



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 6, 2026 – 06:59 AM UTC

PDB ID : 1J0D / pdb_00001j0d
Title : ACC deaminase mutant complexed with ACC
Authors : Ose, T.; Fujino, A.; Yao, M.; Honma, M.; Tanaka, I.
Deposited on : 2002-11-12
Resolution : 2.20 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	:	4-5-2 with Phenix2.0
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	NOT EXECUTED
EDS	:	NOT EXECUTED
Buster-report	:	wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

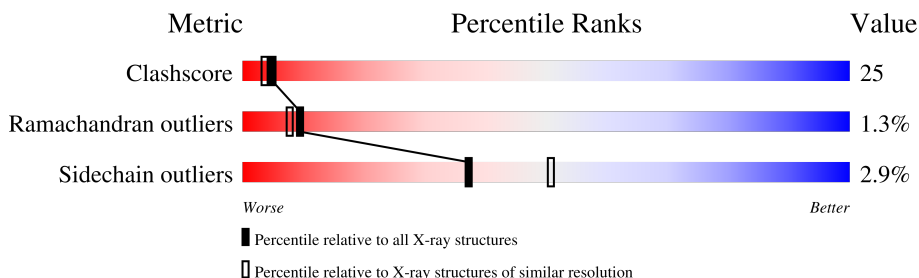
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.20 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	190562	6851 (2.20-2.20)
Ramachandran outliers	187476	6768 (2.20-2.20)
Sidechain outliers	187428	6769 (2.20-2.20)

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 $\leq 5\%$.

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	A	341	
1	B	341	
1	C	341	
1	D	341	

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	5PA	A	1401	-	-	X	-
2	5PA	D	1701	-	-	X	-

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 11443 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.

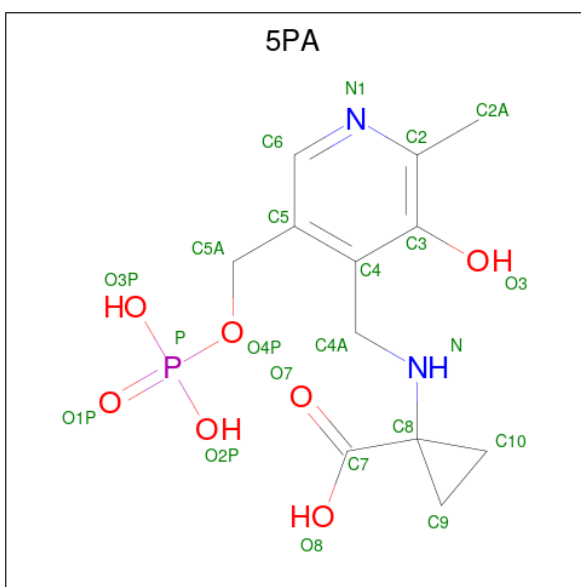
- Molecule 1 is a protein called 1-aminocyclopropane-1-carboxylate deaminase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	341	Total	C	N	O	S	0	0	0
			2605	1653	440	500	12			
1	B	341	Total	C	N	O	S	0	0	0
			2605	1653	440	500	12			
1	C	341	Total	C	N	O	S	0	0	0
			2605	1653	440	500	12			
1	D	341	Total	C	N	O	S	0	0	0
			2605	1653	440	500	12			

There are 8 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	1	ALA	SER	engineered mutation	UNP Q7M523
A	51	THR	LYS	engineered mutation	UNP Q7M523
B	1	ALA	SER	engineered mutation	UNP Q7M523
B	51	THR	LYS	engineered mutation	UNP Q7M523
C	1	ALA	SER	engineered mutation	UNP Q7M523
C	51	THR	LYS	engineered mutation	UNP Q7M523
D	1	ALA	SER	engineered mutation	UNP Q7M523
D	51	THR	LYS	engineered mutation	UNP Q7M523

- Molecule 2 is N-[3-HYDROXY-2-METHYL-5-PHOSPHONOOXYMETHYL-PYRIDIN-4-Y-LMETHYL]-1-AMINO-CYCLOPROPANECARBOXYLIC ACID (CCD ID: 5PA) (formula: C₁₂H₁₇N₂O₇P).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total	C	N	O	P	0	0
			22	12	2	7	1		
2	B	1	Total	C	N	O	P	0	0
			22	12	2	7	1		
2	C	1	Total	C	N	O	P	0	0
			22	12	2	7	1		
2	D	1	Total	C	N	O	P	0	0
			22	12	2	7	1		

- Molecule 3 is water.

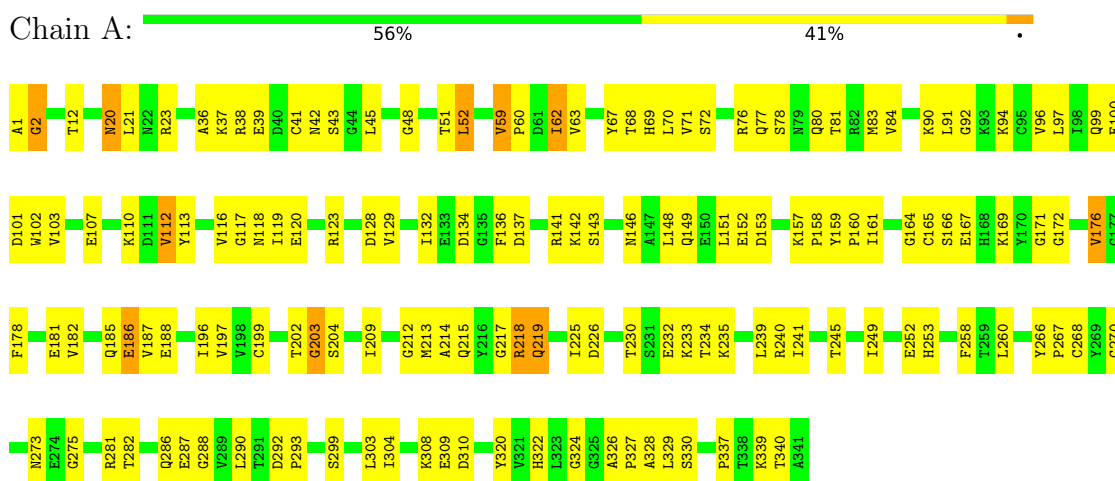
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	126	Total	O	0	0
			126	126		
3	B	125	Total	O	0	0
			125	125		
3	C	366	Total	O	0	0
			366	366		
3	D	318	Total	O	0	0
			318	318		

3 Residue-property plots

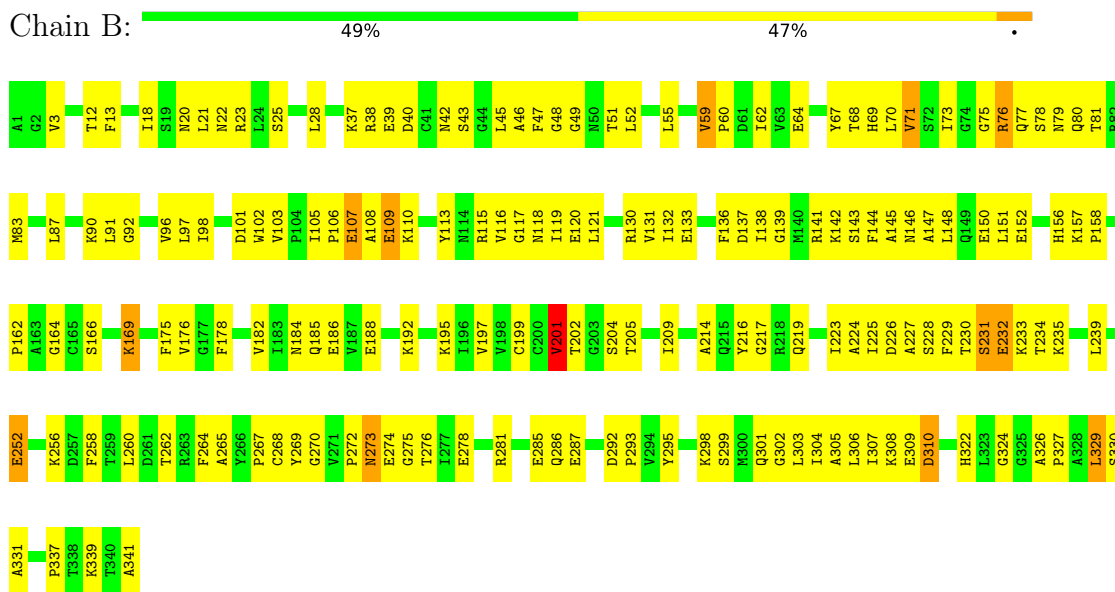
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry. Residues are color-coded 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: 1-aminocyclopropane-1-carboxylate deaminase

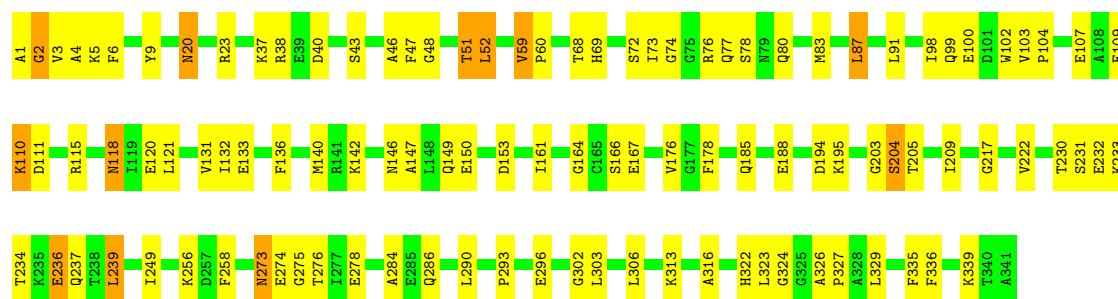


- Molecule 1: 1-aminocyclopropane-1-carboxylate deaminase



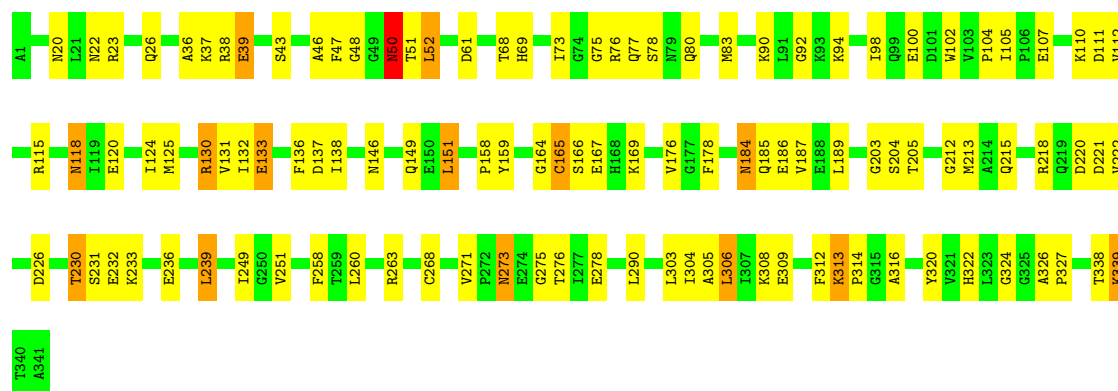
- Molecule 1: 1-aminocyclopropane-1-carboxylate deaminase

Chain C:  68% 28% .



