD	C6-C5	2.72	1.46	1.41
5	C	7802	MGD	C6-C5	2.70	1.46	1.41
5	A	5802	MGD	C21-N20	2.66	1.39	1.34
5	C	7802	MGD	C21-N20	2.54	1.39	1.34
5	C	7801	MGD	C2-N2	2.36	1.38	1.33
5	A	5801	MGD	C6-C5	2.33	1.45	1.41
5	C	7802	MGD	C19-N18	2.32	1.39	1.35
5	A	5801	MGD	C2-N2	2.30	1.38	1.33
5	A	5802	MGD	C19-N18	2.26	1.39	1.35
5	A	5802	MGD	C2-N2	2.22	1.38	1.33
5	A	5801	MGD	C10-C11	2.21	1.55	1.52
5	A	5801	MGD	C4-N3	2.13	1.39	1.35
5	C	7801	MGD	C3'-C4'	2.13	1.58	1.53
5	C	7801	MGD	C6-C5	2.09	1.45	1.41
5	C	7802	MGD	C4-N3	2.08	1.38	1.35
5	C	7802	MGD	C3'-C4'	2.04	1.58	1.53
5	C	7802	MGD	C2-N2	2.02	1.37	1.33

All (58) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	C	7802	MGD	O11-C23-C14	-11.57	101.25	108.96
5	A	5802	MGD	O11-C23-C14	-10.98	101.64	108.96
5	C	7801	MGD	C5-C6-N1	-7.18	113.61	123.43
5	A	5802	MGD	C5-C6-N1	-7.01	113.84	123.43
5	A	5801	MGD	C5-C6-N1	-6.98	113.89	123.43
5	C	7802	MGD	C5-C6-N1	-6.89	114.01	123.43
5	A	5801	MGD	O11-C23-N22	6.30	115.04	108.57
5	C	7801	MGD	O11-C23-N22	5.75	114.48	108.57
5	A	5801	MGD	C17-C16-C21	5.49	119.44	114.57
5	C	7802	MGD	O11-C23-N22	-5.40	103.02	108.57
5	A	5802	MGD	O11-C23-N22	-5.16	103.27	108.57
5	C	7801	MGD	C17-C16-C21	5.03	119.04	114.57
5	C	7802	MGD	C17-N18-C19	4.82	123.59	115.93
5	A	5802	MGD	C17-N18-C19	4.74	123.47	115.93
5	A	5801	MGD	O11-C23-C14	4.68	112.09	108.96
5	C	7801	MGD	C17-N18-C19	4.59	123.22	115.93
5	A	5801	MGD	C6-N1-C2	4.53	123.12	115.93
5	C	7802	MGD	C6-N1-C2	4.50	123.07	115.93

