



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 01:11 PM UTC

PDB ID : 2DQY / pdb_00002dqy
Title : Crystal structure of human carboxylesterase in complex with cholate and palmitate
Authors : Bencharit, S.; Edwards, C.C.; Morton, C.L.; Howard-Williams, E.L.; Potter, P.M.; Redinbo, M.R.
Deposited on : 2006-06-02
Resolution : 3.00 Å(reported)

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

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

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

MolProbity	:	4-5-2 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

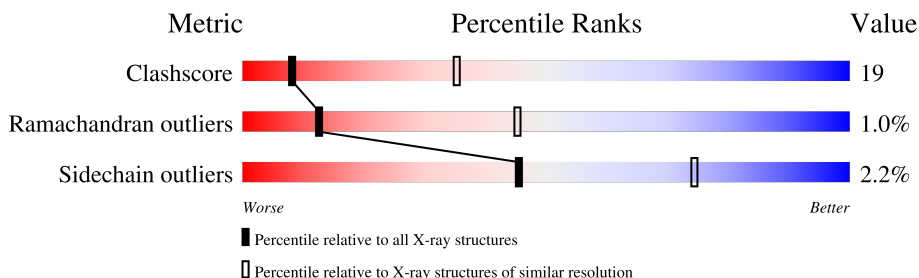
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.00 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
Clashscore	190562	2977 (3.00-3.00)
Ramachandran outliers	187476	2877 (3.00-3.00)
Sidechain outliers	187428	2880 (3.00-3.00)

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

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	A	542	 63% 33% . .
1	B	542	 64% 32% . .
1	C	542	 65% 32% . .

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	NAG	C	379	X	-	-	-
6	PLM	A	11	-	-	X	-

2 Entry composition [i](#)

There are 7 unique types of molecules in this entry. The entry contains 12967 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.

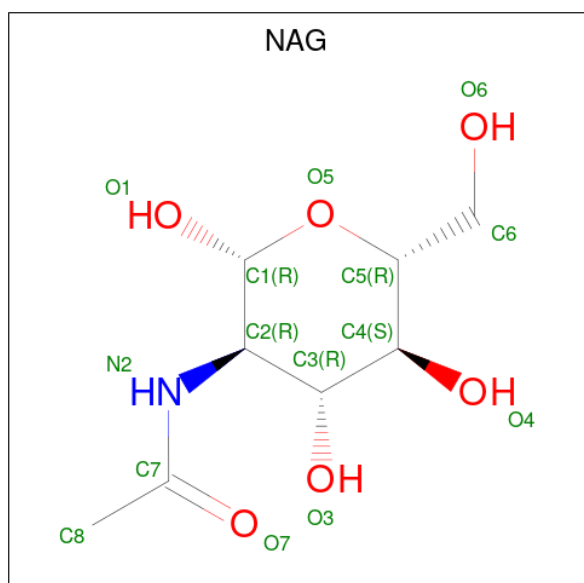
- Molecule 1 is a protein called Liver carboxylesterase 1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	532	Total	C	N	O	S	0	0	0
			4130	2662	685	763	20			
1	B	532	Total	C	N	O	S	0	0	0
			4130	2662	685	763	20			
1	C	532	Total	C	N	O	S	0	0	0
			4130	2662	685	763	20			

There are 3 discrepancies between the modelled and reference sequences:

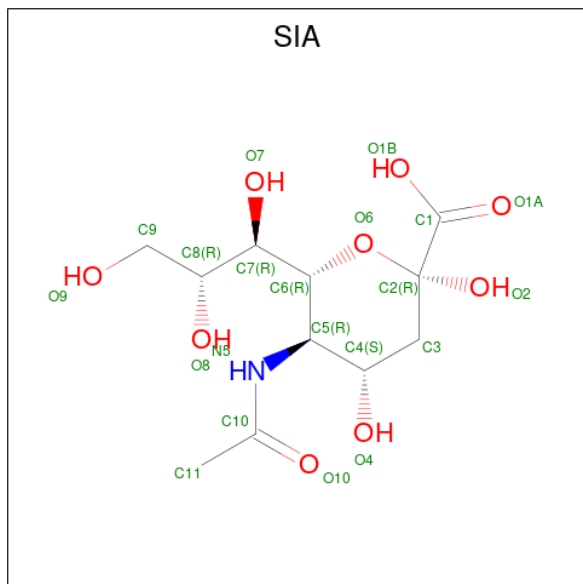
Chain	Residue	Modelled	Actual	Comment	Reference
A	?	-	GLN	deletion	UNP P23141
B	?	-	GLN	deletion	UNP P23141
C	?	-	GLN	deletion	UNP P23141

- Molecule 2 is 2-acetamido-2-deoxy-beta-D-glucopyranose (CCD ID: NAG) (formula: $C_8H_{15}NO_6$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	A	1	Total	C	N	O	0	0
			14	8	1	5		
2	B	1	Total	C	N	O	0	0
			14	8	1	5		
2	C	1	Total	C	N	O	0	0
			14	8	1	5		

- Molecule 3 is N-acetyl-alpha-neuraminic acid (CCD ID: SIA) (formula: $C_{11}H_{19}NO_9$).



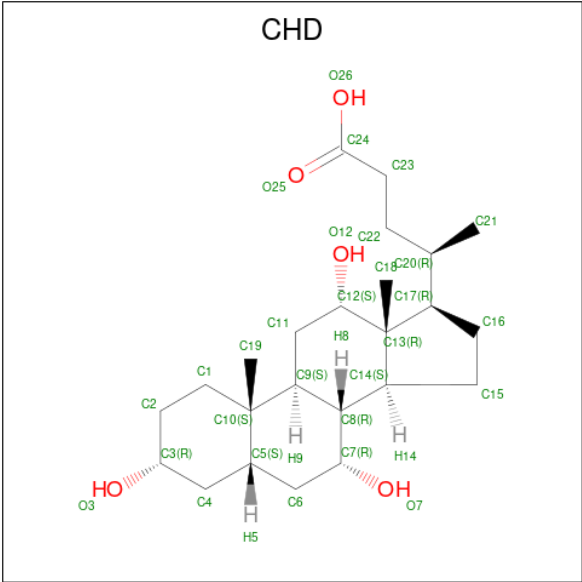
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	A	1	Total	C	N	O	0	0
			21	11	1	9		
3	B	1	Total	C	N	O	0	0
			21	11	1	9		
3	C	1	Total	C	N	O	0	0
			21	11	1	9		

- Molecule 4 is SULFATE ION (CCD ID: SO4) (formula: O_4S).



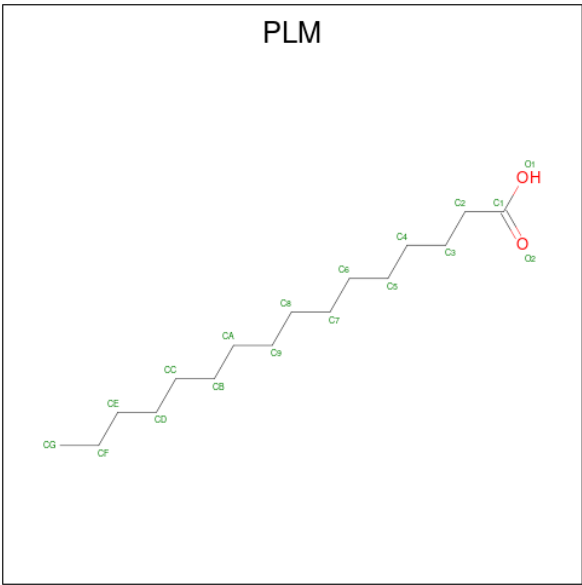
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	A	1	Total	O	S	0	0
			5	4	1		
4	A	1	Total	O	S	0	0
			5	4	1		
4	A	1	Total	O	S	0	0
			5	4	1		
4	B	1	Total	O	S	0	0
			5	4	1		
4	C	1	Total	O	S	0	0
			5	4	1		
4	C	1	Total	O	S	0	0
			5	4	1		

- Molecule 5 is CHOLIC ACID (CCD ID: CHD) (formula: C₂₄H₄₀O₅).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	A	1	Total	C	O	0	0
			29	24	5		
5	B	1	Total	C	O	0	0
			29	24	5		
5	C	1	Total	C	O	0	0
			29	24	5		

- Molecule 6 is PALMITIC ACID (CCD ID: PLM) (formula: C₁₆H₃₂O₂).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
6	A	1	Total	C	O	0	0
			18	16	2		

Continued on next page...

Continued from previous page...

Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
6	B	1	Total	C	O	0	0
			18	16	2		
6	C	1	Total	C	O	0	0
			18	16	2		

- Molecule 7 is water.

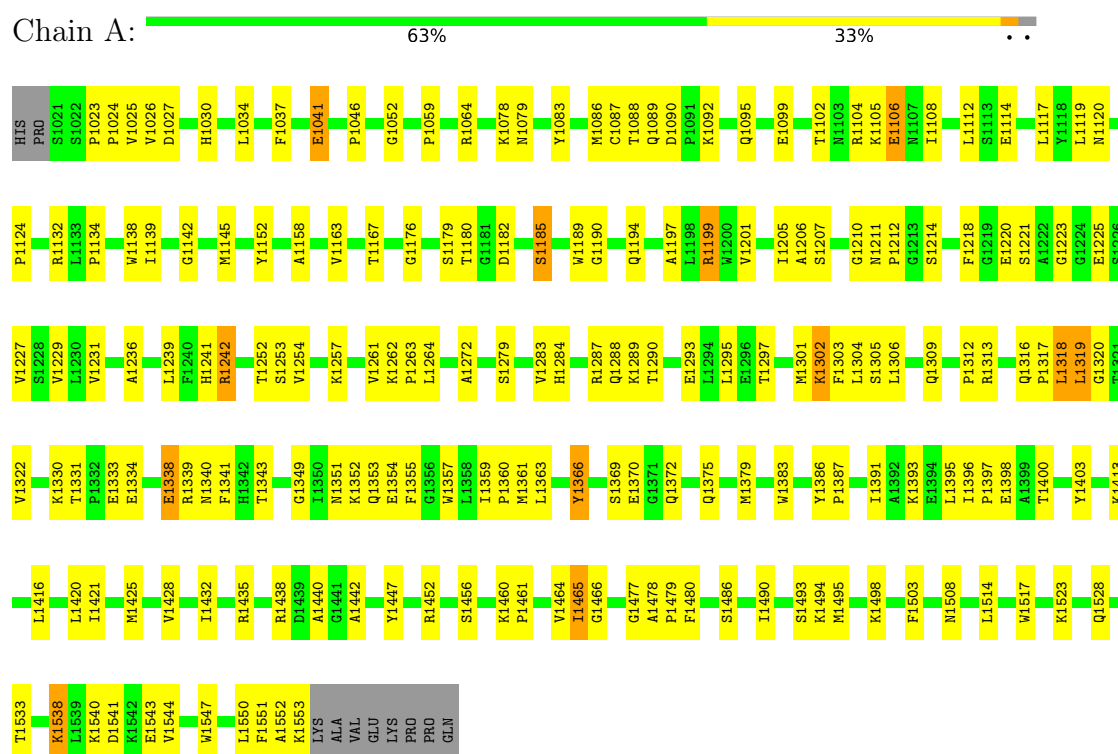
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	A	108	Total	O	0	0
			108	108		
7	B	87	Total	O	0	0
			87	87		
7	C	106	Total	O	0	0
			106	106		

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.