• Molecule 1: 1-aminocyclopropane-1-carboxylate deaminase

Chain D:  67% 28% .



4 Data and refinement statistics

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

Property	Value	Source
Space group	C 2 2 21	Depositor
Cell constants a, b, c, α , β , γ	65.25Å 267.29Å 187.68Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	10.00 – 2.20	Depositor
% Data completeness (in resolution range)	91.1 (10.00-2.20)	Depositor
R_{merge}	0.07	Depositor
R_{sym}	0.06	Depositor
Refinement program	CNS	Depositor
R, R_{free}	0.221 , 0.279	Depositor
Estimated twinning fraction	No twinning to report.	Xtrriage
Total number of atoms	11443	wwPDB-VP
Average B, all atoms (Å ²)	37.0	wwPDB-VP

5 Model quality ⓘ

5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: 5PA

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	0.36	0/2656	0.94	8/3593 (0.2%)
1	B	0.36	0/2656	0.91	4/3593 (0.1%)
1	C	0.44	0/2656	0.97	13/3593 (0.4%)
1	D	0.48	0/2656	0.98	12/3593 (0.3%)
All	All	0.42	0/10624	0.95	37/14372 (0.3%)

There are no bond length outliers.

All (37) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	176	VAL	N-CA-C	-10.63	99.41	111.00
1	C	176	VAL	N-CA-C	-9.88	100.23	111.00
1	A	203	GLY	N-CA-C	8.49	124.79	114.69
1	B	176	VAL	N-CA-C	-8.39	102.25	110.72
1	B	3	VAL	N-CA-C	-8.21	100.93	113.16
1	A	176	VAL	N-CA-C	-7.71	101.45	111.09
1	C	38	ARG	N-CA-C	7.45	121.53	108.56
1	A	38	ARG	N-CA-C	7.11	120.92	108.56
1	C	222	VAL	N-CA-C	7.04	118.96	108.54
1	D	263	ARG	N-CA-C	6.94	121.57	113.18
1	D	105	ILE	N-CA-C	6.15	115.67	108.96
1	C	203	GLY	N-CA-C	6.07	127.57	113.18
1	D	38	ARG	N-CA-C	6.03	119.05	108.56
1	B	59	VAL	CB-CA-C	-6.03	107.97	113.70
1	D	222	VAL	N-CA-C	6.03	117.46	108.54
1	D	50	ASN	N-CA-C	5.96	118.56	111.71
1	A	288	GLY	N-CA-C	-5.94	106.53	115.32
1	C	161	ILE	CA-C-N	5.78	126.10	119.92
1	C	161	ILE	C-N-CA	5.78	126.10	119.92
1	D	118	ASN	N-CA-C	5.66	117.45	111.28

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	292	ASP	CA-C-N	5.65	125.33	119.56
1	A	292	ASP	C-N-CA	5.65	125.33	119.56
1	C	133	GLU	N-CA-C	5.62	119.76	113.02
1	C	118	ASN	N-CA-C	5.61	117.85	111.11
1	D	39	GLU	N-CA-C	-5.61	105.69	112.54
1	D	43	SER	N-CA-C	5.52	117.23	108.79
1	D	230	THR	N-CA-C	-5.52	102.17	110.06
1	C	59	VAL	CB-CA-C	-5.50	108.52	114.35
1	C	204	SER	N-CA-C	5.41	117.94	111.71
1	A	186	GLU	N-CA-C	-5.35	105.53	111.36
1	D	203	GLY	N-CA-C	5.28	122.60	115.32
1	D	165	CYS	N-CA-C	-5.25	106.26	113.56
1	C	43	SER	N-CA-C	5.23	117.02	109.07
1	C	110	LYS	N-CA-C	5.23	117.66	111.33
1	B	38	ARG	N-CA-C	5.21	117.63	108.56
1	C	3	VAL	N-CA-C	-5.20	105.42	113.16
1	A	59	VAL	CB-CA-C	-5.09	108.96	114.35

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	2605	0	2589	155	0
1	B	2605	0	2589	187	0
1	C	2605	0	2589	93	0
1	D	2605	0	2589	112	1
2	A	22	0	13	10	0
2	B	22	0	13	3	0
2	C	22	0	13	3	0
2	D	22	0	13	17	0
3	A	126	0	0	12	0
3	B	125	0	0	13	0
3	C	366	0	0	22	1
3	D	318	0	0	24	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
All	All	11443	0	10408	526	2

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 25.

All (526) 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:B:77:GLN:HE22	1:B:117:GLY:HA3	1.12	1.07
1:B:116:VAL:HG12	1:B:117:GLY:H	1.17	1.04
1:B:214:ALA:HA	1:B:219:GLN:HE21	1.26	0.99
1:D:164:GLY:HA2	2:D:1701:5PA:H91	1.44	0.98
1:A:116:VAL:HG12	1:A:117:GLY:H	1.28	0.97
1:D:164:GLY:CA	2:D:1701:5PA:H91	1.94	0.97
1:A:202:THR:N	2:A:1401:5PA:O3P	1.99	0.95
1:D:164:GLY:N	2:D:1701:5PA:H92	1.81	0.94
1:D:164:GLY:CA	2:D:1701:5PA:C9	2.46	0.94
1:B:185:GLN:HA	1:B:188:GLU:HG2	1.50	0.93
1:B:79:ASN:N	2:B:1501:5PA:O7	2.01	0.92
2:D:1701:5PA:O8	3:D:1760:HOH:O	1.89	0.91
1:D:146:ASN:HB2	3:D:1974:HOH:O	1.69	0.89
1:D:164:GLY:HA2	2:D:1701:5PA:C9	2.03	0.89
1:C:51:THR:HG23	1:C:83:MET:HE3	1.54	0.89
1:A:218:ARG:HH11	1:A:218:ARG:HB3	1.38	0.89
1:A:23:ARG:HH12	1:A:286:GLN:HA	1.39	0.88
1:A:273:ASN:HD22	1:A:275:GLY:H	1.18	0.87
1:A:142:LYS:HG2	1:A:146:ASN:HD21	1.37	0.87
1:B:143:SER:HA	1:B:146:ASN:HD22	1.41	0.85
1:A:23:ARG:NH2	1:B:92:GLY:HA2	1.92	0.85
1:D:132:ILE:HG22	1:D:133:GLU:H	1.41	0.85
1:C:142:LYS:HG2	1:C:146:ASN:HD21	1.43	0.83
1:A:116:VAL:HG12	1:A:117:GLY:N	1.91	0.83
1:B:141:ARG:HA	1:B:141:ARG:HH11	1.42	0.83
1:A:23:ARG:NH1	1:A:286:GLN:HA	1.94	0.82
1:B:252:GLU:CD	1:B:252:GLU:H	1.88	0.82
1:A:92:GLY:HA2	1:B:23:ARG:HH21	1.45	0.82
1:D:164:GLY:H	2:D:1701:5PA:H92	1.43	0.81
1:B:217:GLY:HA2	1:B:219:GLN:HE22	1.45	0.80
1:B:40:ASP:HB3	1:B:324:GLY:HA2	1.62	0.79
1:A:78:SER:OG	2:A:1401:5PA:C7	2.30	0.79
1:B:298:LYS:O	1:B:301:GLN:HG2	1.83	0.78