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	C	7801	MGD	C6-N1-C2	4.49	123.06	115.93
5	A	5802	MGD	C6-N1-C2	4.43	122.97	115.93
5	A	5801	MGD	C17-N18-C19	4.41	122.94	115.93
5	A	5802	MGD	C6-C5-C4	-4.00	116.98	120.80
5	C	7801	MGD	O11-C23-C14	3.90	111.56	108.96
5	A	5802	MGD	C17-C16-C21	3.83	117.97	114.57
5	C	7801	MGD	O4'-C1'-C2'	-3.82	101.35	106.93
5	C	7802	MGD	C17-C16-C21	3.73	117.89	114.57
5	A	5801	MGD	O4'-C1'-C2'	-3.62	101.64	106.93
5	C	7802	MGD	C6-C5-C4	-3.55	117.41	120.80
5	C	7801	MGD	O4'-C4'-C5'	-3.37	98.29	109.37
5	A	5801	MGD	O4'-C4'-C5'	-3.32	98.45	109.37
5	A	5801	MGD	C6-C5-C4	-3.27	117.68	120.80
5	C	7802	MGD	C16-C17-N18	-3.23	114.82	124.01
5	C	7802	MGD	C17-C16-N15	3.21	121.82	119.12
5	C	7801	MGD	C6-C5-C4	-3.20	117.75	120.80
5	A	5802	MGD	C16-C17-N18	-3.19	114.94	124.01
5	C	7802	MGD	C3'-C2'-C1'	3.15	105.72	100.98
5	A	5801	MGD	C2-N3-C4	-3.15	111.76	115.36
5	C	7801	MGD	C2-N3-C4	-3.08	111.84	115.36
5	C	7801	MGD	C16-N15-C14	-3.04	108.96	120.00
5	C	7801	MGD	C16-C17-N18	-3.02	115.44	124.01
5	A	5801	MGD	C16-C17-N18	-3.00	115.48	124.01
5	A	5802	MGD	C17-C16-N15	2.96	121.61	119.12
5	C	7802	MGD	C16-C21-N22	2.92	120.80	118.13
5	A	5801	MGD	C16-C21-N22	2.91	120.79	118.13
5	C	7802	MGD	C2-N3-C4	-2.89	112.05	115.36
5	A	5801	MGD	C16-N15-C14	-2.89	109.52	120.00
5	A	5802	MGD	C3'-C2'-C1'	2.82	105.22	100.98
5	A	5802	MGD	C16-C21-N22	2.79	120.69	118.13
5	C	7801	MGD	C16-C21-N22	2.77	120.66	118.13
5	A	5802	MGD	C2-N3-C4	-2.68	112.30	115.36
5	A	5802	MGD	N3-C2-N1	-2.51	123.88	127.22
5	C	7802	MGD	C16-N15-C14	-2.41	111.24	120.00
5	C	7802	MGD	N3-C2-N1	-2.29	124.17	127.22
5	A	5802	MGD	C16-N15-C14	-2.27	111.76	120.00
5	A	5801	MGD	N3-C2-N1	-2.20	124.29	127.22
5	C	7801	MGD	N3-C2-N1	-2.16	124.34	127.22
5	A	5802	MGD	C21-N22-C23	-2.04	119.67	123.67
5	A	5802	MGD	O4'-C4'-C5'	-2.01	102.76	109.37

There are no chirality outliers.

All (22) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
5	A	5801	MGD	C5'-O5'-PB-O1B
5	C	7801	MGD	C5'-O5'-PB-O1B
5	A	5802	MGD	C5'-O5'-PB-O1B
5	C	7802	MGD	PA-O3B-PB-O5'
5	C	7802	MGD	C5'-O5'-PB-O1B
5	A	5801	MGD	PA-O3B-PB-O1B
5	A	5801	MGD	PA-O3B-PB-O5'
5	C	7801	MGD	PA-O3B-PB-O5'
5	A	5802	MGD	PA-O3B-PB-O5'
5	C	7802	MGD	C5'-O5'-PB-O3B
5	C	7801	MGD	PA-O3B-PB-O1B
5	A	5801	MGD	C5'-O5'-PB-O2B
5	C	7801	MGD	C5'-O5'-PB-O2B
5	A	5802	MGD	C5'-O5'-PB-O2B
5	C	7802	MGD	C5'-O5'-PB-O2B
5	A	5801	MGD	C5'-O5'-PB-O3B
5	C	7801	MGD	C5'-O5'-PB-O3B
5	A	5802	MGD	C5'-O5'-PB-O3B
5	A	5801	MGD	O4'-C4'-C5'-O5'
5	C	7801	MGD	O4'-C4'-C5'-O5'
5	A	5802	MGD	O4'-C4'-C5'-O5'
5	C	7802	MGD	O4'-C4'-C5'-O5'