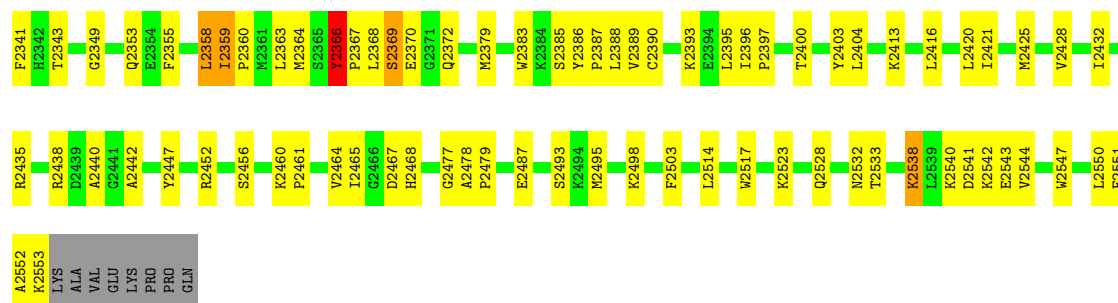
Note EDS was not executed.

- Molecule 1: Liver carboxylesterase 1



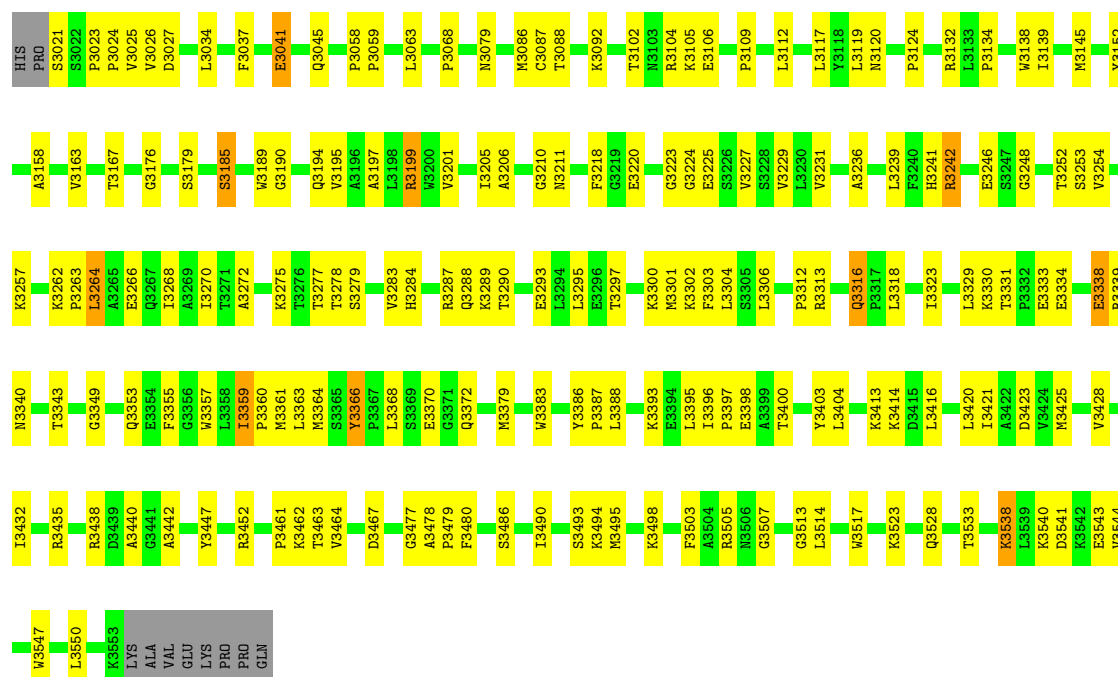
- Molecule 1: Liver carboxylesterase 1





• Molecule 1: Liver carboxylesterase 1

Chain C: 65% 32%



4 Data and refinement statistics

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

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	55.29Å 179.88Å 201.32Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	19.93 – 3.00	Depositor
% Data completeness (in resolution range)	93.0 (19.93-3.00)	Depositor
R_{merge}	(Not available)	Depositor
R_{sym}	0.11	Depositor
Refinement program	CNS 1.1	Depositor
R, R_{free}	0.226 , 0.271	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	12967	wwPDB-VP
Average B, all atoms (Å ²)	31.0	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: SIA, CHD, PLM, NAG, SO4

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	0.53	0/4236	0.92	7/5754 (0.1%)
1	B	0.51	0/4236	0.91	7/5754 (0.1%)
1	C	0.52	1/4236 (0.0%)	0.89	4/5754 (0.1%)
All	All	0.52	1/12708 (0.0%)	0.90	18/17262 (0.1%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	C	3359	ILE	CA-CB	-5.02	1.51	1.54

All (18) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	1318	LEU	N-CA-C	12.59	124.31	108.45
1	A	1319	LEU	N-CA-C	-10.06	90.40	107.80
1	B	2316	GLN	CA-C-N	7.84	129.64	119.84
1	B	2316	GLN	C-N-CA	7.84	129.64	119.84
1	C	3316	GLN	CA-C-N	7.17	126.42	118.97
1	C	3316	GLN	C-N-CA	7.17	126.42	118.97
1	A	1305	SER	N-CA-C	6.19	119.18	109.96
1	A	1552	ALA	N-CA-C	-5.60	106.48	113.15
1	B	2359	ILE	CB-CA-C	-5.59	108.39	113.70
1	C	3366	TYR	CA-C-N	5.46	126.66	119.84
1	C	3366	TYR	C-N-CA	5.46	126.66	119.84
1	B	2366	TYR	CA-C-N	5.39	126.10	120.12
1	B	2366	TYR	C-N-CA	5.39	126.10	120.12
1	A	1366	TYR	CA-C-N	5.34	126.52	119.84
1	A	1366	TYR	C-N-CA	5.34	126.52	119.84
1	B	2114	GLU	N-CA-C	-5.11	106.31	112.54
1	B	2552	ALA	N-CA-C	-5.09	107.36	113.21

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	1221	SER	CB-CA-C	-5.07	110.33	117.23

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	4130	0	4131	170	0
1	B	4130	0	4131	155	0
1	C	4130	0	4131	161	0
2	A	14	0	13	0	0
2	B	14	0	13	0	0
2	C	14	0	13	2	0
3	A	21	0	18	3	0
3	B	21	0	18	2	0
3	C	21	0	18	6	0
4	A	15	0	0	0	0
4	B	5	0	0	0	0
4	C	10	0	0	0	0
5	A	29	0	39	2	0
5	B	29	0	39	0	0
5	C	29	0	39	7	0
6	A	18	0	31	9	0
6	B	18	0	31	2	0
6	C	18	0	31	7	0
7	A	108	0	0	14	0
7	B	87	0	0	11	0
7	C	106	0	0	22	0
All	All	12967	0	12696	492	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 19.

All (492) 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:2317:PRO:HG3	1:B:2387:PRO:HB2	1.29	1.06
1:A:1199:ARG:HH11	1:A:1199:ARG:HB3	1.28	0.97
1:C:3199:ARG:HH11	1:C:3199:ARG:HB3	1.31	0.95
1:B:2199:ARG:HH11	1:B:2199:ARG:HB3	1.26	0.95
1:B:2105:LYS:HE2	1:B:2106:GLU:HG2	1.51	0.93
1:A:1105:LYS:HE2	1:A:1106:GLU:HG2	1.54	0.89
1:B:2363:LEU:HD13	6:B:12:PLM:H72	1.56	0.87
1:C:3134:PRO:HG2	1:C:3163:VAL:HG12	1.56	0.87
1:C:3105:LYS:HE2	1:C:3106:GLU:HG2	1.56	0.86
1:A:1134:PRO:HG2	1:A:1163:VAL:HG12	1.56	0.86
1:B:2134:PRO:HG2	1:B:2163:VAL:HG12	1.56	0.86
1:B:2343:THR:HA	7:B:7069:HOH:O	1.79	0.82
1:B:2338:GLU:HG2	1:B:2340:ASN:H	1.45	0.81
1:A:1257:LYS:HE2	1:A:1320:GLY:H	1.45	0.81
1:A:1338:GLU:HG2	1:A:1340:ASN:H	1.47	0.80
1:B:2199:ARG:HB3	1:B:2199:ARG:NH1	1.96	0.79
3:C:382:SIA:H4	3:C:382:SIA:H113	1.64	0.79
1:A:1359:ILE:HB	1:A:1360:PRO:HD3	1.66	0.78
1:A:1199:ARG:HB3	1:A:1199:ARG:NH1	1.98	0.78
1:A:1052:GLY:O	3:A:182:SIA:H92	1.84	0.77
1:B:2461:PRO:HG2	1:B:2464:VAL:HG23	1.67	0.77
1:B:2318:LEU:HD12	1:B:2318:LEU:O	1.85	0.77
1:C:3343:THR:HA	7:C:7090:HOH:O	1.84	0.77
1:A:1428:VAL:HG13	1:A:1544:VAL:HA	1.67	0.76
1:A:1262:LYS:NZ	3:C:382:SIA:H112	2.00	0.76
1:B:2428:VAL:HG13	1:B:2544:VAL:HA	1.68	0.76
1:C:3338:GLU:HG2	1:C:3340:ASN:H	1.48	0.76
1:A:1252:THR:HG22	1:A:1254:VAL:HG12	1.69	0.75
1:C:3368:LEU:HB2	5:C:3:CHD:H192	1.68	0.75
1:B:2452:ARG:HB2	1:B:2465:ILE:HG12	1.68	0.74
1:A:1375:GLN:HE21	1:A:1413:LYS:NZ	1.85	0.74
1:C:3199:ARG:HB3	1:C:3199:ARG:NH1	2.02	0.74
1:C:3241:HIS:O	1:C:3242:ARG:HG3	1.89	0.73
1:C:3428:VAL:HG13	1:C:3544:VAL:HA	1.70	0.73
1:C:3025:VAL:HG22	1:C:3034:LEU:HD23	1.71	0.72
1:C:3538:LYS:HD2	7:C:7156:HOH:O	1.89	0.72
1:A:1339:ARG:HG3	1:A:1440:ALA:HA	1.72	0.72
1:B:2202:GLN:HB3	7:B:7029:HOH:O	1.88	0.72
1:B:2343:THR:HB	1:B:2442:ALA:HB2	1.71	0.71
1:C:3343:THR:HB	1:C:3442:ALA:HB2	1.71	0.71
1:A:1341:PHE:HB3	7:A:7206:HOH:O	1.89	0.71
1:A:1343:THR:HA	7:A:7012:HOH:O	1.90	0.71