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:23:ARG:HH12	1:B:286:GLN:HA	1.48	0.77
1:B:116:VAL:HG12	1:B:117:GLY:N	1.96	0.76
1:D:77:GLN:HE22	1:D:118:ASN:H	1.32	0.76
1:D:230:THR:OG1	1:D:233:LYS:HE2	1.85	0.76
1:B:12:THR:HA	1:B:43:SER:HB3	1.67	0.76
1:A:78:SER:OG	2:A:1401:5PA:O8	2.04	0.76
1:B:281:ARG:O	1:B:285:GLU:HB2	1.85	0.76
1:C:51:THR:HG23	1:C:83:MET:CE	2.16	0.76
1:D:164:GLY:CA	2:D:1701:5PA:H92	2.15	0.76
1:A:118:ASN:ND2	1:A:328:ALA:HB2	2.01	0.75
1:B:119:ILE:HG23	3:B:1571:HOH:O	1.87	0.74
1:A:116:VAL:CG1	1:A:117:GLY:H	2.00	0.74
1:C:166:SER:HA	1:C:204:SER:HB3	1.70	0.74
1:C:323:LEU:HD12	2:C:1601:5PA:C6	2.17	0.74
2:D:1701:5PA:O1P	3:D:1820:HOH:O	2.04	0.74
1:B:77:GLN:NE2	1:B:117:GLY:HA3	1.98	0.74
1:B:228:SER:HB3	3:B:1567:HOH:O	1.87	0.73
1:B:205:THR:O	1:B:209:ILE:HG13	1.89	0.73
1:B:76:ARG:NH1	1:B:131:VAL:HG13	2.04	0.73
1:C:322:HIS:HD2	1:C:324:GLY:H	1.37	0.72
1:B:78:SER:OG	2:B:1501:5PA:O8	2.04	0.72
1:B:109:GLU:HG2	1:B:331:ALA:O	1.89	0.72
1:A:142:LYS:HG2	1:A:146:ASN:ND2	2.04	0.71
1:A:78:SER:OG	2:A:1401:5PA:O7	2.07	0.71
1:A:21:LEU:HD22	1:A:287:GLU:HG3	1.72	0.71
1:B:304:ILE:O	1:B:308:LYS:HG2	1.91	0.71
1:A:322:HIS:HD2	1:A:324:GLY:H	1.39	0.71
1:B:219:GLN:CD	1:B:219:GLN:H	1.98	0.70
1:D:48:GLY:HA2	1:D:52:LEU:HD22	1.73	0.70
1:B:37:LYS:HG2	1:B:178:PHE:CE1	2.26	0.70
1:B:37:LYS:HG2	1:B:178:PHE:HE1	1.55	0.70
1:A:78:SER:HG	2:A:1401:5PA:C7	2.05	0.70
1:A:273:ASN:HD22	1:A:275:GLY:N	1.90	0.69
1:A:100:GLU:HA	1:A:132:ILE:HG22	1.75	0.69
1:D:313:LYS:HG3	1:D:316:ALA:HB2	1.74	0.68
1:A:166:SER:HA	1:A:204:SER:HB3	1.75	0.68
1:C:302:GLY:O	1:C:306:LEU:HD13	1.94	0.68
1:D:68:THR:OG1	1:D:69:HIS:HD2	1.76	0.67
1:D:308:LYS:HD3	3:D:1919:HOH:O	1.94	0.67
1:D:186:GLU:CD	1:D:218:ARG:HH22	2.02	0.67
1:D:98:ILE:HD13	1:D:130:ARG:HG3	1.77	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:296:GLU:OE1	2:C:1601:5PA:N1	2.28	0.67
1:C:339:LYS:HA	3:C:1946:HOH:O	1.94	0.66
1:D:308:LYS:HG3	3:D:1967:HOH:O	1.93	0.66
1:C:23:ARG:HD2	3:D:1948:HOH:O	1.95	0.66
1:C:48:GLY:HA2	1:C:52:LEU:HD22	1.76	0.66
1:A:102:TRP:CD1	1:A:136:PHE:HA	2.31	0.66
1:D:271:VAL:HG23	3:D:1943:HOH:O	1.96	0.66
1:C:23:ARG:NH1	1:C:286:GLN:HA	2.10	0.66
1:D:107:GLU:OE2	1:D:110:LYS:HD3	1.96	0.65
1:D:313:LYS:HE2	1:D:316:ALA:HA	1.78	0.65
1:A:20:ASN:C	1:A:20:ASN:HD22	2.02	0.65
1:A:62:ILE:HD13	1:A:70:LEU:HD21	1.79	0.65
1:B:175:PHE:O	1:B:178:PHE:HB3	1.97	0.65
1:C:232:GLU:HB2	3:C:1864:HOH:O	1.97	0.64
1:A:23:ARG:HH21	1:B:92:GLY:HA2	1.62	0.64
1:A:51:THR:HG21	1:A:80:GLN:HA	1.80	0.64
1:A:240:ARG:HG3	3:A:1523:HOH:O	1.97	0.64
1:C:1:ALA:HA	1:C:249:ILE:O	1.96	0.64
1:A:92:GLY:HA2	1:B:23:ARG:NH2	2.13	0.64
1:B:132:ILE:HG22	1:B:133:GLU:H	1.63	0.64
1:B:199:CYS:HB2	1:B:299:SER:HB3	1.79	0.64
1:B:132:ILE:HG22	1:B:133:GLU:N	2.13	0.64
1:D:186:GLU:OE1	1:D:218:ARG:NH2	2.31	0.63
1:D:205:THR:OG1	2:D:1701:5PA:O2P	2.16	0.63
1:B:322:HIS:CD2	1:B:324:GLY:H	2.17	0.63
1:B:67:TYR:HA	1:B:157:LYS:HB2	1.80	0.63
1:C:323:LEU:HD12	2:C:1601:5PA:H6	1.80	0.63
1:B:217:GLY:CA	1:B:219:GLN:HE22	2.11	0.62
1:C:23:ARG:NH2	1:D:92:GLY:HA2	2.14	0.62
1:B:217:GLY:HA2	1:B:219:GLN:NE2	2.14	0.62
1:C:51:THR:HG21	1:C:80:GLN:HA	1.81	0.62
1:B:70:LEU:HD11	1:B:87:LEU:HD12	1.81	0.62
1:C:77:GLN:HE22	1:C:118:ASN:H	1.45	0.62
1:C:80:GLN:OE1	1:C:164:GLY:HA2	1.99	0.62
1:A:70:LEU:HD23	1:A:159:TYR:HB3	1.81	0.62
1:A:266:TYR:CD1	1:A:267:PRO:HA	2.36	0.61
1:C:142:LYS:HG2	1:C:146:ASN:ND2	2.11	0.61
1:C:87:LEU:HD22	1:C:91:LEU:HG	1.82	0.61
1:A:185:GLN:HA	1:A:188:GLU:HG2	1.82	0.61
1:B:195:LYS:HD2	1:B:223:ILE:HD11	1.81	0.61
1:A:232:GLU:HG2	1:A:233:LYS:H	1.66	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:322:HIS:HD2	1:B:324:GLY:H	1.47	0.60
1:A:1:ALA:HB1	1:A:215:GLN:OE1	2.02	0.60
1:B:23:ARG:NH1	1:B:286:GLN:HA	2.16	0.60
1:D:324:GLY:O	2:D:1701:5PA:H2A3	2.02	0.60
1:A:203:GLY:H	2:A:1401:5PA:P	2.24	0.60
1:B:184:ASN:HB2	1:D:184:ASN:HD21	1.65	0.60
1:A:137:ASP:HB3	1:A:141:ARG:HD3	1.83	0.60
1:A:214:ALA:HA	1:A:219:GLN:HG3	1.84	0.59
1:B:71:VAL:HG11	1:B:148:LEU:HD23	1.84	0.59
1:B:142:LYS:O	1:B:142:LYS:HG2	2.02	0.59
1:B:302:GLY:O	1:B:306:LEU:HD13	2.02	0.59
1:A:77:GLN:HE22	1:A:118:ASN:H	1.50	0.59
1:B:252:GLU:HB3	3:B:1561:HOH:O	2.02	0.59
3:C:1916:HOH:O	1:D:23:ARG:HD2	2.01	0.59
1:B:201:VAL:HG22	1:B:202:THR:HG23	1.84	0.59
1:A:59:VAL:HG13	1:A:91:LEU:HD11	1.84	0.59
1:B:46:ALA:O	1:B:47:PHE:HB2	2.01	0.59
1:B:73:ILE:HG13	1:B:98:ILE:HB	1.85	0.59
1:D:322:HIS:HD2	1:D:324:GLY:H	1.50	0.59
1:B:116:VAL:CG1	1:B:117:GLY:H	2.02	0.59
1:D:164:GLY:HA3	2:D:1701:5PA:H91	1.81	0.59
1:D:231:SER:HB3	3:D:2002:HOH:O	2.02	0.59
1:D:167:GLU:HG2	3:D:1824:HOH:O	2.01	0.59
1:B:272:PRO:HG3	1:B:293:PRO:HB3	1.83	0.59
1:C:68:THR:OG1	1:C:69:HIS:HD2	1.86	0.58
1:C:273:ASN:HD22	1:C:275:GLY:H	1.51	0.58
1:C:273:ASN:ND2	1:C:276:THR:H	2.01	0.58
1:D:37:LYS:HD3	1:D:178:PHE:CE1	2.38	0.58
1:B:107:GLU:C	1:B:109:GLU:H	2.11	0.58
1:C:109:GLU:HG3	3:C:1881:HOH:O	2.03	0.58
1:C:51:THR:CG2	1:C:83:MET:HE3	2.32	0.58
1:C:274:GLU:O	1:C:278:GLU:HG3	2.03	0.58
1:D:273:ASN:HD22	1:D:275:GLY:N	2.01	0.58
1:A:304:ILE:O	1:A:308:LYS:HG2	2.04	0.58
1:D:273:ASN:HD22	1:D:275:GLY:H	1.52	0.58
1:C:185:GLN:HA	1:C:188:GLU:HG2	1.86	0.57
1:D:220:ASP:HA	3:D:1936:HOH:O	2.04	0.57
1:A:187:VAL:O	1:D:169:LYS:CE	2.52	0.57
1:B:40:ASP:CB	1:B:324:GLY:HA2	2.33	0.57
1:C:20:ASN:C	1:C:20:ASN:HD22	2.12	0.57
1:D:339:LYS:NZ	1:D:339:LYS:HB3	2.18	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:23:ARG:HH11	1:B:23:ARG:HG2	1.69	0.57
1:B:42:ASN:HD22	1:B:49:GLY:H	1.53	0.57
1:D:132:ILE:HG22	1:D:133:GLU:N	2.17	0.57
1:A:217:GLY:C	1:A:219:GLN:HE21	2.12	0.57
1:D:151:LEU:HD23	1:D:158:PRO:HB3	1.87	0.57
1:D:138:ILE:HG12	1:D:233:LYS:HE3	1.87	0.56
1:D:164:GLY:N	2:D:1701:5PA:C9	2.60	0.56
1:B:81:THR:HB	1:B:97:LEU:HD13	1.87	0.56
1:C:290:LEU:O	1:C:322:HIS:HE1	1.87	0.56
1:A:232:GLU:CD	1:A:232:GLU:H	2.12	0.56
1:D:77:GLN:HE22	1:D:118:ASN:N	2.03	0.56
1:C:230:THR:OG1	1:C:233:LYS:HE2	2.05	0.56
1:A:2:GLY:HA2	3:A:1494:HOH:O	2.04	0.56
1:A:166:SER:HB3	1:A:241:ILE:HD11	1.86	0.56
1:A:166:SER:HB3	1:A:241:ILE:CD1	2.36	0.56
1:B:107:GLU:O	1:B:110:LYS:HG2	2.06	0.56
1:B:164:GLY:C	1:B:166:SER:H	2.12	0.56
1:B:273:ASN:ND2	1:B:276:THR:H	2.03	0.56
1:C:52:LEU:HD13	1:C:83:MET:SD	2.46	0.56
1:C:164:GLY:C	1:C:166:SER:H	2.14	0.56
1:B:40:ASP:HB3	1:B:324:GLY:CA	2.34	0.56
1:B:51:THR:OG1	1:B:83:MET:SD	2.64	0.56
1:B:224:ALA:O	1:B:260:LEU:HD12	2.06	0.56
1:D:205:THR:N	2:D:1701:5PA:O2P	2.35	0.56
1:A:239:LEU:HD13	1:A:258:PHE:HD2	1.71	0.56
1:C:273:ASN:HD22	1:C:275:GLY:N	2.03	0.56
1:A:187:VAL:O	1:D:169:LYS:NZ	2.38	0.55
1:B:48:GLY:HA2	1:B:52:LEU:HD12	1.88	0.55
1:D:51:THR:HG21	1:D:80:GLN:HA	1.88	0.55
1:A:202:THR:CA	2:A:1401:5PA:O3P	2.54	0.55
1:A:196:ILE:HD12	1:A:213:MET:HE2	1.88	0.55
1:B:70:LEU:CD1	1:B:87:LEU:HD12	2.36	0.55
1:B:21:LEU:HD22	1:B:287:GLU:HG3	1.88	0.55
1:A:45:LEU:HD21	1:A:90:LYS:HD2	1.88	0.55
1:C:40:ASP:HB3	1:C:324:GLY:HA2	1.89	0.55
1:B:197:VAL:HG21	1:B:303:LEU:HD23	1.89	0.54
1:B:226:ASP:OD2	1:B:227:ALA:N	2.39	0.54
1:D:305:ALA:O	1:D:309:GLU:HG2	2.07	0.54
1:A:123:ARG:HG3	1:A:129:VAL:HG21	1.89	0.54
1:C:37:LYS:HD3	1:C:178:PHE:CZ	2.42	0.54