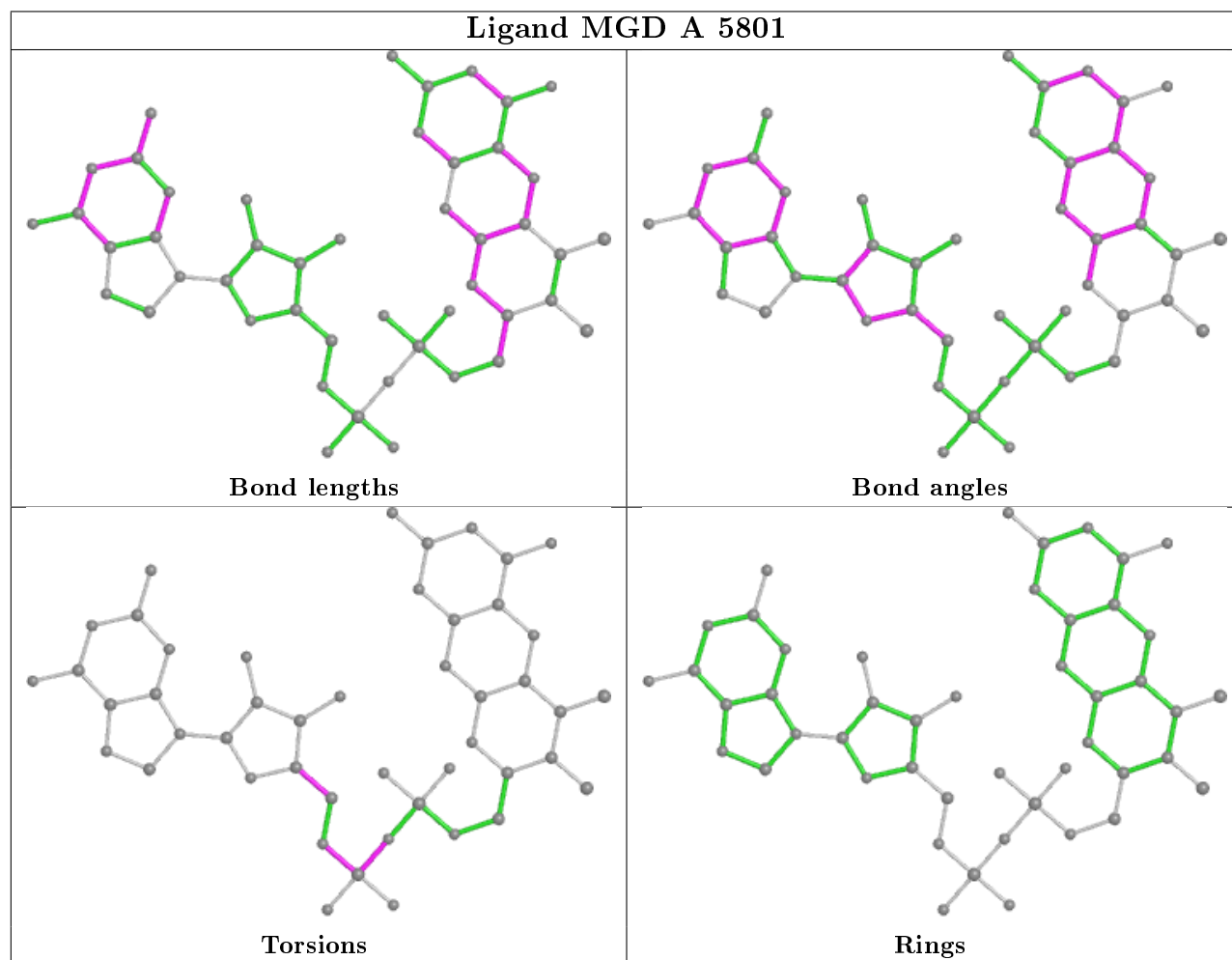
There are no ring outliers.