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:3339:ARG:HG3	1:C:3440:ALA:HA	1.72	0.70
1:A:1343:THR:HB	1:A:1442:ALA:HB2	1.72	0.70
1:B:2339:ARG:HG3	1:B:2440:ALA:HA	1.73	0.70
1:A:1105:LYS:HG3	1:A:1106:GLU:H	1.54	0.70
1:B:2290:THR:OG1	1:B:2293:GLU:HG3	1.90	0.70
1:A:1421:ILE:HG22	1:A:1425:MET:HE2	1.74	0.69
1:B:2025:VAL:HG22	1:B:2034:LEU:HD23	1.74	0.69
1:B:2105:LYS:HG3	1:B:2106:GLU:H	1.55	0.69
1:C:3105:LYS:HG3	1:C:3106:GLU:H	1.57	0.69
1:B:2024:PRO:HG3	1:B:2037:PHE:CZ	2.27	0.69
1:B:2130:LYS:HD3	7:B:7190:HOH:O	1.91	0.69
1:A:1333:GLU:H	1:A:1333:GLU:CD	2.01	0.68
1:A:1398:GLU:HB2	7:A:7100:HOH:O	1.94	0.68
1:B:2331:THR:OG1	1:B:2334:GLU:HG3	1.93	0.68
1:B:2333:GLU:H	1:B:2333:GLU:CD	2.01	0.68
1:A:1241:HIS:O	1:A:1242:ARG:HG3	1.93	0.67
1:A:1396:ILE:HB	1:A:1397:PRO:HD3	1.76	0.67
1:C:3414:LYS:NZ	5:C:3:CHD:H42	2.09	0.67
1:A:1025:VAL:HG22	1:A:1034:LEU:HD23	1.73	0.67
1:B:2421:ILE:HG22	1:B:2425:MET:HE2	1.74	0.67
1:B:2262:LYS:HB3	1:B:2263:PRO:HD3	1.77	0.67
1:C:3304:LEU:HD13	6:C:13:PLM:H91	1.76	0.67
1:C:3290:THR:OG1	1:C:3293:GLU:HG3	1.95	0.67
1:A:1262:LYS:HB3	1:A:1263:PRO:HD3	1.77	0.66
1:C:3331:THR:OG1	1:C:3334:GLU:HG3	1.96	0.66
1:C:3333:GLU:H	1:C:3333:GLU:CD	2.03	0.66
1:C:3262:LYS:HB3	1:C:3263:PRO:HD3	1.77	0.66
1:C:3421:ILE:HG22	1:C:3425:MET:HE2	1.76	0.66
1:A:1304:LEU:HB2	6:A:11:PLM:HB1	1.77	0.66
1:B:2241:HIS:O	1:B:2242:ARG:HG3	1.95	0.65
1:A:1355:PHE:CE1	1:A:1360:PRO:HG3	2.31	0.65
1:A:1024:PRO:HG3	1:A:1037:PHE:CZ	2.32	0.65
1:A:1078:LYS:HG3	3:A:182:SIA:O1B	1.96	0.65
1:A:1290:THR:OG1	1:A:1293:GLU:HG3	1.97	0.65
1:A:1331:THR:OG1	1:A:1334:GLU:HG3	1.97	0.65
3:B:282:SIA:H6	3:B:282:SIA:H113	1.79	0.65
1:C:3363:LEU:HD13	6:C:13:PLM:H81	1.77	0.65
1:A:1403:TYR:O	1:A:1416:LEU:HD13	1.98	0.64
1:B:2370:GLU:HB3	1:B:2372:GLN:NE2	2.12	0.64
1:B:2341:PHE:HB3	7:B:7221:HOH:O	1.99	0.63
1:C:3396:ILE:HB	1:C:3397:PRO:HD3	1.79	0.63

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:3403:TYR:O	1:C:3416:LEU:HD13	1.99	0.63
1:A:1538:LYS:HB3	1:A:1541:ASP:HB2	1.80	0.63
1:B:2252:THR:HG22	1:B:2254:VAL:HG12	1.81	0.63
1:B:2396:ILE:HB	1:B:2397:PRO:HD3	1.80	0.62
1:B:2551:PHE:C	1:B:2553:LYS:H	2.07	0.62
1:C:3236:ALA:HA	1:C:3239:LEU:HD12	1.80	0.62
1:A:1375:GLN:HG2	1:A:1413:LYS:HE3	1.80	0.62
1:B:2254:VAL:HG21	1:B:2388:LEU:HD23	1.81	0.62
1:A:1306:LEU:HD22	1:A:1366:TYR:CE1	2.35	0.62
1:B:2363:LEU:HB3	6:B:12:PLM:HA1	1.81	0.62
1:A:1262:LYS:HZ1	3:C:382:SIA:H112	1.62	0.62
1:B:2538:LYS:HB3	1:B:2541:ASP:HB2	1.81	0.62
1:C:3145:MET:HE2	1:C:3303:PHE:CD1	2.35	0.61
1:A:1079:ASN:HB2	3:A:182:SIA:O2	2.01	0.61
1:B:2498:LYS:HB3	1:B:2514:LEU:HD11	1.81	0.61
1:C:3300:LYS:O	1:C:3302:LYS:HG3	2.00	0.61
1:C:3498:LYS:HB3	1:C:3514:LEU:HD11	1.82	0.61
5:C:3:CHD:H7	7:C:7166:HOH:O	2.01	0.61
1:C:3199:ARG:HD2	7:C:7172:HOH:O	2.00	0.61
1:B:2227:VAL:O	1:B:2231:VAL:HG23	2.00	0.61
1:C:3538:LYS:HB3	1:C:3541:ASP:HB2	1.81	0.61
1:B:2403:TYR:O	1:B:2416:LEU:HD13	2.01	0.60
1:C:3304:LEU:HD22	6:C:13:PLM:H71	1.83	0.60
1:B:2225:GLU:O	1:B:2229:VAL:HG23	2.02	0.60
1:A:1297:THR:O	1:A:1301:MET:HG2	2.01	0.60
1:A:1304:LEU:HB2	6:A:11:PLM:CB	2.32	0.60
1:B:2236:ALA:HA	1:B:2239:LEU:HD12	1.83	0.60
1:A:1498:LYS:HB3	1:A:1514:LEU:HD11	1.84	0.60
1:A:1306:LEU:HD22	1:A:1366:TYR:CZ	2.37	0.60
1:C:3024:PRO:HG3	1:C:3037:PHE:CZ	2.37	0.60
1:A:1254:VAL:O	1:A:1318:LEU:HD13	2.02	0.60
1:C:3414:LYS:HZ1	5:C:3:CHD:H42	1.65	0.59
1:A:1428:VAL:O	1:A:1432:ILE:HG13	2.03	0.59
1:B:2390:CYS:HB2	7:B:7140:HOH:O	2.03	0.59
1:A:1375:GLN:HE21	1:A:1413:LYS:HZ1	1.50	0.59
1:A:1452:ARG:HB2	1:A:1465:ILE:HG12	1.85	0.58
1:A:1227:VAL:O	1:A:1231:VAL:HG23	2.03	0.58
1:A:1225:GLU:O	1:A:1229:VAL:HG23	2.04	0.58
1:A:1370:GLU:HB3	1:A:1372:GLN:NE2	2.17	0.58
1:C:3428:VAL:O	1:C:3432:ILE:HG13	2.03	0.58
1:B:2428:VAL:O	1:B:2432:ILE:HG13	2.03	0.58

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1312:PRO:HG2	1:A:1383:TRP:CD1	2.39	0.57
1:C:3297:THR:O	1:C:3301:MET:HG2	2.04	0.57
1:B:2386:TYR:N	1:B:2387:PRO:HD2	2.19	0.57
1:A:1318:LEU:HD12	1:A:1320:GLY:HA3	1.86	0.57
1:B:2461:PRO:HG2	1:B:2464:VAL:CG2	2.34	0.57
1:C:3370:GLU:HB3	1:C:3372:GLN:NE2	2.18	0.57
1:A:1386:TYR:N	1:A:1387:PRO:HD2	2.20	0.56
1:B:2255:LEU:HD23	1:B:2318:LEU:HD11	1.86	0.56
1:A:1236:ALA:HA	1:A:1239:LEU:HD12	1.85	0.56
1:A:1355:PHE:CZ	1:A:1360:PRO:HG3	2.41	0.56
1:C:3225:GLU:O	1:C:3229:VAL:HG23	2.04	0.56
1:B:2242:ARG:HG2	1:B:2242:ARG:HH11	1.69	0.56
1:B:2359:ILE:HB	1:B:2360:PRO:HD3	1.86	0.56
1:B:2086:MET:HG3	1:B:2112:LEU:HD23	1.88	0.56
1:C:3227:VAL:O	1:C:3231:VAL:HG23	2.06	0.56
1:C:3242:ARG:NH2	7:C:7118:HOH:O	2.39	0.56
1:A:1540:LYS:O	1:A:1544:VAL:HG23	2.06	0.56
1:C:3359:ILE:HB	1:C:3360:PRO:HD3	1.87	0.56
1:C:3386:TYR:N	1:C:3387:PRO:HD2	2.20	0.56
1:B:2242:ARG:HH11	1:B:2242:ARG:CG	2.19	0.56
1:A:1086:MET:HG3	1:A:1112:LEU:HD23	1.88	0.56
1:A:1252:THR:HG22	1:A:1254:VAL:CG1	2.35	0.56
1:B:2102:THR:OG1	1:B:2104:ARG:HG2	2.06	0.56
1:B:2317:PRO:HG3	1:B:2387:PRO:CB	2.20	0.55
1:A:1102:THR:OG1	1:A:1104:ARG:HG2	2.06	0.55
2:C:379:NAG:H5	7:C:7208:HOH:O	2.05	0.55
1:A:1393:LYS:HA	1:A:1396:ILE:HG12	1.89	0.55
1:C:3312:PRO:HG2	1:C:3383:TRP:CD1	2.41	0.55
1:C:3241:HIS:C	1:C:3242:ARG:HG3	2.30	0.55
1:A:1428:VAL:HG12	1:A:1432:ILE:HD11	1.89	0.55
1:C:3242:ARG:HG2	1:C:3242:ARG:HH11	1.72	0.55
1:B:2403:TYR:CG	1:B:2420:LEU:HD23	2.42	0.55
1:C:3393:LYS:HA	1:C:3396:ILE:HG12	1.89	0.55
1:C:3540:LYS:O	1:C:3544:VAL:HG23	2.07	0.55
1:A:1304:LEU:HD13	6:A:11:PLM:HA2	1.89	0.54
1:A:1375:GLN:HE21	1:A:1413:LYS:HZ2	1.55	0.54
1:C:3275:LYS:HD3	7:C:7176:HOH:O	2.06	0.54
1:A:1318:LEU:HG	1:A:1319:LEU:N	2.18	0.54
1:B:2313:ARG:HG2	1:B:2386:TYR:CE2	2.42	0.54
1:A:1456:SER:HB3	1:A:1460:LYS:HD3	1.88	0.54
1:C:3313:ARG:HG2	1:C:3386:TYR:CE2	2.43	0.54