1:C:217:GLY:HA2	3:C:1645:HOH:O	2.06	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:37:LYS:HD3	1:D:178:PHE:CZ	2.43	0.54
1:A:230:THR:HG22	3:A:1433:HOH:O	2.08	0.54
1:B:272:PRO:CG	1:B:293:PRO:HB3	2.38	0.54
1:B:64:GLU:HA	3:B:1547:HOH:O	2.07	0.54
1:B:201:VAL:HG11	1:B:295:TYR:CE2	2.43	0.53
1:C:322:HIS:CD2	1:C:324:GLY:H	2.23	0.53
1:A:218:ARG:HB3	1:A:218:ARG:NH1	2.17	0.53
1:B:185:GLN:HG2	1:B:188:GLU:OE2	2.08	0.53
1:B:201:VAL:HG11	1:B:295:TYR:HE2	1.73	0.53
1:C:46:ALA:O	1:C:47:PHE:HB2	2.07	0.53
1:D:166:SER:OG	1:D:204:SER:HB2	2.09	0.53
1:B:23:ARG:NH1	1:B:23:ARG:HG2	2.22	0.53
1:D:205:THR:HB	3:D:1820:HOH:O	2.08	0.53
1:A:232:GLU:CD	1:A:232:GLU:N	2.66	0.53
1:B:156:HIS:O	1:B:158:PRO:HD3	2.08	0.53
1:B:273:ASN:HD22	1:B:275:GLY:H	1.55	0.53
1:D:77:GLN:NE2	1:D:118:ASN:H	2.03	0.53
1:C:23:ARG:CZ	3:C:1811:HOH:O	2.57	0.53
1:C:274:GLU:HG3	3:C:1748:HOH:O	2.09	0.53
1:A:116:VAL:HG13	1:B:330:SER:HB3	1.91	0.53
1:A:290:LEU:O	1:A:322:HIS:HE1	1.91	0.53
1:C:313:LYS:HE2	3:C:1920:HOH:O	2.09	0.53
1:D:130:ARG:HB2	1:D:132:ILE:HD11	1.90	0.53
1:D:212:GLY:O	1:D:215:GLN:HG3	2.08	0.53
1:A:36:ALA:HA	1:A:320:TYR:O	2.08	0.53
1:A:112:VAL:HG13	1:A:116:VAL:HG21	1.92	0.52
1:C:100:GLU:HG2	1:C:132:ILE:HD11	1.92	0.52
1:C:231:SER:HB2	3:C:1753:HOH:O	2.09	0.52
1:C:23:ARG:NH1	1:C:286:GLN:OE1	2.43	0.52
1:C:98:ILE:HD11	1:C:147:ALA:HB2	1.90	0.52
1:B:326:ALA:N	1:B:327:PRO:CD	2.72	0.52
1:D:324:GLY:O	3:D:1706:HOH:O	2.19	0.52
1:A:116:VAL:O	1:A:119:ILE:HG22	2.10	0.52
1:B:252:GLU:CD	1:B:252:GLU:N	2.63	0.52
1:A:149:GLN:HG3	1:A:153:ASP:OD2	2.10	0.51
1:A:116:VAL:CG1	1:A:117:GLY:N	2.61	0.51
1:C:2:GLY:O	1:C:5:LYS:HG2	2.09	0.51
1:A:134:ASP:HB3	1:A:141:ARG:HH21	1.74	0.51
1:A:169:LYS:HD3	3:A:1497:HOH:O	2.11	0.51
1:B:185:GLN:CA	1:B:188:GLU:HG2	2.33	0.51
1:A:39:GLU:HB2	1:A:322:HIS:O	2.11	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:68:THR:OG1	1:B:69:HIS:HD2	1.94	0.51
1:A:100:GLU:HG2	1:A:132:ILE:HG21	1.93	0.51
1:B:182:VAL:O	1:B:186:GLU:HG3	2.10	0.51
1:C:69:HIS:HE1	3:C:1730:HOH:O	1.93	0.51
1:C:107:GLU:O	1:C:110:LYS:HG2	2.11	0.51
1:D:73:ILE:HD11	1:D:100:GLU:CD	2.36	0.51
1:D:61:ASP:HB2	3:D:1838:HOH:O	2.11	0.50
1:A:112:VAL:HG13	1:A:116:VAL:CG2	2.41	0.50
1:B:235:LYS:HB2	1:B:260:LEU:HD23	1.93	0.50
1:B:137:ASP:C	1:B:139:GLY:H	2.20	0.50
1:A:100:GLU:HA	1:A:132:ILE:CG2	2.40	0.50
1:B:109:GLU:O	1:B:113:TYR:HB2	2.12	0.50
1:D:278:GLU:HG2	3:D:1970:HOH:O	2.11	0.50
1:B:42:ASN:ND2	1:B:49:GLY:O	2.45	0.50
1:B:71:VAL:HG22	1:B:144:PHE:CE1	2.47	0.50
1:B:269:TYR:HA	3:B:1586:HOH:O	2.12	0.50
1:D:339:LYS:HB3	1:D:339:LYS:HZ2	1.75	0.50
1:A:99:GLN:HE21	1:A:99:GLN:HA	1.76	0.50
1:B:23:ARG:HB3	1:B:287:GLU:OE2	2.12	0.50
1:B:28:LEU:HD22	1:B:304:ILE:HG23	1.94	0.50
1:C:73:ILE:HG12	1:C:74:GLY:N	2.27	0.50
1:B:39:GLU:O	1:B:42:ASN:ND2	2.45	0.49
1:B:339:LYS:HE3	1:B:341:ALA:OXT	2.12	0.49
1:D:290:LEU:O	1:D:322:HIS:HE1	1.95	0.49
1:A:182:VAL:O	1:A:186:GLU:HG3	2.11	0.49
1:B:103:VAL:HG22	1:B:269:TYR:O	2.13	0.49
1:B:293:PRO:HD3	1:B:329:LEU:CD1	2.42	0.49
1:C:23:ARG:NH1	3:C:1811:HOH:O	2.44	0.49
1:D:313:LYS:HE2	1:D:316:ALA:CA	2.42	0.49
1:A:152:GLU:HG2	3:A:1486:HOH:O	2.12	0.49
1:C:77:GLN:HE22	1:C:118:ASN:N	2.10	0.49
1:A:20:ASN:C	1:A:20:ASN:ND2	2.68	0.49
1:B:274:GLU:O	1:B:278:GLU:HB2	2.13	0.49
1:D:239:LEU:HD13	1:D:258:PHE:CD2	2.47	0.49
1:A:340:THR:HG21	3:A:1488:HOH:O	2.11	0.49
1:B:115:ARG:C	3:B:1571:HOH:O	2.56	0.49
1:B:184:ASN:HB2	1:D:184:ASN:ND2	2.26	0.49
1:D:149:GLN:HG2	3:D:1951:HOH:O	2.12	0.49
1:A:63:VAL:HG22	3:A:1476:HOH:O	2.13	0.49
1:A:81:THR:HB	1:A:97:LEU:HD13	1.93	0.49
1:A:118:ASN:HD21	1:A:328:ALA:HB2	1.74	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:76:ARG:NH2	1:D:132:ILE:O	2.31	0.49
1:D:102:TRP:CD1	1:D:136:PHE:HA	2.47	0.49
1:B:145:ALA:HA	1:B:148:LEU:HD12	1.95	0.49
1:D:268:CYS:HB3	3:D:1943:HOH:O	2.13	0.49
1:A:290:LEU:O	1:A:322:HIS:CE1	2.66	0.48
1:B:142:LYS:O	1:B:146:ASN:ND2	2.46	0.48
1:A:23:ARG:HH21	1:B:92:GLY:CA	2.25	0.48
1:B:219:GLN:H	1:B:219:GLN:NE2	2.09	0.48
1:B:225:ILE:HG21	1:B:299:SER:HA	1.96	0.48
1:C:110:LYS:HB3	3:C:1925:HOH:O	2.12	0.48
1:A:143:SER:HA	1:A:146:ASN:HD22	1.78	0.48
1:A:148:LEU:HD11	1:A:160:PRO:HB3	1.95	0.48
1:C:293:PRO:HD3	1:C:329:LEU:HD23	1.95	0.48
1:A:281:ARG:HH21	1:A:337:PRO:HD2	1.78	0.48
1:B:308:LYS:C	1:B:310:ASP:H	2.20	0.48
1:A:69:HIS:CG	1:A:94:LYS:HB2	2.49	0.48
1:A:69:HIS:O	1:A:158:PRO:HA	2.13	0.48
1:A:282:THR:O	1:A:286:GLN:HG2	2.14	0.48
1:B:22:ASN:O	1:B:25:SER:HB2	2.14	0.48
1:B:164:GLY:C	1:B:166:SER:N	2.71	0.48
1:B:214:ALA:HB2	1:B:219:GLN:HG3	1.96	0.48
1:B:272:PRO:HG3	1:B:293:PRO:CB	2.43	0.48
1:D:326:ALA:N	1:D:327:PRO:CD	2.77	0.48
1:A:21:LEU:HD22	1:A:287:GLU:CG	2.42	0.48
1:A:120:GLU:OE1	1:B:330:SER:HA	2.13	0.48
1:A:308:LYS:C	1:A:310:ASP:H	2.22	0.48
1:B:141:ARG:HA	1:B:141:ARG:NH1	2.18	0.48
1:C:142:LYS:HE3	3:C:1905:HOH:O	2.14	0.48
1:A:324:GLY:HA2	3:A:1407:HOH:O	2.13	0.48
1:A:100:GLU:HG2	1:A:132:ILE:CG2	2.44	0.48
1:B:76:ARG:HH12	1:B:131:VAL:HG13	1.76	0.48
1:B:239:LEU:HD21	1:B:256:LYS:O	2.14	0.48
1:B:292:ASP:HA	1:B:329:LEU:HD13	1.96	0.48
1:B:116:VAL:O	1:B:119:ILE:HG22	2.14	0.47
1:B:202:THR:OG1	2:B:1501:5PA:O3P	2.23	0.47
1:A:48:GLY:HA2	1:A:52:LEU:HD22	1.96	0.47
1:D:20:ASN:ND2	3:D:1724:HOH:O	2.45	0.47
1:A:72:SER:HA	1:A:161:ILE:O	2.14	0.47
1:B:216:TYR:HD2	1:D:187:VAL:HG12	1.78	0.47
1:C:335:PHE:HE1	3:C:1881:HOH:O	1.97	0.47
1:B:45:LEU:HD21	1:B:90:LYS:HD2	1.96	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:185:GLN:O	1:D:189:LEU:HG	2.15	0.47
1:A:68:THR:OG1	1:A:69:HIS:HD2	1.98	0.47
1:A:165:CYS:O	1:A:171:GLY:HA3	2.14	0.47
1:B:217:GLY:CA	1:B:219:GLN:NE2	2.77	0.47
1:B:217:GLY:C	1:B:219:GLN:HE22	2.22	0.47
1:D:80:GLN:OE1	1:D:164:GLY:CA	2.63	0.47
1:A:273:ASN:ND2	1:A:275:GLY:H	1.99	0.47
1:B:42:ASN:HB2	1:B:49:GLY:H	1.80	0.47
1:C:284:ALA:HB1	1:D:125:MET:HG2	1.97	0.47
1:D:115:ARG:O	1:D:120:GLU:HB2	2.15	0.47
1:A:212:GLY:O	1:A:215:GLN:HG3	2.15	0.47
1:B:102:TRP:CD1	1:B:136:PHE:HA	2.51	0.46
1:A:107:GLU:O	1:A:110:LYS:HG2	2.15	0.46
1:B:105:ILE:HG21	1:B:110:LYS:HA	1.98	0.46
1:C:5:LYS:HG3	1:C:6:PHE:CD1	2.51	0.46
1:D:46:ALA:O	1:D:47:PHE:HB2	2.14	0.46
1:A:252:GLU:O	1:A:253:HIS:C	2.58	0.46
1:B:144:PHE:O	1:B:148:LEU:HG	2.15	0.46
1:C:4:ALA:HA	3:C:1815:HOH:O	2.16	0.46
1:A:41:CYS:HA	3:A:1472:HOH:O	2.16	0.46
1:B:264:PHE:HB3	1:B:301:GLN:NE2	2.30	0.46
1:A:235:LYS:O	1:A:239:LEU:HB2	2.16	0.46
1:C:59:VAL:N	1:C:60:PRO:CD	2.79	0.46
1:C:290:LEU:O	1:C:322:HIS:CE1	2.69	0.46
1:C:98:ILE:HD11	1:C:147:ALA:CB	2.46	0.46
1:D:39:GLU:HB2	1:D:322:HIS:O	2.15	0.46
1:A:225:ILE:HG21	1:A:299:SER:HA	1.97	0.46
1:C:23:ARG:HH21	1:D:92:GLY:HA2	1.81	0.46
1:A:339:LYS:HG2	1:A:340:THR:N	2.30	0.45
1:C:102:TRP:CD1	1:C:136:PHE:HA	2.51	0.45
1:D:313:LYS:HD2	1:D:314:PRO:O	2.16	0.45
1:A:267:PRO:O	1:A:268:CYS:HB3	2.16	0.45
1:B:87:LEU:HD13	1:B:91:LEU:HG	1.98	0.45
1:B:239:LEU:HD13	1:B:258:PHE:CD2	2.51	0.45
2:D:1701:5PA:H2A3	3:D:1710:HOH:O	2.16	0.45
1:A:176:VAL:HG11	1:A:249:ILE:HG21	1.98	0.45
1:D:51:THR:OG1	1:D:83:MET:SD	2.72	0.45
1:A:185:GLN:HA	1:A:188:GLU:CG	2.47	0.45
1:A:239:LEU:HD13	1:A:258:PHE:CD2	2.51	0.45
1:A:326:ALA:N	1:A:327:PRO:CD	2.79	0.45
1:A:245:THR:O	1:A:249:ILE:HG12	2.15	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:75:GLY:O	1:B:78:SER:N	2.49	0.45