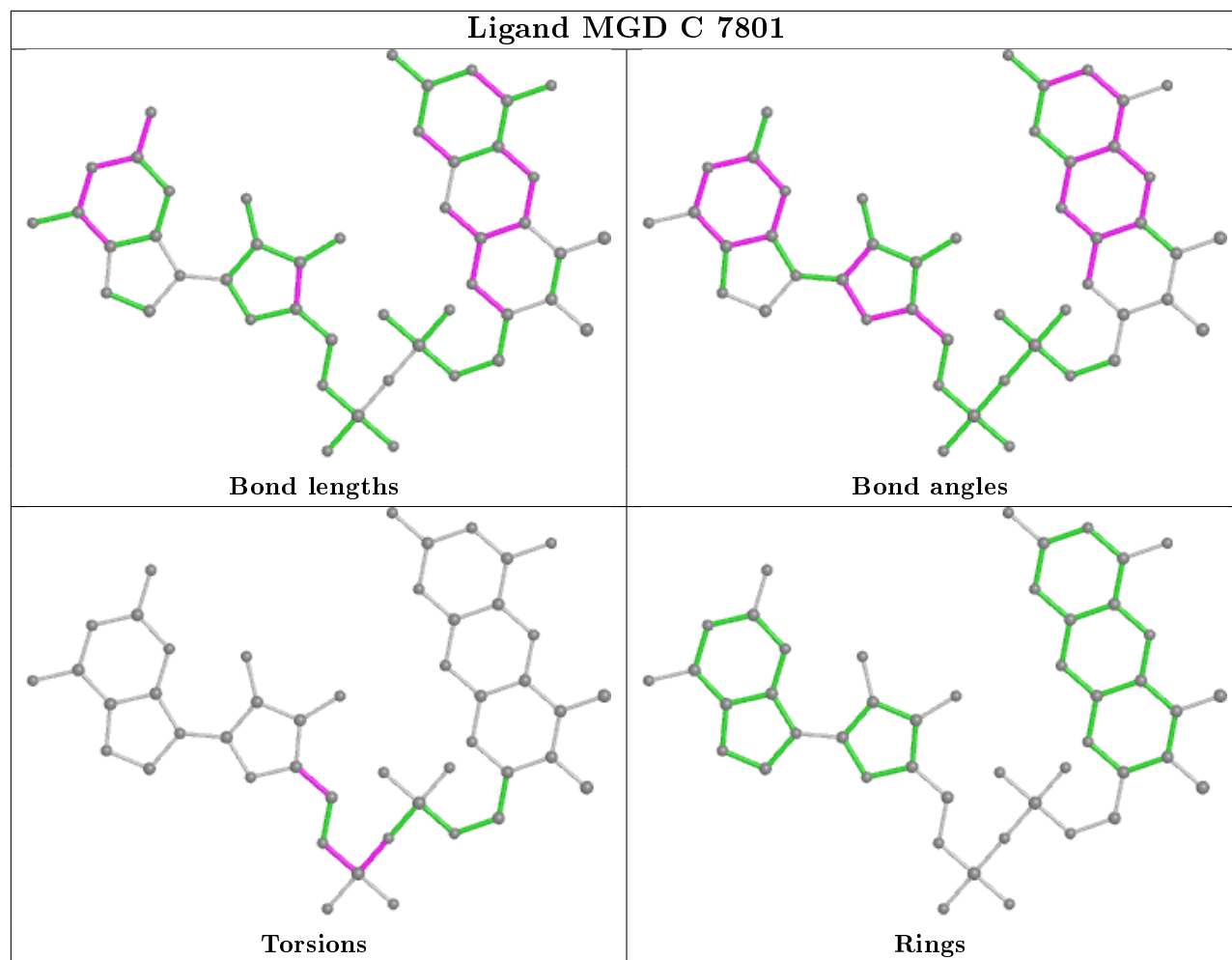
6 monomers are involved in 16 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	A	5801	MGD	1	0
4	B	5800	SF4	2	0
5	C	7801	MGD	3	0
5	A	5802	MGD	5	0
4	D	7800	SF4	1	0
5	C	7802	MGD	4	0