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:2540:LYS:O	1:B:2544:VAL:HG23	2.08	0.54
1:C:3086:MET:HG3	1:C:3112:LEU:HD23	1.89	0.54
1:B:2312:PRO:HG2	1:B:2383:TRP:CD1	2.42	0.54
1:A:1242:ARG:HG2	1:A:1242:ARG:HH11	1.73	0.54
1:A:1272:ALA:O	1:A:1289:LYS:HE3	2.08	0.54
1:C:3102:THR:OG1	1:C:3104:ARG:HG2	2.07	0.54
1:C:3316:GLN:HA	1:C:3316:GLN:NE2	2.23	0.53
3:C:382:SIA:H111	7:C:7211:HOH:O	2.07	0.53
1:C:3505:ARG:HB3	7:C:7115:HOH:O	2.08	0.53
1:A:1403:TYR:CG	1:A:1420:LEU:HD23	2.42	0.53
1:B:2338:GLU:CG	1:B:2340:ASN:H	2.20	0.53
1:B:2105:LYS:HE2	1:B:2106:GLU:CG	2.33	0.53
1:A:1242:ARG:HH11	1:A:1242:ARG:CG	2.21	0.53
1:C:3357:TRP:CH2	1:C:3361:MET:HE2	2.44	0.53
1:B:2393:LYS:HA	1:B:2396:ILE:HG12	1.91	0.53
1:B:2495:MET:HE1	1:B:2533:THR:OG1	2.09	0.53
1:A:1284:HIS:O	1:A:1288:GLN:HG2	2.09	0.52
1:B:2284:HIS:O	1:B:2288:GLN:HG2	2.08	0.52
1:A:1420:LEU:HD22	1:A:1547:TRP:HZ2	1.75	0.52
1:A:1105:LYS:HE2	1:A:1106:GLU:CG	2.35	0.52
1:A:1313:ARG:HG2	1:A:1386:TYR:CE2	2.44	0.52
1:A:1551:PHE:C	1:A:1553:LYS:H	2.15	0.52
1:C:3316:GLN:HA	1:C:3316:GLN:HE21	1.75	0.52
1:B:2241:HIS:C	1:B:2242:ARG:HG3	2.34	0.52
1:B:2447:TYR:HB3	1:B:2517:TRP:CZ2	2.45	0.52
1:A:1460:LYS:HD2	7:A:7088:HOH:O	2.09	0.52
1:C:3132:ARG:HB3	1:C:3211:ASN:HB2	1.92	0.52
1:A:1261:VAL:HG22	7:A:7108:HOH:O	2.08	0.52
1:B:2355:PHE:CE1	1:B:2360:PRO:HG3	2.45	0.52
1:C:3063:LEU:HD11	7:C:7196:HOH:O	2.09	0.52
1:A:1461:PRO:HD3	5:A:1:CHD:O12	2.10	0.51
1:C:3242:ARG:HH11	1:C:3242:ARG:CG	2.23	0.51
1:B:2420:LEU:HD22	1:B:2547:TRP:HZ2	1.75	0.51
1:C:3139:ILE:HG22	1:C:3223:GLY:HA2	1.91	0.51
1:A:1283:VAL:O	1:A:1287:ARG:HG3	2.10	0.51
1:A:1316:GLN:HA	1:A:1316:GLN:NE2	2.25	0.51
1:B:2306:LEU:HB2	1:B:2364:MET:HE2	1.92	0.51
1:B:2428:VAL:HG12	1:B:2432:ILE:HD11	1.91	0.51
1:A:1241:HIS:C	1:A:1242:ARG:HG3	2.34	0.51
1:A:1316:GLN:HA	1:A:1316:GLN:HE21	1.75	0.51
1:A:1338:GLU:CG	1:A:1340:ASN:H	2.21	0.51

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1349:GLY:HA3	1:A:1447:TYR:CE1	2.46	0.51
1:A:1452:ARG:HG2	1:A:1452:ARG:HH11	1.75	0.51
1:C:3079:ASN:HB2	3:C:382:SIA:O2	2.10	0.51
1:A:1478:ALA:N	1:A:1479:PRO:CD	2.74	0.51
1:B:2318:LEU:O	1:B:2319:LEU:C	2.53	0.51
1:C:3403:TYR:CG	1:C:3420:LEU:HD23	2.45	0.51
1:A:1304:LEU:HB2	6:A:11:PLM:HA2	1.93	0.51
1:B:2487:GLU:N	7:B:7191:HOH:O	2.39	0.51
1:C:3338:GLU:CG	1:C:3340:ASN:H	2.23	0.51
1:C:3452:ARG:HG2	1:C:3452:ARG:HH11	1.76	0.51
1:A:1316:GLN:OE1	1:A:1318:LEU:HD23	2.11	0.51
1:C:3021:SER:N	7:C:7235:HOH:O	2.44	0.51
1:A:1317:PRO:HB3	1:A:1387:PRO:HB2	1.93	0.50
1:B:2452:ARG:HG2	1:B:2452:ARG:HH11	1.76	0.50
1:A:1302:LYS:HA	6:A:11:PLM:HG1	1.94	0.50
1:B:2024:PRO:HG3	1:B:2037:PHE:CE1	2.46	0.50
1:A:1024:PRO:HG3	1:A:1037:PHE:CE1	2.47	0.50
1:A:1087:CYS:HB3	7:A:7048:HOH:O	2.11	0.50
1:C:3284:HIS:O	1:C:3288:GLN:HG2	2.12	0.50
1:C:3428:VAL:HG12	1:C:3432:ILE:HD11	1.92	0.50
1:A:1095:GLN:O	1:A:1099:GLU:HG3	2.12	0.49
1:C:3447:TYR:HB3	1:C:3517:TRP:CZ2	2.47	0.49
1:B:2242:ARG:CG	1:B:2242:ARG:NH1	2.76	0.49
1:C:3152:TYR:CD1	1:C:3152:TYR:N	2.80	0.49
1:C:3398:GLU:HB2	7:C:7244:HOH:O	2.12	0.49
1:C:3477:GLY:HA2	1:C:3493:SER:OG	2.13	0.49
1:C:3119:LEU:HD12	1:C:3119:LEU:C	2.37	0.49
1:A:1369:SER:HA	5:A:1:CHD:H191	1.95	0.49
1:B:2543:GLU:OE2	1:B:2543:GLU:N	2.37	0.49
1:C:3257:LYS:HE2	1:C:3318:LEU:O	2.13	0.49
1:C:3423:ASP:HA	7:C:7003:HOH:O	2.13	0.49
1:A:1132:ARG:HB3	1:A:1211:ASN:HB2	1.95	0.49
1:A:1206:ALA:HA	1:A:1210:GLY:O	2.12	0.49
1:B:2132:ARG:HB3	1:B:2211:ASN:HB2	1.95	0.49
1:C:3206:ALA:HA	1:C:3210:GLY:O	2.13	0.49
1:B:2152:TYR:CD1	1:B:2152:TYR:N	2.80	0.49
1:C:3068:PRO:HA	7:C:7201:HOH:O	2.13	0.49
1:A:1152:TYR:N	1:A:1152:TYR:CD1	2.80	0.49
1:A:1354:GLU:HG2	7:A:7101:HOH:O	2.13	0.49
1:C:3543:GLU:OE2	1:C:3543:GLU:N	2.38	0.49
1:A:1142:GLY:HA2	6:A:11:PLM:H62	1.94	0.49

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1447:TYR:HB3	1:A:1517:TRP:CZ2	2.48	0.49
1:B:2283:VAL:O	1:B:2287:ARG:HG3	2.11	0.49
1:C:3290:THR:HG23	1:C:3293:GLU:OE2	2.13	0.48
1:C:3339:ARG:CG	1:C:3440:ALA:HA	2.42	0.48
1:A:1357:TRP:CH2	1:A:1361:MET:HE2	2.48	0.48
1:B:2206:ALA:HA	1:B:2210:GLY:O	2.14	0.48
1:B:2478:ALA:N	1:B:2479:PRO:CD	2.76	0.48
1:C:3045:GLN:HA	7:C:7111:HOH:O	2.13	0.48
1:A:1477:GLY:HA2	1:A:1493:SER:OG	2.12	0.48
1:C:3026:VAL:HG12	1:C:3027:ASP:N	2.29	0.48
1:C:3363:LEU:HB3	6:C:13:PLM:HA1	1.95	0.48
1:B:2358:LEU:HD22	1:B:2468:HIS:O	2.13	0.48
1:C:3252:THR:HG22	1:C:3254:VAL:HG12	1.94	0.48
1:C:3283:VAL:HG12	1:C:3287:ARG:NH1	2.28	0.48
1:C:3303:PHE:CD2	1:C:3318:LEU:HA	2.49	0.48
1:B:2435:ARG:O	1:B:2438:ARG:HB3	2.14	0.48
1:C:3224:GLY:HA3	7:C:7279:HOH:O	2.14	0.48
1:A:1034:LEU:HD13	1:A:1034:LEU:C	2.39	0.48
1:C:3109:PRO:HA	7:C:7068:HOH:O	2.13	0.48
1:C:3357:TRP:O	1:C:3360:PRO:HD2	2.14	0.48
1:C:3420:LEU:HD22	1:C:3547:TRP:HZ2	1.79	0.48
1:A:1138:TRP:HH2	1:A:1220:GLU:HB2	1.79	0.47
1:A:1317:PRO:HG2	1:A:1318:LEU:HD22	1.95	0.47
1:C:3254:VAL:HG21	1:C:3388:LEU:HD23	1.96	0.47
1:C:3353:GLN:OE1	1:C:3464:VAL:HG13	2.14	0.47
1:A:1375:GLN:HG2	1:A:1413:LYS:CE	2.44	0.47
1:A:1312:PRO:HG2	1:A:1383:TRP:NE1	2.29	0.47
1:A:1495:MET:HE1	1:A:1533:THR:OG1	2.14	0.47
1:B:2456:SER:HB3	1:B:2460:LYS:HD3	1.96	0.47
1:C:3138:TRP:HH2	1:C:3220:GLU:HB2	1.79	0.47
1:C:3034:LEU:HD13	1:C:3034:LEU:C	2.38	0.47
1:A:1119:LEU:HD12	1:A:1119:LEU:C	2.40	0.47
1:B:2026:VAL:HG12	1:B:2027:ASP:N	2.29	0.47
1:B:2064:ARG:NH2	1:B:2114:GLU:OE2	2.47	0.47
1:B:2087:CYS:O	1:B:2088:THR:C	2.58	0.47
1:C:3087:CYS:O	1:C:3088:THR:C	2.57	0.47
1:A:1353:GLN:OE1	1:A:1464:VAL:HG13	2.15	0.47
1:B:2316:GLN:HA	1:B:2316:GLN:NE2	2.29	0.47
1:C:3368:LEU:O	5:C:3:CHD:H62	2.15	0.47
1:A:1543:GLU:OE2	1:A:1543:GLU:N	2.40	0.47
1:B:2395:LEU:HD22	1:B:2550:LEU:CD1	2.45	0.47