1:B:169:LYS:NZ	1:B:169:LYS:HB3	2.31	0.45
1:D:164:GLY:O	1:D:165:CYS:HB2	2.15	0.45
1:A:1:ALA:HA	1:A:249:ILE:HB	1.98	0.45
1:D:75:GLY:N	1:D:78:SER:OG	2.50	0.45
1:A:167:GLU:HG3	3:A:1495:HOH:O	2.15	0.45
1:C:233:LYS:HG3	1:C:234:THR:N	2.31	0.45
1:A:71:VAL:HG23	1:A:96:VAL:O	2.17	0.45
1:B:217:GLY:C	1:B:219:GLN:NE2	2.75	0.45
1:C:205:THR:O	1:C:209:ILE:HG13	2.16	0.45
1:C:313:LYS:HG3	1:C:316:ALA:HB2	1.98	0.45
1:D:313:LYS:HD2	1:D:313:LYS:C	2.42	0.45
1:A:110:LYS:HB3	3:A:1487:HOH:O	2.17	0.45
1:A:116:VAL:HG13	1:B:330:SER:CB	2.46	0.45
1:A:203:GLY:N	2:A:1401:5PA:P	2.90	0.45
1:B:162:PRO:HB2	3:B:1616:HOH:O	2.17	0.45
1:B:273:ASN:HD22	1:B:275:GLY:N	2.14	0.45
1:C:20:ASN:C	1:C:20:ASN:ND2	2.75	0.45
1:B:51:THR:HG21	1:B:80:GLN:HA	1.99	0.45
1:B:96:VAL:HG21	1:B:151:LEU:HD11	1.98	0.45
1:A:37:LYS:HD3	1:A:178:PHE:CZ	2.52	0.44
1:B:148:LEU:O	1:B:152:GLU:HG3	2.16	0.44
1:D:312:PHE:HA	3:D:1996:HOH:O	2.17	0.44
1:A:219:GLN:H	1:A:219:GLN:NE2	2.16	0.44
1:A:290:LEU:HD13	1:B:121:LEU:HD22	2.00	0.44
1:B:13:PHE:CE1	1:B:43:SER:HA	2.53	0.44
1:B:120:GLU:HB2	3:B:1571:HOH:O	2.17	0.44
1:A:164:GLY:C	1:A:166:SER:N	2.73	0.44
1:D:22:ASN:O	1:D:26:GLN:HG3	2.16	0.44
1:A:23:ARG:NH2	1:B:92:GLY:CA	2.73	0.44
1:A:71:VAL:HG11	1:A:148:LEU:CD2	2.48	0.44
1:B:230:THR:O	1:B:232:GLU:N	2.51	0.44
1:C:76:ARG:NH1	1:C:100:GLU:C	2.75	0.44
1:A:103:VAL:CG2	1:A:270:GLY:HA3	2.48	0.44
1:B:106:PRO:O	1:B:107:GLU:C	2.61	0.44
1:D:226:ASP:HB2	1:D:260:LEU:HD11	2.00	0.44
1:A:232:GLU:HG2	1:A:233:LYS:N	2.32	0.44
1:B:118:ASN:OD1	1:B:327:PRO:HB2	2.18	0.44
1:C:23:ARG:HH11	1:C:286:GLN:HA	1.82	0.44
1:C:103:VAL:HA	1:C:104:PRO:HD3	1.87	0.44
1:C:256:LYS:HE2	3:C:1959:HOH:O	2.17	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:20:ASN:C	1:B:20:ASN:HD22	2.24	0.44
1:C:140:MET:HG2	1:C:167:GLU:OE1	2.18	0.44
1:D:36:ALA:HA	1:D:320:TYR:O	2.18	0.44
1:D:273:ASN:ND2	1:D:276:THR:H	2.15	0.44
1:D:338:THR:HB	3:D:1983:HOH:O	2.17	0.44
1:A:107:GLU:HB3	3:A:1510:HOH:O	2.17	0.44
1:B:55:LEU:O	1:B:59:VAL:HG23	2.18	0.44
1:C:236:GLU:HG3	1:C:237:GLN:N	2.33	0.43
1:A:76:ARG:HH12	1:A:101:ASP:HB2	1.82	0.43
1:B:76:ARG:HH12	1:B:131:VAL:CG1	2.31	0.43
1:B:226:ASP:HB2	1:B:260:LEU:HD11	2.01	0.43
1:A:59:VAL:N	1:A:60:PRO:CD	2.82	0.43
1:A:303:LEU:HD13	1:A:303:LEU:C	2.43	0.43
1:C:293:PRO:HD3	1:C:329:LEU:CD2	2.47	0.43
1:A:43:SER:HB3	1:A:52:LEU:HD23	2.00	0.43
1:B:20:ASN:C	1:B:20:ASN:ND2	2.76	0.43
1:B:59:VAL:O	1:B:60:PRO:C	2.61	0.43
1:B:303:LEU:O	1:B:307:ILE:HG13	2.19	0.43
1:B:326:ALA:O	1:B:329:LEU:HB2	2.18	0.43
1:C:37:LYS:HD3	1:C:178:PHE:CE1	2.53	0.43
1:A:209:ILE:O	1:A:213:MET:HG2	2.19	0.43
1:D:20:ASN:C	1:D:20:ASN:HD22	2.26	0.43
1:D:61:ASP:OD2	1:D:159:TYR:CE1	2.72	0.43
1:A:67:TYR:HA	1:A:157:LYS:HB3	2.01	0.43
1:A:77:GLN:HE22	1:A:118:ASN:N	2.14	0.43
1:A:233:LYS:HG3	1:A:234:THR:N	2.33	0.43
1:B:235:LYS:HD2	1:B:260:LEU:HD23	2.00	0.43
1:C:121:LEU:HD22	1:D:290:LEU:HD13	2.00	0.43
1:C:149:GLN:HE21	1:C:153:ASP:CG	2.26	0.43
1:A:172:GLY:O	1:A:176:VAL:HG23	2.19	0.43
1:D:239:LEU:HD13	1:D:258:PHE:HD2	1.84	0.43
1:D:306:LEU:HD12	1:D:306:LEU:HA	1.91	0.43
1:D:232:GLU:HB3	3:D:1942:HOH:O	2.19	0.43
1:B:59:VAL:HA	1:B:62:ILE:HD12	1.99	0.42
1:B:235:LYS:HG3	1:B:258:PHE:CE2	2.54	0.42
1:C:274:GLU:HG2	3:C:1702:HOH:O	2.18	0.42
1:D:80:GLN:OE1	1:D:164:GLY:HA2	2.19	0.42
1:A:330:SER:HB3	1:B:116:VAL:HG11	2.02	0.42
1:B:120:GLU:N	3:B:1571:HOH:O	2.52	0.42
1:B:233:LYS:HG3	1:B:234:THR:N	2.34	0.42
1:C:9:TYR:CD2	1:C:59:VAL:HG11	2.54	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:50:ASN:HD22	1:D:50:ASN:N	2.16	0.42
1:B:130:ARG:HH12	1:B:150:GLU:CD	2.27	0.42
1:B:132:ILE:CG2	1:B:133:GLU:N	2.82	0.42
1:A:199:CYS:HB2	1:A:299:SER:HB3	2.00	0.42
1:A:273:ASN:ND2	1:A:275:GLY:N	2.63	0.42
1:B:18:ILE:HG12	1:B:37:LYS:HD2	2.00	0.42
1:B:42:ASN:HD22	1:B:49:GLY:N	2.17	0.42
1:B:137:ASP:HB3	1:B:141:ARG:NE	2.35	0.42
1:B:192:LYS:HD3	3:B:1609:HOH:O	2.20	0.42
1:C:107:GLU:HB3	3:C:1726:HOH:O	2.19	0.42
1:C:194:ASP:O	1:C:195:LYS:HD3	2.18	0.42
1:A:68:THR:CB	1:A:69:HIS:HD2	2.31	0.42
1:A:330:SER:HB3	1:B:116:VAL:CG1	2.49	0.42
1:B:28:LEU:CD2	1:B:304:ILE:HG23	2.50	0.42
1:B:184:ASN:ND2	3:B:1579:HOH:O	2.53	0.42
1:C:110:LYS:HE3	1:C:111:ASP:OD2	2.20	0.42
1:D:51:THR:HG21	1:D:80:GLN:CA	2.49	0.42
1:D:104:PRO:HD2	3:D:1943:HOH:O	2.19	0.42
1:D:137:ASP:HA	1:D:233:LYS:NZ	2.35	0.42
1:B:216:TYR:CD1	1:B:216:TYR:N	2.87	0.42
1:B:143:SER:HA	1:B:146:ASN:ND2	2.22	0.42
1:D:80:GLN:HB3	2:D:1701:5PA:C7	2.50	0.42
1:D:324:GLY:O	2:D:1701:5PA:C2A	2.67	0.42
1:A:293:PRO:HD3	1:A:329:LEU:HD13	2.02	0.42
1:D:111:ASP:O	1:D:115:ARG:NH2	2.53	0.42
1:B:23:ARG:NH1	1:B:286:GLN:O	2.53	0.42
1:C:115:ARG:O	1:C:120:GLU:HB2	2.20	0.42
1:B:147:ALA:O	1:B:150:GLU:HB3	2.20	0.41
1:B:239:LEU:HD13	1:B:258:PHE:HD2	1.83	0.41
1:B:274:GLU:HG3	3:B:1526:HOH:O	2.20	0.41
1:A:151:LEU:HB2	1:A:158:PRO:HG2	2.03	0.41
1:B:298:LYS:NZ	3:B:1586:HOH:O	2.53	0.41
1:D:304:ILE:CG2	1:D:308:LYS:HE3	2.50	0.41
1:D:339:LYS:HE3	3:D:2019:HOH:O	2.20	0.41
1:B:75:GLY:O	1:B:77:GLN:N	2.54	0.41
1:B:229:PHE:HD1	1:B:265:ALA:HB3	1.86	0.41
1:B:230:THR:O	1:B:231:SER:C	2.64	0.41
1:B:267:PRO:O	1:B:268:CYS:HB2	2.20	0.41
1:C:150:GLU:HA	3:C:1804:HOH:O	2.20	0.41
1:B:87:LEU:HD13	1:B:87:LEU:C	2.45	0.41
1:D:61:ASP:OD2	1:D:159:TYR:HE1	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:116:VAL:CG1	1:B:330:SER:HB3	2.50	0.41
1:B:260:LEU:O	1:B:262:THR:HG23	2.21	0.41
1:C:78:SER:HB2	3:C:1611:HOH:O	2.20	0.41
1:A:51:THR:OG1	1:A:83:MET:SD	2.77	0.41
1:A:217:GLY:C	1:A:219:GLN:NE2	2.78	0.41
1:A:281:ARG:NH2	1:A:337:PRO:HD2	2.36	0.41
1:C:336:PHE:CD2	1:D:124:ILE:HG12	2.56	0.41
1:D:76:ARG:NE	1:D:131:VAL:HG13	2.36	0.41
1:D:213:MET:HE3	1:D:218:ARG:HB2	2.03	0.41
1:A:37:LYS:NZ	1:A:185:GLN:OE1	2.53	0.41
1:C:76:ARG:CZ	1:C:131:VAL:HG13	2.51	0.41
1:C:278:GLU:HB3	3:C:1929:HOH:O	2.21	0.41
1:C:326:ALA:N	1:C:327:PRO:CD	2.84	0.41
1:D:52:LEU:HD12	1:D:52:LEU:HA	1.92	0.41
1:B:42:ASN:HD22	1:B:49:GLY:C	2.29	0.41
1:B:48:GLY:HA2	1:B:52:LEU:CD1	2.49	0.41
1:B:76:ARG:NH2	1:B:101:ASP:HB2	2.36	0.41
3:C:1650:HOH:O	1:D:90:LYS:HE3	2.21	0.41
1:D:48:GLY:HA2	1:D:52:LEU:CD2	2.46	0.41
1:D:218:ARG:HD2	1:D:221:ASP:OD2	2.20	0.41
1:A:80:GLN:O	1:A:84:VAL:HG23	2.21	0.41
1:A:203:GLY:N	2:A:1401:5PA:O3P	2.54	0.41
1:B:305:ALA:O	1:B:308:LYS:HB2	2.21	0.41
1:A:102:TRP:HZ3	2:A:1401:5PA:H101	1.86	0.40
1:A:329:LEU:HD23	1:B:121:LEU:CD2	2.51	0.40
1:B:71:VAL:HG11	1:B:148:LEU:CD2	2.49	0.40
1:B:103:VAL:CG2	1:B:270:GLY:HA3	2.51	0.40
1:B:301:GLN:HG3	1:B:302:GLY:N	2.35	0.40
1:C:164:GLY:C	1:C:166:SER:N	2.77	0.40
1:C:76:ARG:NH1	1:C:99:GLN:O	2.53	0.40
1:A:77:GLN:NE2	1:A:77:GLN:HA	2.37	0.40
1:A:226:ASP:HB2	1:A:260:LEU:HD11	2.03	0.40
1:B:281:ARG:NH2	1:B:337:PRO:O	2.50	0.40
1:D:94:LYS:NZ	3:D:1867:HOH:O	2.53	0.40
1:A:12:THR:HB	1:A:42:ASN:O	2.21	0.40
1:A:181:GLU:O	1:A:185:GLN:HG3	2.21	0.40
1:A:197:VAL:HG21	1:A:303:LEU:HD23	2.03	0.40
1:A:59:VAL:HB	1:A:60:PRO:HD3	2.03	0.40
1:A:96:VAL:HA	1:A:128:ASP:HB3	2.03	0.40
1:A:157:LYS:N	1:A:158:PRO:HD3	2.36	0.40
1:C:239:LEU:HD13	1:C:258:PHE:CD2	2.57	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:249:ILE:HG13	1:D:251:VAL:HG23	2.04	0.40