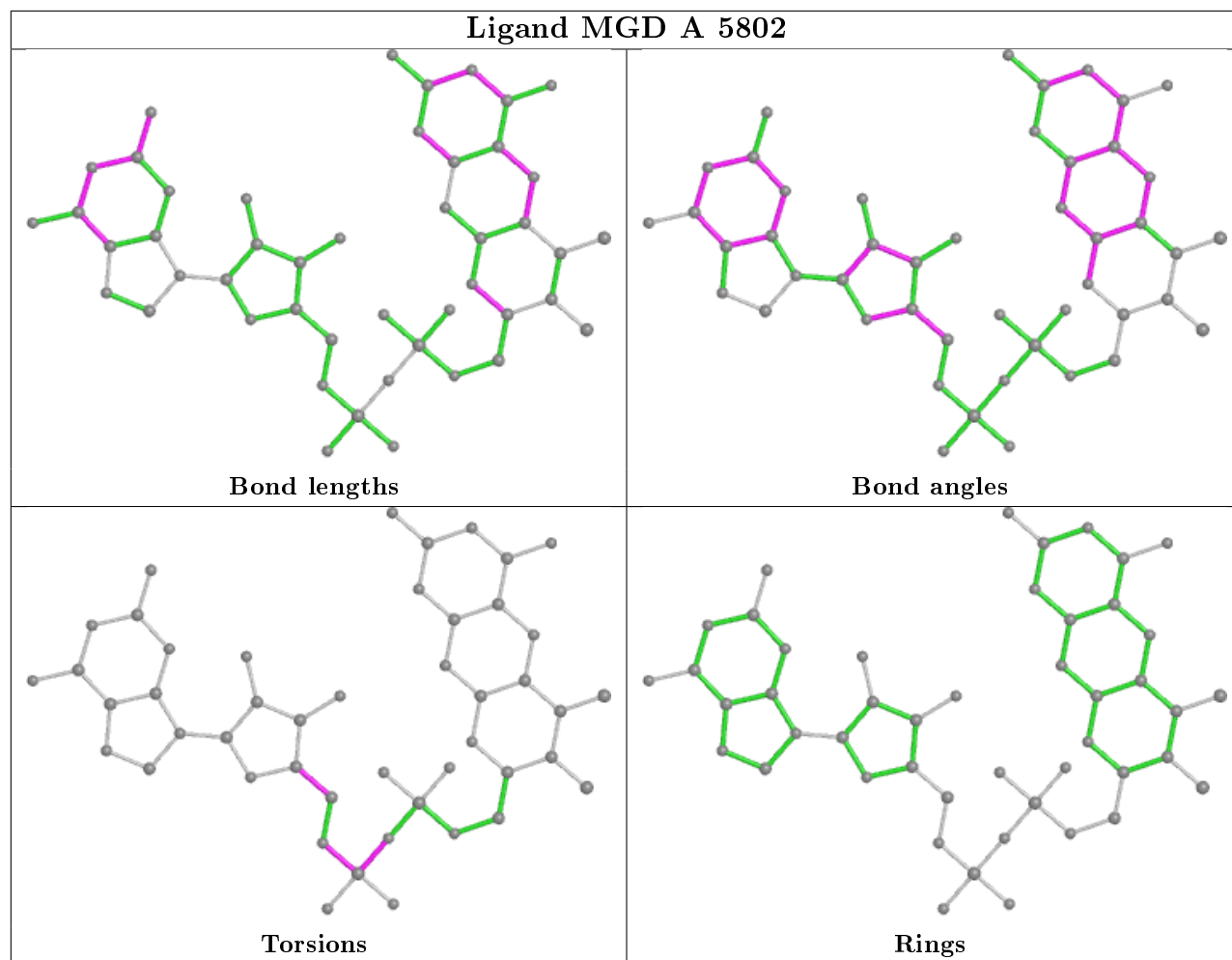
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included.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