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1139:ILE:HG22	1:A:1223:GLY:HA2	1.95	0.47
1:B:2421:ILE:CG2	1:B:2425:MET:HE2	2.43	0.47
1:C:3268:ILE:HG12	1:C:3301:MET:HE2	1.97	0.47
1:B:2138:TRP:HH2	1:B:2220:GLU:HB2	1.79	0.46
1:B:2339:ARG:CG	1:B:2440:ALA:HA	2.43	0.46
1:C:3312:PRO:HG2	1:C:3383:TRP:NE1	2.29	0.46
1:C:3197:ALA:O	1:C:3201:VAL:HG23	2.14	0.46
1:A:1353:GLN:OE1	1:A:1464:VAL:HA	2.16	0.46
1:A:1391:ILE:HB	7:A:7219:HOH:O	2.15	0.46
1:C:3478:ALA:N	1:C:3479:PRO:CD	2.78	0.46
1:A:1359:ILE:HB	1:A:1360:PRO:CD	2.43	0.46
1:B:2134:PRO:CG	1:B:2163:VAL:HG12	2.38	0.46
1:B:2395:LEU:HD22	1:B:2550:LEU:HD12	1.97	0.46
1:C:3395:LEU:HD22	1:C:3550:LEU:CD1	2.45	0.46
1:B:2221:SER:O	1:B:2224:GLY:N	2.47	0.46
1:B:2316:GLN:HA	1:B:2316:GLN:HE21	1.80	0.46
1:C:3242:ARG:CG	1:C:3242:ARG:NH1	2.78	0.46
1:C:3304:LEU:HB3	6:C:13:PLM:H91	1.97	0.46
1:C:3495:MET:HE1	1:C:3533:THR:OG1	2.16	0.46
1:A:1030:HIS:HD2	7:A:7089:HOH:O	1.99	0.46
1:B:2139:ILE:HG22	1:B:2223:GLY:HA2	1.97	0.46
1:B:2272:ALA:O	1:B:2289:LYS:HE3	2.16	0.46
1:C:3223:GLY:O	1:C:3227:VAL:HG23	2.16	0.46
1:C:3349:GLY:HA3	1:C:3447:TYR:CE1	2.50	0.46
1:A:1242:ARG:CG	1:A:1242:ARG:NH1	2.78	0.46
1:B:2262:LYS:HE3	1:B:2279:SER:OG	2.15	0.46
1:C:3024:PRO:HG3	1:C:3037:PHE:CE1	2.51	0.46
1:A:1318:LEU:HD23	1:A:1318:LEU:H	1.81	0.46
1:B:2266:GLU:O	1:B:2270:ILE:HG13	2.16	0.46
1:C:3105:LYS:HE2	1:C:3106:GLU:CG	2.38	0.46
1:C:3414:LYS:HZ2	5:C:3:CHD:H42	1.81	0.46
1:A:1421:ILE:CG2	1:A:1425:MET:HE2	2.44	0.45
1:C:3304:LEU:HD22	6:C:13:PLM:H91	1.98	0.45
1:A:1395:LEU:HD22	1:A:1550:LEU:CD1	2.46	0.45
1:B:2370:GLU:HB3	1:B:2372:GLN:HE21	1.81	0.45
1:C:3283:VAL:O	1:C:3287:ARG:HG3	2.16	0.45
1:A:1351:ASN:HB3	1:A:1466:GLY:O	2.17	0.45
1:B:2312:PRO:HG2	1:B:2383:TRP:NE1	2.32	0.45
1:C:3486:SER:O	1:C:3490:ILE:HG13	2.16	0.45
1:A:1026:VAL:CG1	1:A:1207:SER:HB3	2.46	0.45
1:A:1242:ARG:HD3	1:A:1503:PHE:O	2.17	0.45

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:2034:LEU:HD13	1:B:2034:LEU:C	2.42	0.45
1:A:1090:ASP:OD1	1:A:1090:ASP:C	2.60	0.45
1:B:2477:GLY:HA2	1:B:2493:SER:OG	2.17	0.45
1:C:3538:LYS:HE2	7:C:7024:HOH:O	2.16	0.45
1:A:1059:PRO:HD3	1:A:1117:LEU:HD12	1.98	0.45
1:B:2542:LYS:HD3	7:B:7073:HOH:O	2.16	0.45
1:A:1339:ARG:CG	1:A:1440:ALA:HA	2.42	0.45
1:B:2306:LEU:HD22	1:B:2366:TYR:CE1	2.52	0.45
1:C:3395:LEU:HD22	1:C:3550:LEU:HD12	1.97	0.45
1:B:2026:VAL:CG1	1:B:2207:SER:HB3	2.47	0.44
1:C:3262:LYS:HE3	1:C:3279:SER:OG	2.17	0.44
1:A:1120:ASN:HB2	1:A:1167:THR:OG1	2.18	0.44
1:A:1370:GLU:HB3	1:A:1372:GLN:HE21	1.82	0.44
1:B:2039:SER:OG	1:B:2046:PRO:HB3	2.17	0.44
1:B:2095:GLN:O	1:B:2099:GLU:HG3	2.18	0.44
1:B:2242:ARG:HD3	1:B:2503:PHE:O	2.16	0.44
1:B:2364:MET:SD	1:B:2388:LEU:HD11	2.58	0.44
1:C:3272:ALA:O	1:C:3289:LYS:HE3	2.17	0.44
1:A:1088:THR:HG22	1:A:1295:LEU:HD13	1.99	0.44
1:C:3088:THR:HG22	1:C:3295:LEU:HD13	2.00	0.44
1:B:2283:VAL:HG12	1:B:2287:ARG:NH1	2.31	0.44
1:B:2349:GLY:HA3	1:B:2447:TYR:CE1	2.52	0.44
1:C:3120:ASN:HB2	1:C:3167:THR:OG1	2.18	0.44
1:C:3205:ILE:HD12	1:C:3205:ILE:HA	1.88	0.44
1:C:3266:GLU:O	1:C:3270:ILE:HG13	2.16	0.44
1:C:3355:PHE:CE1	1:C:3360:PRO:HG3	2.52	0.44
1:A:1262:LYS:HE3	1:A:1279:SER:OG	2.18	0.44
1:B:2355:PHE:CD1	1:B:2360:PRO:HG3	2.53	0.44
1:C:3421:ILE:CG2	1:C:3425:MET:HE2	2.46	0.44
1:A:1026:VAL:HG12	1:A:1027:ASP:N	2.33	0.44
1:A:1435:ARG:O	1:A:1438:ARG:HB3	2.18	0.44
1:B:2323:ILE:HG21	1:B:2330:LYS:HA	1.99	0.44
1:C:3357:TRP:HA	5:C:3:CHD:H22	1.99	0.44
1:A:1508:ASN:HB3	7:A:7128:HOH:O	2.16	0.44
1:C:3025:VAL:HG22	1:C:3034:LEU:CD2	2.44	0.44
1:C:3246:GLU:HG2	1:C:3447:TYR:OH	2.18	0.44
1:C:3353:GLN:O	1:C:3467:ASP:HA	2.18	0.44
1:A:1395:LEU:HD22	1:A:1550:LEU:HD12	1.98	0.44
1:C:3364:MET:HE2	1:C:3364:MET:HB3	1.94	0.44
1:B:2119:LEU:HD12	1:B:2119:LEU:C	2.43	0.43
1:C:3041:GLU:O	1:C:3041:GLU:HG3	2.18	0.43

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1304:LEU:HB2	6:A:11:PLM:HD2	2.00	0.43
1:C:3353:GLN:OE1	1:C:3464:VAL:HA	2.18	0.43
1:A:1197:ALA:O	1:A:1201:VAL:HG23	2.18	0.43
1:A:1283:VAL:HG12	1:A:1287:ARG:NH1	2.34	0.43
1:C:3304:LEU:HD22	6:C:13:PLM:C7	2.49	0.43
1:C:3329:LEU:HD23	7:C:7174:HOH:O	2.19	0.43
1:C:3357:TRP:C	1:C:3360:PRO:HD2	2.43	0.43
1:B:2330:LYS:HB2	1:B:2334:GLU:OE2	2.18	0.43
1:C:3059:PRO:HD3	1:C:3117:LEU:HD12	2.00	0.43
1:A:1025:VAL:HG22	1:A:1034:LEU:CD2	2.46	0.43
1:A:1041:GLU:O	1:A:1041:GLU:HG3	2.18	0.43
1:A:1124:PRO:HD3	1:A:1158:ALA:HB1	2.00	0.43
1:B:2379:MET:HG2	1:B:2400:THR:OG1	2.17	0.43
1:B:2528:GLN:O	1:B:2533:THR:HA	2.19	0.43
1:C:3330:LYS:HB2	1:C:3334:GLU:OE2	2.18	0.43
1:A:1105:LYS:HG3	1:A:1106:GLU:N	2.30	0.43
1:A:1330:LYS:HB2	1:A:1334:GLU:OE2	2.19	0.43
1:C:3023:PRO:HB2	1:C:3034:LEU:HD21	2.01	0.43
1:A:1190:GLY:O	1:A:1194:GLN:HG3	2.18	0.43
1:B:2120:ASN:HB2	1:B:2167:THR:OG1	2.19	0.43
1:B:2253:SER:O	1:B:2255:LEU:N	2.51	0.43
3:B:282:SIA:H6	3:B:282:SIA:C11	2.48	0.43
1:A:1023:PRO:HA	1:A:1024:PRO:HD3	1.81	0.42
1:A:1304:LEU:HD11	1:A:1363:LEU:HB3	2.01	0.42
1:A:1318:LEU:HD23	1:A:1318:LEU:N	2.33	0.42
1:B:2113:SER:HB2	1:C:3277:THR:HG21	2.01	0.42
1:B:2246:GLU:HG2	1:B:2447:TYR:OH	2.20	0.42
1:A:1176:GLY:HA2	1:A:1189:TRP:HB2	2.01	0.42
1:B:2366:TYR:HA	1:B:2367:PRO:HD3	1.78	0.42
1:C:3306:LEU:HD22	1:C:3366:TYR:CE1	2.54	0.42
1:C:3452:ARG:NE	1:C:3462:LYS:HA	2.33	0.42
1:C:3495:MET:O	1:C:3498:LYS:HB2	2.19	0.42
1:A:1304:LEU:HB2	6:A:11:PLM:CA	2.49	0.42
1:A:1349:GLY:HA3	1:A:1447:TYR:CZ	2.54	0.42
1:C:3058:PRO:HA	1:C:3059:PRO:HD2	1.98	0.42
1:C:3242:ARG:HD3	1:C:3503:PHE:O	2.19	0.42
1:C:3248:GLY:HA3	7:C:7279:HOH:O	2.18	0.42
1:C:3323:ILE:HG21	1:C:3330:LYS:HA	2.02	0.42
1:A:1023:PRO:HB2	1:A:1034:LEU:HD21	2.02	0.42
1:A:1214:SER:HA	7:A:7017:HOH:O	2.19	0.42
1:A:1301:MET:HE3	1:A:1301:MET:HB3	1.92	0.42