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

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:1808:HOH:O	3:C:1808:HOH:O[3_655]	1.49	0.71
1:D:26:GLN:NE2	1:D:26:GLN:NE2[3_655]	2.17	0.03

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	339/341 (99%)	311 (92%)	23 (7%)	5 (2%)	8 6
1	B	339/341 (99%)	286 (84%)	42 (12%)	11 (3%)	3 1
1	C	339/341 (99%)	322 (95%)	16 (5%)	1 (0%)	36 42
1	D	339/341 (99%)	320 (94%)	18 (5%)	1 (0%)	36 42
All	All	1356/1364 (99%)	1239 (91%)	99 (7%)	18 (1%)	9 8

All (18) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	76	ARG
1	B	204	SER
1	B	232	GLU
1	A	2	GLY
1	B	231	SER
1	A	112	VAL
1	A	113	TYR
1	B	107	GLU

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Mol	Chain	Res	Type
1	B	108	ALA
1	B	309	GLU
1	B	310	ASP
1	B	109	GLU
1	A	309	GLU
1	A	62	ILE
1	B	138	ILE
1	B	201	VAL
1	D	112	VAL
1	C	2	GLY

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	275/275 (100%)	271 (98%)	4 (2%)	57	73
1	B	275/275 (100%)	269 (98%)	6 (2%)	45	61
1	C	275/275 (100%)	266 (97%)	9 (3%)	33	45
1	D	275/275 (100%)	262 (95%)	13 (5%)	23	31
All	All	1100/1100 (100%)	1068 (97%)	32 (3%)	37	51

All (32) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	20	ASN
1	A	52	LEU
1	A	218	ARG
1	A	219	GLN
1	B	71	VAL
1	B	169	LYS
1	B	201	VAL
1	B	252	GLU
1	B	273	ASN
1	B	329	LEU
1	C	20	ASN

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Mol	Chain	Res	Type
1	C	51	THR
1	C	52	LEU
1	C	72	SER
1	C	87	LEU
1	C	236	GLU
1	C	239	LEU
1	C	273	ASN
1	C	303	LEU
1	D	50	ASN
1	D	52	LEU
1	D	130	ARG
1	D	133	GLU
1	D	151	LEU
1	D	184	ASN
1	D	236	GLU
1	D	239	LEU
1	D	273	ASN
1	D	303	LEU
1	D	306	LEU
1	D	313	LYS
1	D	339	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (40) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	20	ASN
1	A	69	HIS
1	A	77	GLN
1	A	99	GLN
1	A	146	ASN
1	A	149	GLN
1	A	184	ASN
1	A	219	GLN
1	A	273	ASN
1	A	301	GLN
1	A	322	HIS
1	B	20	ASN
1	B	42	ASN
1	B	69	HIS
1	B	77	GLN
1	B	99	GLN
1	B	114	ASN

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Mol	Chain	Res	Type
1	B	146	ASN
1	B	219	GLN
1	B	273	ASN
1	B	301	GLN
1	B	322	HIS
1	C	20	ASN
1	C	69	HIS
1	C	77	GLN
1	C	99	GLN
1	C	146	ASN
1	C	149	GLN
1	C	273	ASN
1	C	301	GLN
1	C	322	HIS
1	D	20	ASN
1	D	50	ASN
1	D	69	HIS
1	D	77	GLN
1	D	99	GLN
1	D	184	ASN
1	D	273	ASN
1	D	301	GLN
1	D	322	HIS

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

5.6 Ligand geometry ⓘ

4 ligands are modelled in this entry.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# $ Z > 2$	Counts	RMSZ	# $ Z > 2$
2	5PA	C	1601	-	22,23,23	2.60	8 (36%)	33,35,35	3.88	9 (27%)
2	5PA	B	1501	-	22,23,23	2.62	8 (36%)	33,35,35	3.88	9 (27%)
2	5PA	A	1401	-	22,23,23	2.60	8 (36%)	33,35,35	3.88	9 (27%)
2	5PA	D	1701	-	22,23,23	2.60	8 (36%)	33,35,35	3.87	8 (24%)

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	5PA	C	1601	-	-	3/15/22/22	0/2/2/2
2	5PA	B	1501	-	-	3/15/22/22	0/2/2/2
2	5PA	A	1401	-	-	6/15/22/22	0/2/2/2
2	5PA	D	1701	-	-	3/15/22/22	0/2/2/2