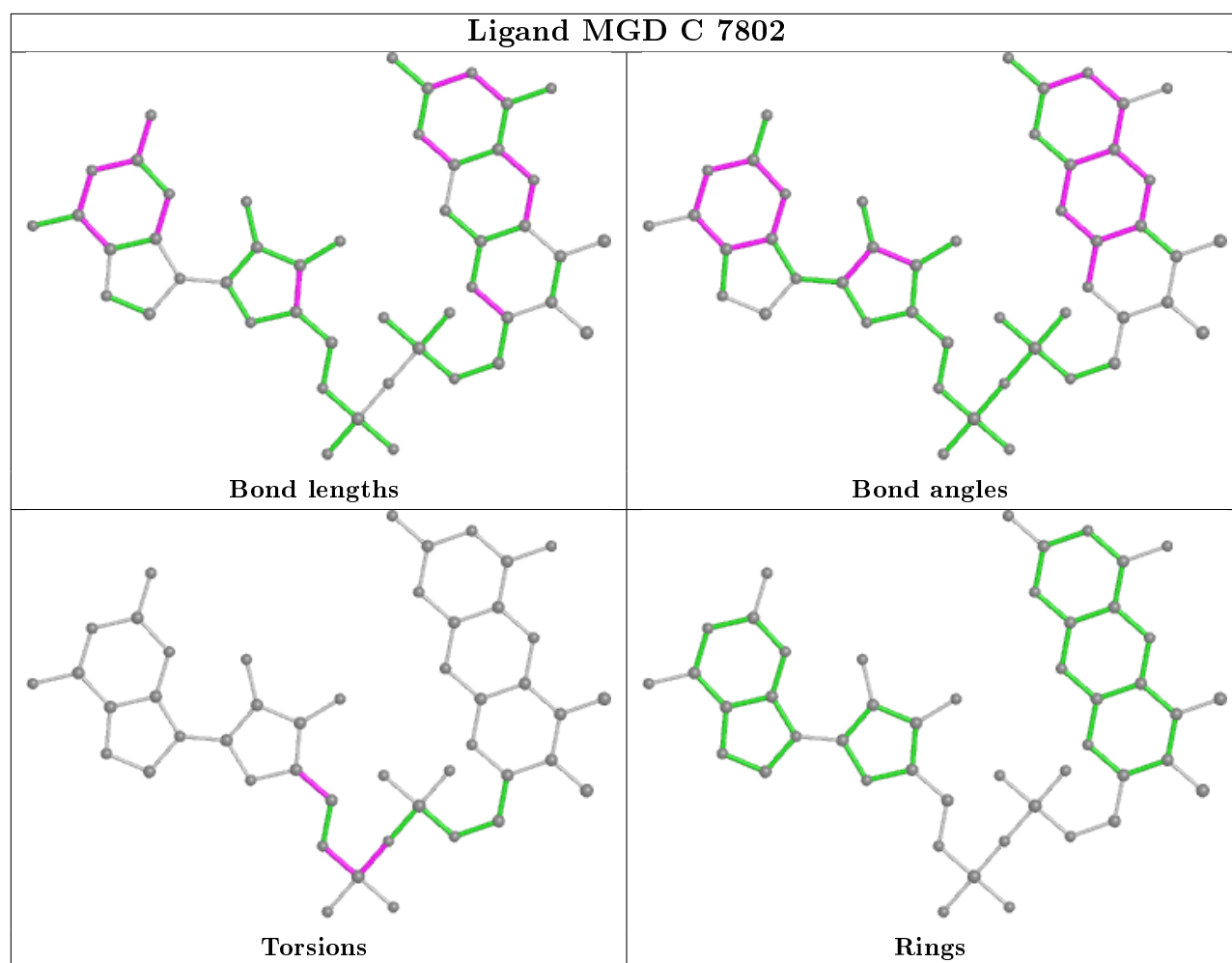
average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.





Ligand MGD A 5802





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 ⓘ

EDS was not executed - this section is therefore empty.

6.2 Non-standard residues in protein, DNA, RNA chains ⓘ

EDS was not executed - this section is therefore empty.

6.3 Carbohydrates ⓘ

EDS was not executed - this section is therefore empty.

6.4 Ligands ⓘ

EDS was not executed - this section is therefore empty.

6.5 Other polymers ⓘ

EDS was not executed - this section is therefore empty.