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:2290:THR:HG23	1:B:2293:GLU:OE2	2.19	0.42
1:C:3513:GLY:N	7:C:7182:HOH:O	2.52	0.42
1:B:2140:HIS:CE1	1:B:2147:GLY:HA3	2.55	0.42
1:B:2190:GLY:O	1:B:2194:GLN:HG3	2.19	0.42
1:B:2220:GLU:HB3	7:B:7149:HOH:O	2.20	0.42
1:B:2318:LEU:C	1:B:2319:LEU:O	2.62	0.42
1:B:2532:ASN:HB3	7:B:7015:HOH:O	2.19	0.42
1:A:1379:MET:HG2	1:A:1400:THR:OG1	2.19	0.42
1:B:2023:PRO:HB2	1:B:2034:LEU:HD21	2.02	0.42
1:C:3379:MET:HG2	1:C:3400:THR:OG1	2.20	0.42
1:A:1180:THR:OG1	1:A:1182:ASP:OD2	2.35	0.42
1:B:2064:ARG:CZ	7:B:7253:HOH:O	2.68	0.42
1:A:1257:LYS:HE3	1:A:1322:VAL:CG1	2.50	0.42
1:B:2318:LEU:O	1:B:2319:LEU:O	2.38	0.42
1:B:2404:LEU:HD22	1:B:2413:LYS:O	2.20	0.42
1:C:3370:GLU:HB3	1:C:3372:GLN:HE21	1.83	0.42
1:A:1352:LYS:HB3	1:A:1465:ILE:O	2.20	0.42
1:A:1383:TRP:CZ3	1:A:1393:LYS:HB2	2.54	0.42
1:B:2551:PHE:C	1:B:2553:LYS:N	2.75	0.42
1:C:3176:GLY:HA2	1:C:3189:TRP:HB2	2.01	0.42
1:B:2197:ALA:O	1:B:2201:VAL:HG23	2.20	0.41
1:B:2205:ILE:HD12	1:B:2205:ILE:HA	1.87	0.41
1:C:3124:PRO:HD3	1:C:3158:ALA:HB1	2.02	0.41
1:A:1046:PRO:HA	7:A:7027:HOH:O	2.20	0.41
1:B:2353:GLN:O	1:B:2467:ASP:HA	2.20	0.41
1:B:2385:SER:O	1:B:2389:VAL:HG22	2.20	0.41
1:C:3503:PHE:O	1:C:3507:GLY:N	2.49	0.41
1:B:2257:LYS:HA	1:B:2257:LYS:HD3	1.92	0.41
1:B:2297:THR:HA	1:B:2300:LYS:HE3	2.02	0.41
1:B:2025:VAL:HG22	1:B:2034:LEU:CD2	2.46	0.41
1:C:3435:ARG:O	1:C:3438:ARG:HB3	2.21	0.41
1:A:1179:SER:HA	1:A:1185:SER:O	2.21	0.41
1:B:2367:PRO:C	1:B:2369:SER:H	2.29	0.41
1:C:3264:LEU:O	1:C:3268:ILE:HG13	2.19	0.41
2:C:379:NAG:H3	2:C:379:NAG:H83	2.02	0.41
3:C:382:SIA:H4	3:C:382:SIA:C11	2.34	0.41
1:C:3179:SER:HA	1:C:3185:SER:O	2.20	0.41
1:C:3190:GLY:O	1:C:3194:GLN:HG3	2.20	0.41
1:C:3528:GLN:O	1:C:3533:THR:HA	2.20	0.41
1:A:1465:ILE:HD11	7:A:7255:HOH:O	2.21	0.41
1:B:2034:LEU:HB3	1:B:2079:ASN:HA	2.03	0.41

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:2124:PRO:HD3	1:B:2158:ALA:HB1	2.03	0.41
1:B:2317:PRO:HD2	7:B:7164:HOH:O	2.20	0.41
1:C:3134:PRO:CG	1:C:3163:VAL:HG12	2.39	0.41
1:A:1064:ARG:NH2	1:A:1114:GLU:OE2	2.54	0.41
1:A:1205:ILE:HD12	1:A:1205:ILE:HA	1.90	0.41
1:A:1309:GLN:CB	7:A:7065:HOH:O	2.69	0.41
1:A:1480:PHE:HZ	1:A:1494:LYS:HG3	1.86	0.41
1:B:2023:PRO:HA	1:B:2024:PRO:HD3	1.82	0.41
1:B:2254:VAL:CG2	1:B:2388:LEU:HD23	2.50	0.41
1:C:3304:LEU:O	1:C:3364:MET:HA	2.21	0.41
1:C:3349:GLY:HA3	1:C:3447:TYR:CZ	2.55	0.41
1:A:1528:GLN:O	1:A:1533:THR:HA	2.20	0.41
1:B:2115:ASP:OD2	1:C:3278:THR:OG1	2.33	0.41
1:B:2383:TRP:CZ3	1:B:2393:LYS:HB2	2.56	0.41
1:B:2447:TYR:CD2	1:B:2447:TYR:C	2.98	0.41
1:B:2301:MET:HE3	1:B:2301:MET:HB3	2.00	0.41
1:B:2364:MET:HE1	1:B:2388:LEU:HD11	2.03	0.41
1:B:2176:GLY:HA2	1:B:2189:TRP:HB2	2.04	0.40
1:B:2252:THR:O	1:B:2253:SER:C	2.64	0.40
1:C:3063:LEU:HB3	7:C:7053:HOH:O	2.20	0.40
1:C:3461:PRO:HG2	1:C:3464:VAL:HG23	2.02	0.40
1:A:1087:CYS:O	1:A:1089:GLN:HG2	2.21	0.40
1:A:1318:LEU:CG	1:A:1319:LEU:N	2.77	0.40
1:A:1331:THR:HB	1:A:1333:GLU:OE1	2.21	0.40
1:A:1486:SER:O	1:A:1490:ILE:HG13	2.22	0.40
1:B:2145:MET:HE2	1:B:2303:PHE:HB2	2.03	0.40
1:B:2331:THR:HB	1:B:2333:GLU:OE1	2.20	0.40
1:B:2495:MET:O	1:B:2498:LYS:HB2	2.21	0.40
1:C:3480:PHE:HZ	1:C:3494:LYS:HG3	1.85	0.40
1:A:1083:TYR:CD2	1:A:1108:ILE:HG21	2.57	0.40
1:A:1145:MET:HE2	1:A:1303:PHE:CD1	2.56	0.40
1:B:2090:ASP:HA	1:B:2091:PRO:HD2	1.92	0.40
1:B:2223:GLY:O	1:B:2227:VAL:HG23	2.21	0.40
1:C:3195:VAL:HG13	1:C:3239:LEU:CD1	2.51	0.40
1:A:1211:ASN:HA	1:A:1212:PRO:HD2	1.99	0.40
1:A:1304:LEU:HD11	1:A:1363:LEU:C	2.47	0.40
1:B:2179:SER:HA	1:B:2185:SER:O	2.22	0.40
1:C:3257:LYS:CE	1:C:3316:GLN:OE1	2.70	0.40
1:C:3404:LEU:HD22	1:C:3413:LYS:O	2.22	0.40
1:A:1304:LEU:CB	6:A:11:PLM:HD2	2.51	0.40

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	530/542 (98%)	481 (91%)	45 (8%)	4 (1%)	16	50
1	B	343/542 (63%)	309 (90%)	27 (8%)	7 (2%)	6	28
1	C	530/542 (98%)	484 (91%)	43 (8%)	3 (1%)	21	56
All	All	1403/1626 (86%)	1274 (91%)	115 (8%)	14 (1%)	12	45

All (14) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	1185	SER
1	B	2319	LEU
1	B	2369	SER
1	C	3185	SER
1	A	1538	LYS
1	B	2538	LYS
1	C	3538	LYS
1	A	1253	SER
1	B	2254	VAL
1	B	2358	LEU
1	B	2368	LEU
1	A	1302	LYS
1	C	3253	SER
1	B	2317	PRO

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	448/457 (98%)	438 (98%)	10 (2%)	45	74
1	B	448/457 (98%)	437 (98%)	11 (2%)	42	72
1	C	448/457 (98%)	439 (98%)	9 (2%)	48	76
All	All	1344/1371 (98%)	1314 (98%)	30 (2%)	45	74

All (30) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	1041	GLU
1	A	1092	LYS
1	A	1106	GLU
1	A	1199	ARG
1	A	1218	PHE
1	A	1242	ARG
1	A	1264	LEU
1	A	1338	GLU
1	A	1465	ILE
1	A	1523	LYS
1	B	2041	GLU
1	B	2092	LYS
1	B	2106	GLU
1	B	2199	ARG
1	B	2218	PHE
1	B	2242	ARG
1	B	2264	LEU
1	B	2318	LEU
1	B	2338	GLU
1	B	2366	TYR
1	B	2523	LYS
1	C	3041	GLU
1	C	3092	LYS
1	C	3199	ARG
1	C	3218	PHE
1	C	3242	ARG
1	C	3264	LEU
1	C	3338	GLU
1	C	3463	THR
1	C	3523	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (27) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	1030	HIS
1	A	1045	GLN
1	A	1069	GLN
1	A	1162	ASN
1	A	1238	ASN
1	A	1316	GLN
1	A	1372	GLN
1	A	1375	GLN
1	A	1450	GLN
1	A	1549	ASN
1	B	2045	GLN
1	B	2069	GLN
1	B	2162	ASN
1	B	2184	HIS
1	B	2316	GLN
1	B	2372	GLN
1	B	2375	GLN
1	B	2450	GLN
1	B	2549	ASN
1	C	3030	HIS
1	C	3045	GLN
1	C	3069	GLN
1	C	3131	ASN
1	C	3162	ASN
1	C	3372	GLN
1	C	3516	HIS
1	C	3549	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 ⓘ

There are no oligosaccharides in this entry.

5.6 Ligand geometry

18 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
3	SIA	A	182	-	21,21,21	0.97	1 (4%)	24,31,31	1.06	3 (12%)
3	SIA	C	382	-	21,21,21	0.99	2 (9%)	24,31,31	1.28	3 (12%)
5	CHD	C	3	-	32,32,32	2.29	17 (53%)	51,51,51	1.37	8 (15%)
4	SO4	A	184	-	4,4,4	0.41	0	6,6,6	0.08	0
5	CHD	B	2	-	32,32,32	2.36	18 (56%)	51,51,51	1.39	7 (13%)
2	NAG	B	279	1	14,14,15	0.54	0	17,19,21	1.05	1 (5%)
4	SO4	A	285	-	4,4,4	0.41	0	6,6,6	0.10	0
4	SO4	A	185	-	4,4,4	0.41	0	6,6,6	0.10	0
4	SO4	B	284	-	4,4,4	0.37	0	6,6,6	0.15	0
5	CHD	A	1	-	32,32,32	2.24	18 (56%)	51,51,51	1.36	8 (15%)
6	PLM	C	13	-	17,17,17	0.69	0	17,17,17	0.58	0
6	PLM	B	12	-	17,17,17	0.69	0	17,17,17	0.64	0
4	SO4	C	385	-	4,4,4	0.42	0	6,6,6	0.12	0
2	NAG	A	179	1	14,14,15	0.80	0	17,19,21	1.15	2 (11%)
2	NAG	C	379	1	14,14,15	0.63	0	17,19,21	1.13	2 (11%)
6	PLM	A	11	-	17,17,17	0.63	0	17,17,17	0.63	0
3	SIA	B	282	-	21,21,21	0.86	0	24,31,31	1.26	4 (16%)
4	SO4	C	384	-	4,4,4	0.39	0	6,6,6	0.15	0

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	SIA	A	182	-	-	9/20/38/38	0/1/1/1
3	SIA	C	382	-	-	14/20/38/38	0/1/1/1
5	CHD	C	3	-	-	5/9/74/74	0/4/4/4
5	CHD	B	2	-	-	5/9/74/74	0/4/4/4

Continued on next page...

Continued from previous page...