All (32) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	1501	5PA	C9-C8	6.82	1.58	1.51
2	C	1601	5PA	C9-C8	6.78	1.58	1.51
2	D	1701	5PA	C9-C8	6.77	1.58	1.51
2	A	1401	5PA	C9-C8	6.77	1.58	1.51
2	B	1501	5PA	C10-C8	6.16	1.58	1.51
2	A	1401	5PA	C10-C8	6.13	1.58	1.51
2	D	1701	5PA	C10-C8	6.12	1.58	1.51
2	C	1601	5PA	C10-C8	6.12	1.58	1.51
2	A	1401	5PA	C8-C7	3.51	1.61	1.53
2	B	1501	5PA	C8-C7	3.50	1.60	1.53
2	C	1601	5PA	C8-C7	3.50	1.60	1.53
2	D	1701	5PA	C8-C7	3.47	1.60	1.53
2	B	1501	5PA	C2-N1	3.05	1.39	1.33
2	A	1401	5PA	C2-N1	3.01	1.39	1.33

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	C	1601	5PA	C2-N1	3.01	1.39	1.33
2	D	1701	5PA	C2-N1	3.00	1.39	1.33
2	A	1401	5PA	C4A-C4	2.65	1.55	1.52
2	C	1601	5PA	C4A-C4	2.64	1.55	1.52
2	D	1701	5PA	C4A-C4	2.64	1.55	1.52
2	B	1501	5PA	C4A-C4	2.64	1.55	1.52
2	B	1501	5PA	C5-C4	2.53	1.44	1.40
2	D	1701	5PA	C5-C4	2.49	1.43	1.40
2	C	1601	5PA	C5-C4	2.48	1.43	1.40
2	A	1401	5PA	C5-C4	2.47	1.43	1.40
2	A	1401	5PA	P-O3P	-2.40	1.45	1.54
2	D	1701	5PA	P-O3P	-2.39	1.45	1.54
2	C	1601	5PA	P-O3P	-2.39	1.45	1.54
2	B	1501	5PA	P-O3P	-2.39	1.45	1.54
2	B	1501	5PA	C4A-N	-2.37	1.32	1.45
2	C	1601	5PA	C4A-N	-2.37	1.32	1.45
2	D	1701	5PA	C4A-N	-2.37	1.32	1.45
2	A	1401	5PA	C4A-N	-2.36	1.32	1.45

All (35) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	1401	5PA	C4A-N-C8	14.58	145.30	116.47
2	B	1501	5PA	C4A-N-C8	14.56	145.28	116.47
2	C	1601	5PA	C4A-N-C8	14.55	145.25	116.47
2	D	1701	5PA	C4A-N-C8	14.55	145.24	116.47
2	A	1401	5PA	C4-C4A-N	13.89	141.26	110.74
2	B	1501	5PA	C4-C4A-N	13.89	141.26	110.74
2	C	1601	5PA	C4-C4A-N	13.87	141.22	110.74
2	D	1701	5PA	C4-C4A-N	13.86	141.19	110.74
2	B	1501	5PA	O4P-C5A-C5	5.08	118.88	109.36
2	D	1701	5PA	O4P-C5A-C5	5.07	118.87	109.36
2	C	1601	5PA	O4P-C5A-C5	5.07	118.85	109.36
2	A	1401	5PA	O4P-C5A-C5	5.06	118.84	109.36
2	A	1401	5PA	C4A-C4-C5	2.68	122.67	119.75
2	B	1501	5PA	C4A-C4-C5	2.68	122.67	119.75
2	C	1601	5PA	C4A-C4-C5	2.68	122.67	119.75
2	D	1701	5PA	C4A-C4-C5	2.68	122.66	119.75
2	D	1701	5PA	C6-C5-C4	2.61	120.03	118.06
2	C	1601	5PA	C6-C5-C4	2.58	120.02	118.06
2	A	1401	5PA	C6-C5-C4	2.54	119.98	118.06
2	B	1501	5PA	C6-C5-C4	2.53	119.98	118.06

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	C	1601	5PA	C5-C6-N1	-2.51	119.75	123.83
2	D	1701	5PA	C5-C6-N1	-2.51	119.75	123.83
2	A	1401	5PA	C5-C6-N1	-2.50	119.76	123.83
2	B	1501	5PA	C5-C6-N1	-2.47	119.82	123.83
2	A	1401	5PA	O2P-P-O4P	-2.37	100.49	106.67
2	D	1701	5PA	O2P-P-O4P	-2.37	100.50	106.67
2	B	1501	5PA	O2P-P-O4P	-2.36	100.51	106.67
2	C	1601	5PA	O2P-P-O4P	-2.36	100.52	106.67
2	D	1701	5PA	O8-C7-C8	2.13	118.95	113.59
2	C	1601	5PA	O8-C7-C8	2.12	118.91	113.59
2	B	1501	5PA	O8-C7-C8	2.11	118.90	113.59
2	A	1401	5PA	O8-C7-C8	2.11	118.88	113.59
2	A	1401	5PA	O7-C7-C8	-2.01	117.96	122.93
2	B	1501	5PA	O7-C7-C8	-2.01	117.97	122.93
2	C	1601	5PA	O7-C7-C8	-2.00	117.98	122.93

There are no chirality outliers.

All (15) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	1401	5PA	C5A-O4P-P-O2P
2	A	1401	5PA	C5A-O4P-P-O3P
2	A	1401	5PA	C5-C4-C4A-N
2	B	1501	5PA	C5-C4-C4A-N
2	C	1601	5PA	C5-C4-C4A-N
2	D	1701	5PA	C5-C4-C4A-N
2	A	1401	5PA	C5A-O4P-P-O1P
2	A	1401	5PA	C3-C4-C4A-N
2	B	1501	5PA	C3-C4-C4A-N
2	C	1601	5PA	C3-C4-C4A-N
2	D	1701	5PA	C3-C4-C4A-N
2	A	1401	5PA	C4-C4A-N-C8
2	B	1501	5PA	C4-C4A-N-C8
2	C	1601	5PA	C4-C4A-N-C8
2	D	1701	5PA	C4-C4A-N-C8

There are no ring outliers.

4 monomers are involved in 33 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	C	1601	5PA	3	0

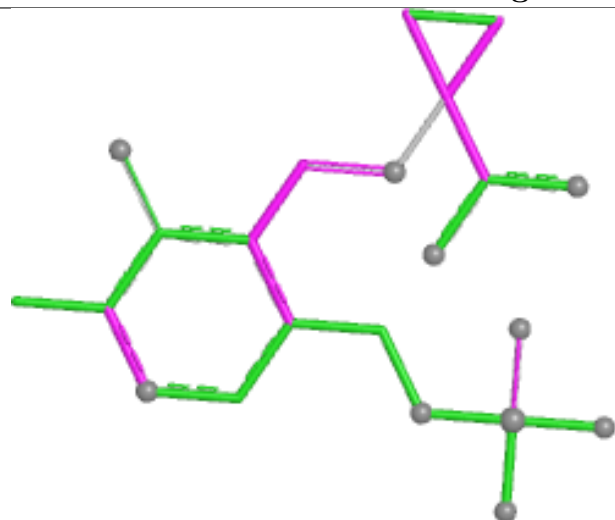
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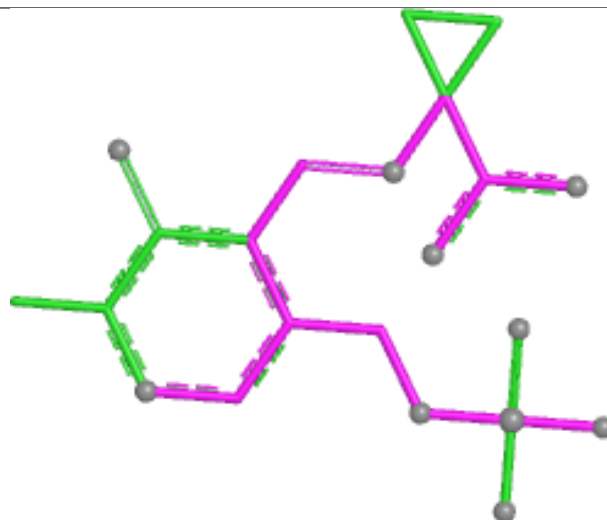
Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	B	1501	5PA	3	0
2	A	1401	5PA	10	0
2	D	1701	5PA	17	0

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.

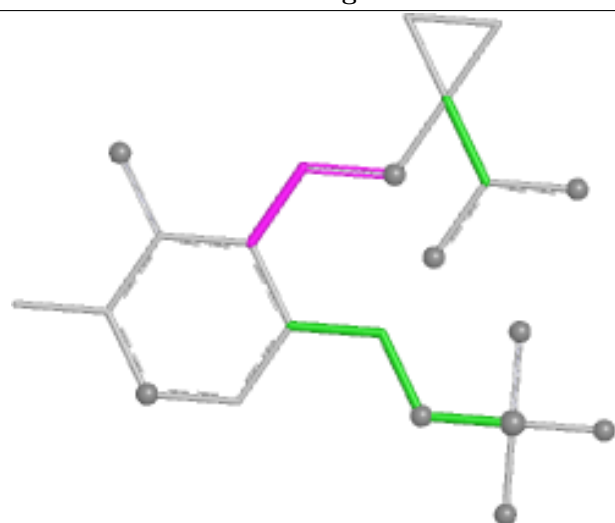
Ligand 5PA C 1601



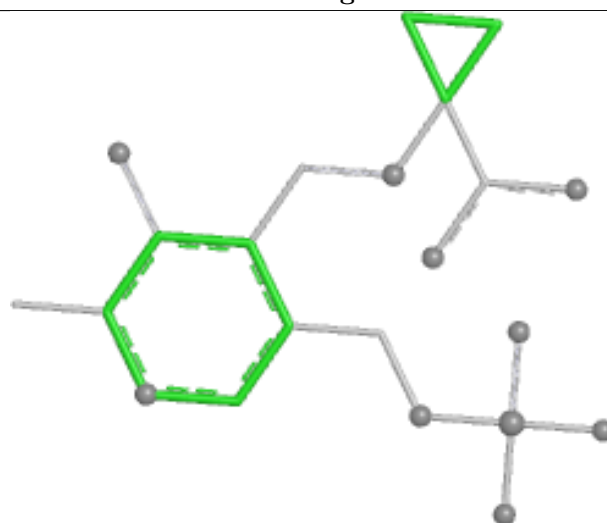
Bond lengths



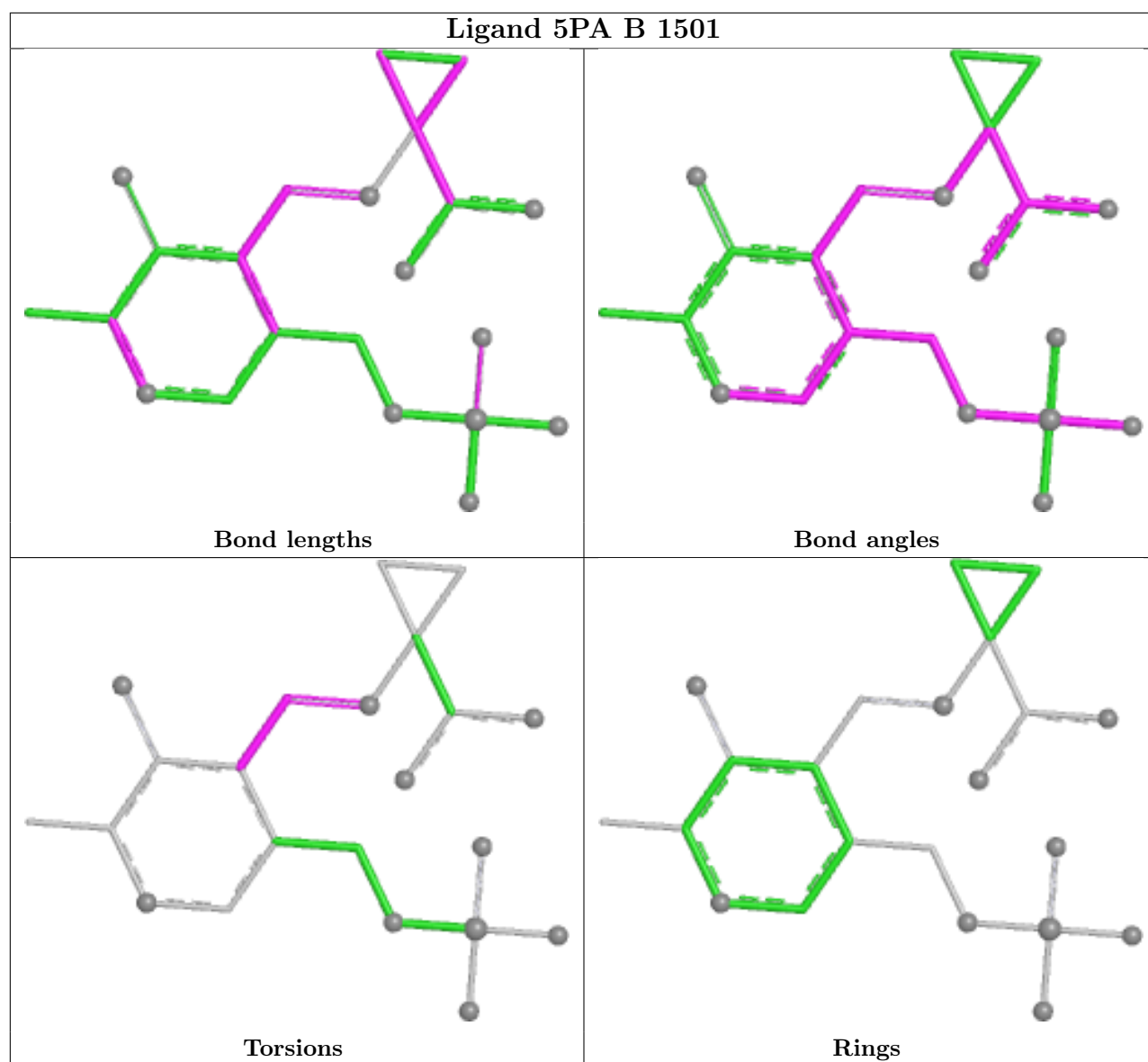
Bond angles

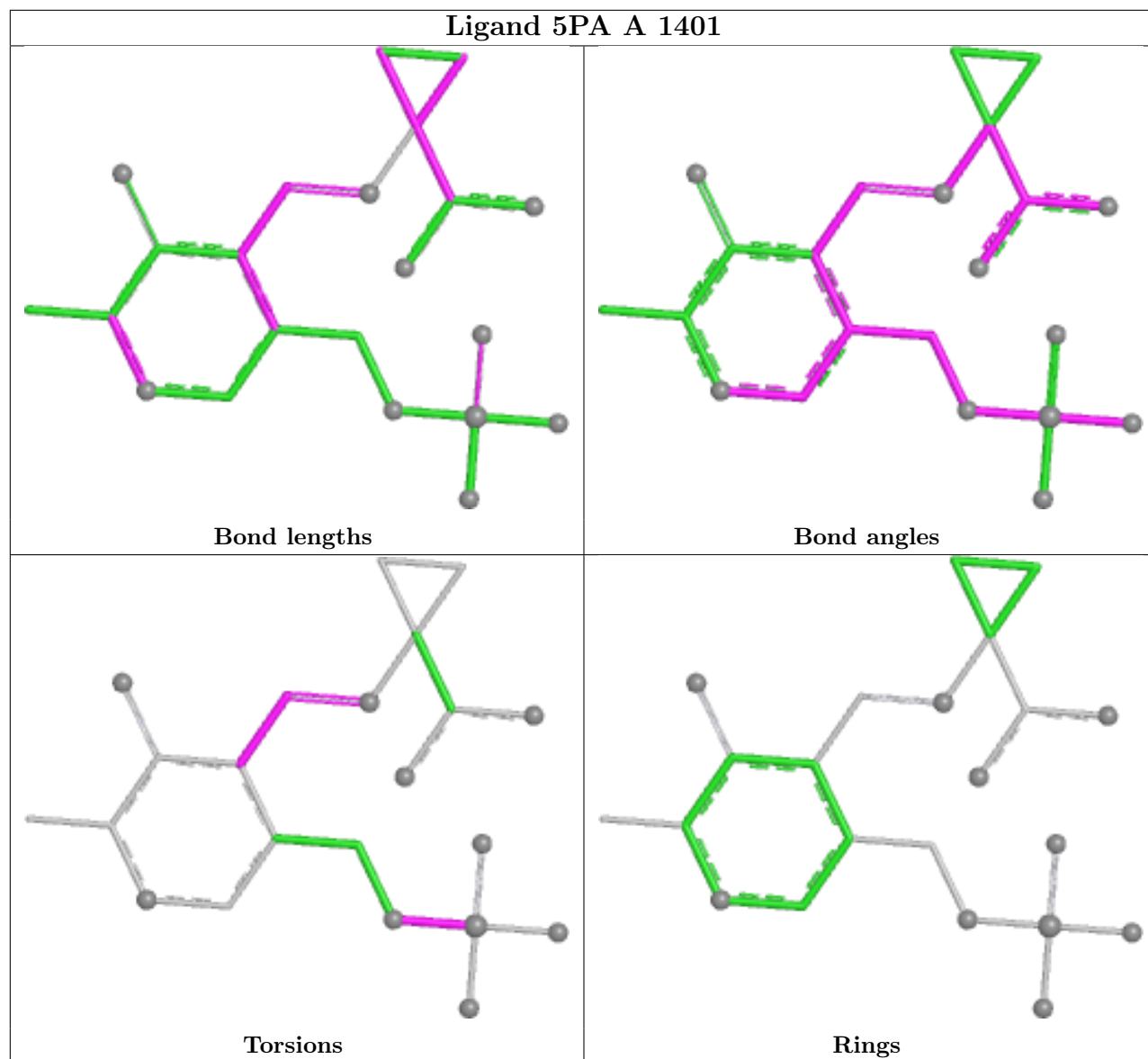


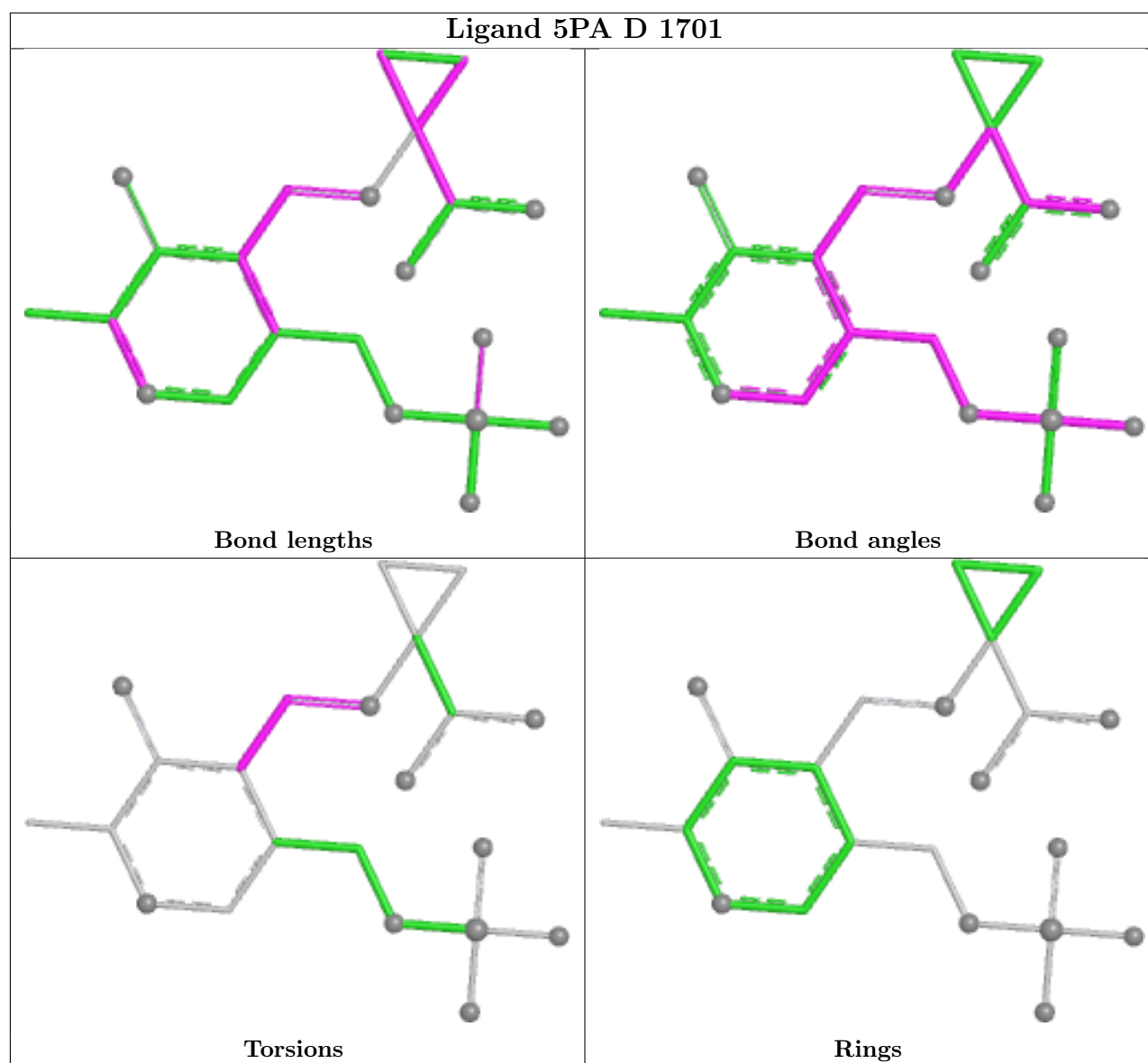
Torsions



Rings







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.