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	NAG	B	279	1	-	2/6/23/26	0/1/1/1
5	CHD	A	1	-	-	3/9/74/74	0/4/4/4
6	PLM	C	13	-	-	11/15/15/15	-
6	PLM	B	12	-	-	9/15/15/15	-
2	NAG	A	179	1	-	3/6/23/26	0/1/1/1
2	NAG	C	379	1	1/1/5/7	3/6/23/26	0/1/1/1
6	PLM	A	11	-	-	13/15/15/15	-
3	SIA	B	282	-	-	6/20/38/38	0/1/1/1

All (56) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	C	3	CHD	C20-C17	4.85	1.62	1.54
5	C	3	CHD	O25-C24	4.04	1.35	1.22
5	B	2	CHD	C11-C12	4.03	1.59	1.53
5	B	2	CHD	C10-C9	3.92	1.62	1.56
5	B	2	CHD	O25-C24	3.80	1.34	1.22
5	C	3	CHD	C11-C12	3.76	1.59	1.53
5	A	1	CHD	C11-C12	3.74	1.59	1.53
5	A	1	CHD	O25-C24	3.63	1.34	1.22
5	C	3	CHD	C11-C9	3.61	1.59	1.53
5	B	2	CHD	C20-C17	3.49	1.60	1.54
5	A	1	CHD	C20-C17	3.47	1.60	1.54
5	B	2	CHD	C11-C9	3.46	1.59	1.53
5	C	3	CHD	C18-C13	3.40	1.59	1.54
5	B	2	CHD	C4-C5	3.25	1.59	1.53
5	A	1	CHD	C18-C13	3.14	1.59	1.54
5	A	1	CHD	C11-C9	3.05	1.58	1.53
5	A	1	CHD	C6-C5	3.04	1.58	1.53
5	C	3	CHD	C10-C9	3.04	1.61	1.56
5	B	2	CHD	C18-C13	3.01	1.59	1.54
5	A	1	CHD	C4-C5	2.89	1.58	1.53
5	C	3	CHD	C8-C9	2.83	1.59	1.53
5	B	2	CHD	C6-C5	2.81	1.58	1.53
5	A	1	CHD	O26-C24	-2.80	1.21	1.30
5	A	1	CHD	C8-C9	2.78	1.59	1.53
5	A	1	CHD	C10-C5	2.73	1.59	1.55
5	C	3	CHD	O26-C24	-2.64	1.22	1.30
5	A	1	CHD	C10-C9	2.59	1.60	1.56
5	B	2	CHD	C10-C5	2.58	1.59	1.55

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	B	2	CHD	C8-C9	2.56	1.58	1.53
5	C	3	CHD	C10-C5	2.54	1.59	1.55
5	C	3	CHD	C6-C5	2.50	1.57	1.53
5	B	2	CHD	O26-C24	-2.48	1.22	1.30
5	A	1	CHD	C13-C17	2.43	1.59	1.55
5	B	2	CHD	C8-C14	2.41	1.58	1.53
5	B	2	CHD	C1-C2	2.40	1.58	1.53
3	A	182	SIA	C3-C2	2.39	1.55	1.51
5	C	3	CHD	C23-C24	2.37	1.56	1.50
5	B	2	CHD	C8-C7	2.35	1.57	1.53
5	B	2	CHD	C13-C17	2.35	1.59	1.55
5	B	2	CHD	C2-C3	2.35	1.57	1.51
5	C	3	CHD	C13-C12	2.31	1.58	1.54
5	A	1	CHD	C2-C3	2.29	1.56	1.51
5	C	3	CHD	C2-C3	2.29	1.56	1.51
3	C	382	SIA	C7-C6	2.26	1.55	1.52
5	C	3	CHD	C6-C7	2.23	1.57	1.52
5	A	1	CHD	C4-C3	2.19	1.55	1.52
5	A	1	CHD	C8-C7	2.18	1.57	1.53
3	C	382	SIA	O6-C2	2.17	1.45	1.43
5	B	2	CHD	C4-C3	2.15	1.55	1.52
5	A	1	CHD	C1-C2	2.13	1.57	1.53
5	B	2	CHD	C6-C7	2.13	1.56	1.52
5	C	3	CHD	C8-C7	2.05	1.57	1.53
5	C	3	CHD	C13-C17	2.03	1.58	1.55
5	C	3	CHD	C8-C14	2.02	1.57	1.53
5	A	1	CHD	C13-C12	2.01	1.57	1.54
5	A	1	CHD	C8-C14	2.01	1.57	1.53

All (38) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	B	2	CHD	C17-C13-C14	-4.20	95.90	100.11
5	C	3	CHD	C19-C10-C1	-3.87	102.16	108.31
2	B	279	NAG	C2-N2-C7	-3.71	117.92	122.90
5	A	1	CHD	C17-C13-C14	-3.32	96.79	100.11
3	C	382	SIA	O1A-C1-C2	-3.26	118.42	123.85
5	A	1	CHD	C9-C11-C12	-3.21	110.09	114.29
2	C	379	NAG	C4-C3-C2	3.21	115.72	111.02
3	B	282	SIA	O1A-C1-C2	-2.95	118.93	123.85
5	B	2	CHD	C9-C11-C12	-2.88	110.52	114.29
3	A	182	SIA	O1A-C1-C2	-2.88	119.05	123.85

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	B	2	CHD	C19-C10-C1	-2.86	103.75	108.31
5	A	1	CHD	C19-C10-C1	-2.74	103.95	108.31
3	C	382	SIA	C9-C8-C7	-2.60	106.88	112.17
5	A	1	CHD	C16-C17-C20	-2.58	108.28	112.18
3	B	282	SIA	C3-C4-C5	2.53	113.63	109.72
5	C	3	CHD	C9-C11-C12	-2.45	111.08	114.29
2	A	179	NAG	C2-N2-C7	-2.43	119.64	122.90
5	C	3	CHD	C21-C20-C22	-2.43	106.57	110.34
5	B	2	CHD	C16-C17-C20	-2.42	108.51	112.18
2	A	179	NAG	C3-C4-C5	2.41	114.61	110.23
5	C	3	CHD	C16-C15-C14	-2.40	100.44	105.14
5	A	1	CHD	C14-C13-C12	-2.40	105.22	107.42
5	C	3	CHD	C1-C2-C3	-2.34	107.38	110.48
5	B	2	CHD	C14-C13-C12	-2.33	105.28	107.42
5	B	2	CHD	C6-C5-C10	-2.32	110.19	112.66
5	C	3	CHD	C18-C13-C12	2.29	111.35	109.06
3	B	282	SIA	O6-C6-C7	2.29	110.23	106.65
3	A	182	SIA	C9-C8-C7	-2.23	107.62	112.17
5	C	3	CHD	O26-C24-C23	2.23	121.04	114.00
3	A	182	SIA	O6-C6-C7	2.23	110.13	106.65
5	B	2	CHD	O26-C24-C23	2.22	121.01	114.00
5	A	1	CHD	C16-C15-C14	-2.20	100.84	105.14
5	A	1	CHD	O26-C24-C23	2.15	120.81	114.00
3	C	382	SIA	O6-C6-C7	2.14	110.00	106.65
5	C	3	CHD	C17-C13-C14	-2.14	97.97	100.11
2	C	379	NAG	C2-N2-C7	-2.08	120.11	122.90
3	B	282	SIA	C9-C8-C7	-2.02	108.06	112.17
5	A	1	CHD	C6-C5-C10	-2.00	110.53	112.66

All (1) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
2	C	379	NAG	C1

All (83) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	C	379	NAG	C3-C2-N2-C7
2	C	379	NAG	C8-C7-N2-C2
2	C	379	NAG	O7-C7-N2-C2
3	A	182	SIA	O1A-C1-C2-O2
3	A	182	SIA	O1B-C1-C2-O2

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms
3	A	182	SIA	O1B-C1-C2-O6
3	A	182	SIA	O6-C6-C7-O7
3	A	182	SIA	C11-C10-N5-C5
3	A	182	SIA	O10-C10-N5-C5
3	B	282	SIA	C4-C5-N5-C10
3	B	282	SIA	C11-C10-N5-C5
3	B	282	SIA	O10-C10-N5-C5
3	C	382	SIA	C5-C6-C7-C8
3	C	382	SIA	C5-C6-C7-O7
3	C	382	SIA	O6-C6-C7-C8
3	C	382	SIA	O6-C6-C7-O7
3	C	382	SIA	C11-C10-N5-C5
3	C	382	SIA	O10-C10-N5-C5
2	B	279	NAG	C8-C7-N2-C2
2	B	279	NAG	O7-C7-N2-C2
2	A	179	NAG	C8-C7-N2-C2
5	C	3	CHD	C17-C20-C22-C23
5	C	3	CHD	C21-C20-C22-C23
5	B	2	CHD	C20-C22-C23-C24
2	A	179	NAG	O7-C7-N2-C2
5	C	3	CHD	C20-C22-C23-C24
6	C	13	PLM	CB-CC-CD-CE
6	B	12	PLM	C4-C5-C6-C7
6	A	11	PLM	C4-C5-C6-C7
5	A	1	CHD	C20-C22-C23-C24
6	B	12	PLM	C5-C6-C7-C8
6	C	13	PLM	C9-CA-CB-CC
6	A	11	PLM	CA-CB-CC-CD
6	B	12	PLM	CC-CD-CE-CF
6	A	11	PLM	CB-CC-CD-CE
6	B	12	PLM	C9-CA-CB-CC
6	C	13	PLM	C5-C6-C7-C8
6	A	11	PLM	CC-CD-CE-CF
6	A	11	PLM	C7-C8-C9-CA
6	A	11	PLM	C2-C3-C4-C5
6	A	11	PLM	C1-C2-C3-C4
6	C	13	PLM	C3-C4-C5-C6
3	C	382	SIA	O7-C7-C8-O8
6	A	11	PLM	C3-C4-C5-C6
3	C	382	SIA	C6-C5-N5-C10
6	C	13	PLM	C2-C3-C4-C5
6	A	11	PLM	C5-C6-C7-C8

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms
6	C	13	PLM	C6-C7-C8-C9
6	B	12	PLM	CB-CC-CD-CE
6	C	13	PLM	CD-CE-CF-CG
6	B	12	PLM	C6-C7-C8-C9
6	A	11	PLM	CD-CE-CF-CG
6	B	12	PLM	C3-C4-C5-C6
3	C	382	SIA	O7-C7-C8-C9
2	A	179	NAG	O5-C5-C6-O6
6	C	13	PLM	C4-C5-C6-C7
3	C	382	SIA	O1A-C1-C2-C3
3	C	382	SIA	O1B-C1-C2-C3
6	C	13	PLM	CA-CB-CC-CD
3	A	182	SIA	O1A-C1-C2-O6
3	B	282	SIA	O1A-C1-C2-O2
3	B	282	SIA	O1A-C1-C2-O6
6	A	11	PLM	C6-C7-C8-C9
3	C	382	SIA	C6-C7-C8-O8
5	B	2	CHD	C21-C20-C22-C23
3	C	382	SIA	C4-C5-N5-C10
6	A	11	PLM	O2-C1-C2-C3
6	A	11	PLM	O1-C1-C2-C3
6	C	13	PLM	O1-C1-C2-C3
3	A	182	SIA	C5-C6-C7-O7
5	B	2	CHD	C22-C23-C24-O26
5	A	1	CHD	C22-C23-C24-O26
5	C	3	CHD	C22-C23-C24-O26
6	C	13	PLM	O2-C1-C2-C3
6	B	12	PLM	O2-C1-C2-C3
3	C	382	SIA	O1B-C1-C2-O2
5	B	2	CHD	C22-C23-C24-O25
5	A	1	CHD	C22-C23-C24-O25
6	B	12	PLM	O1-C1-C2-C3
5	C	3	CHD	C22-C23-C24-O25
5	B	2	CHD	C17-C20-C22-C23
3	A	182	SIA	O1B-C1-C2-C3
3	B	282	SIA	C6-C5-N5-C10

There are no ring outliers.

9 monomers are involved in 40 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	182	SIA	3	0

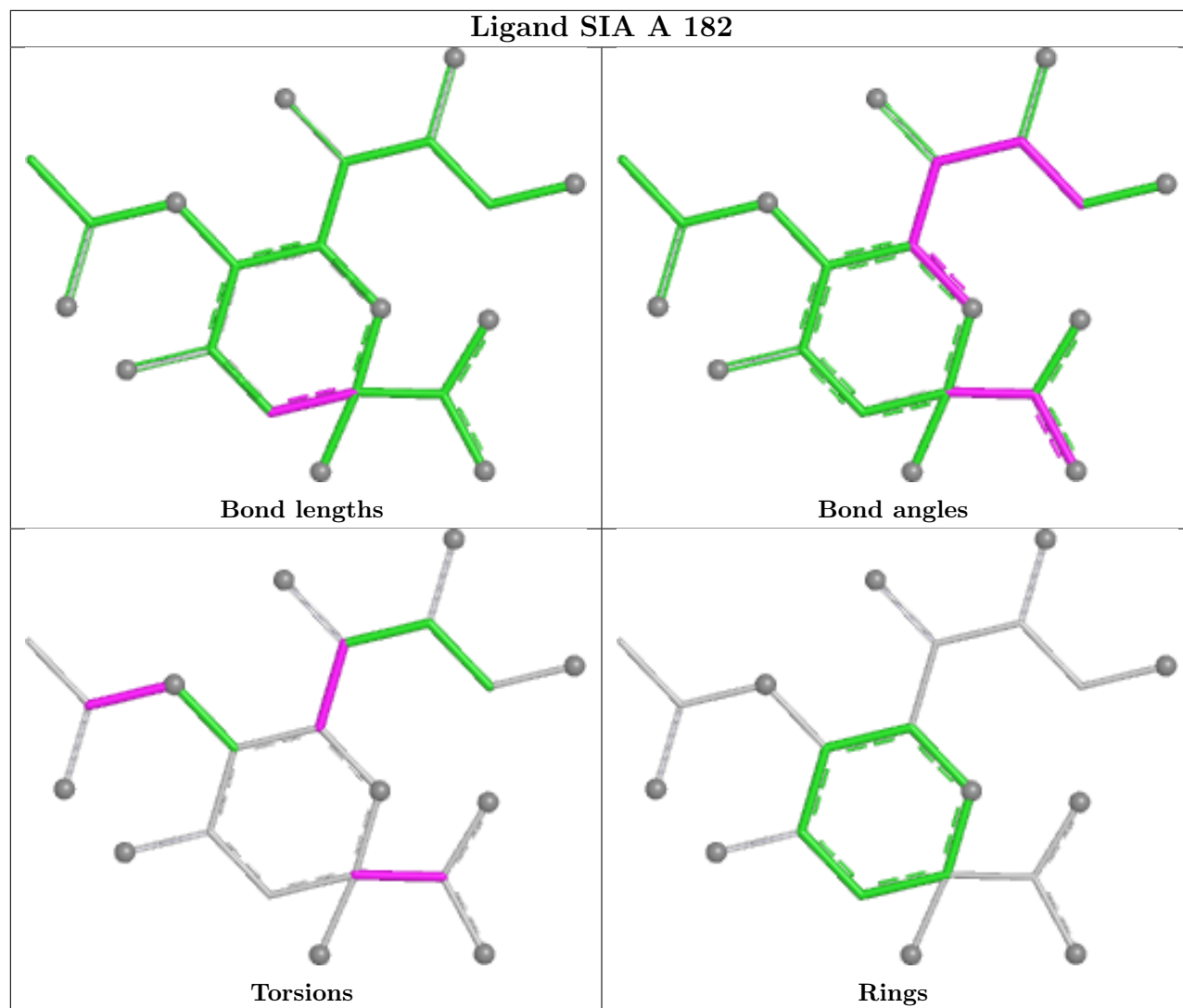
Continued on next page...

Continued from previous page...

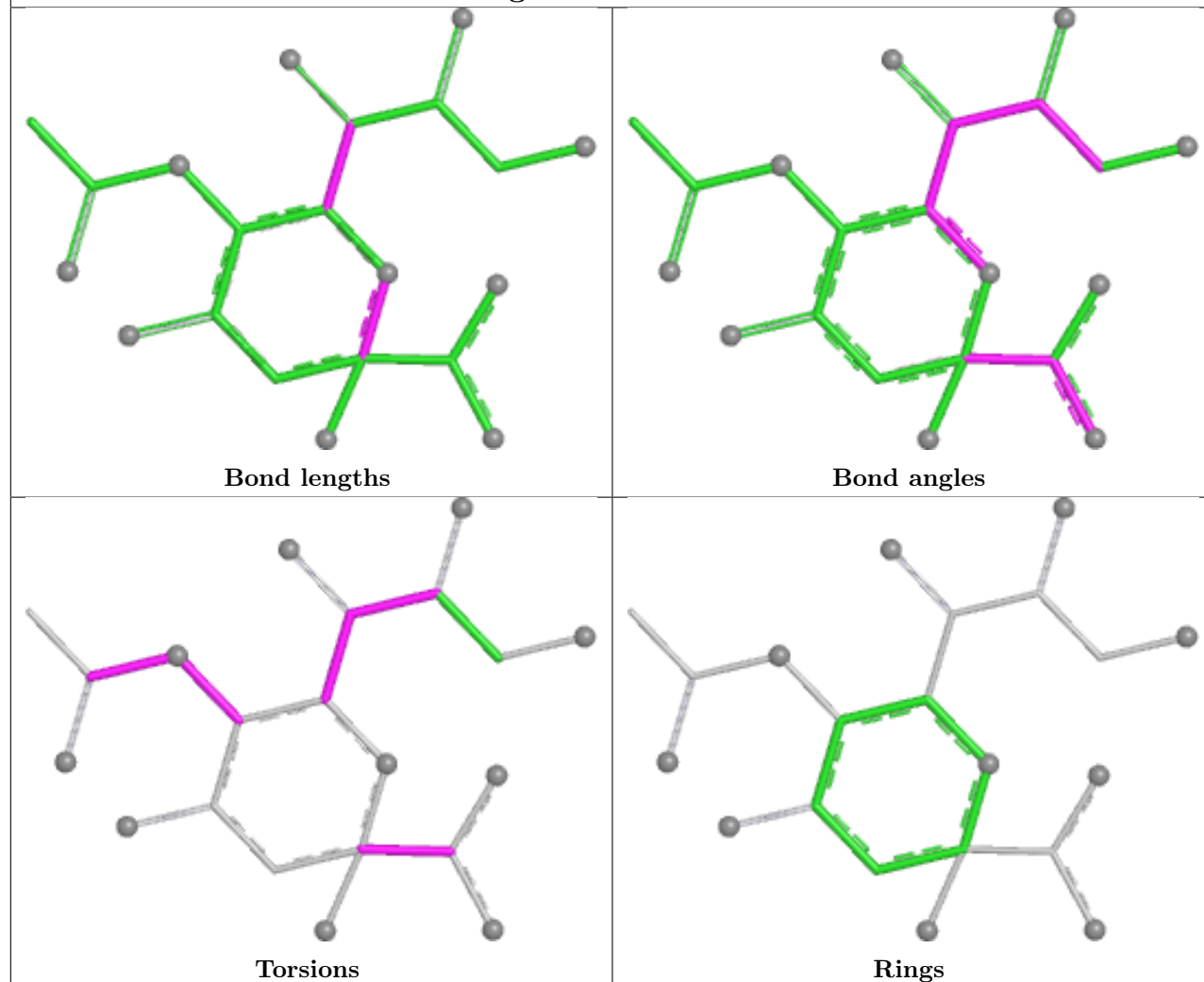
Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	C	382	SIA	6	0
5	C	3	CHD	7	0
5	A	1	CHD	2	0
6	C	13	PLM	7	0
6	B	12	PLM	2	0
2	C	379	NAG	2	0
6	A	11	PLM	9	0
3	B	282	SIA	2	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.

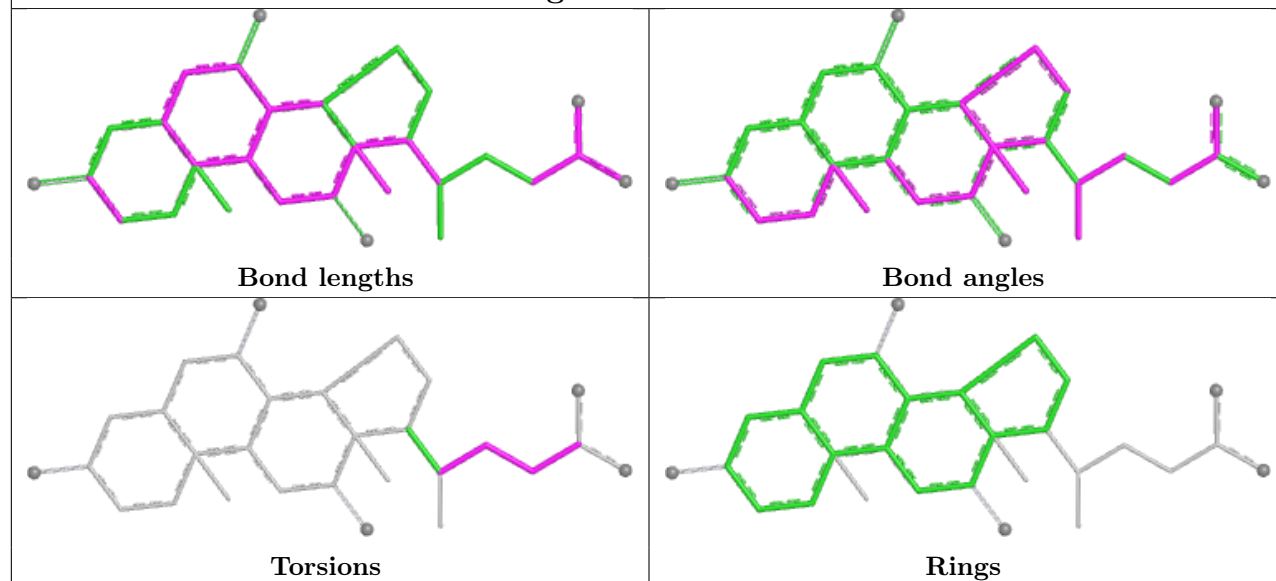
Ligand SIA A 182



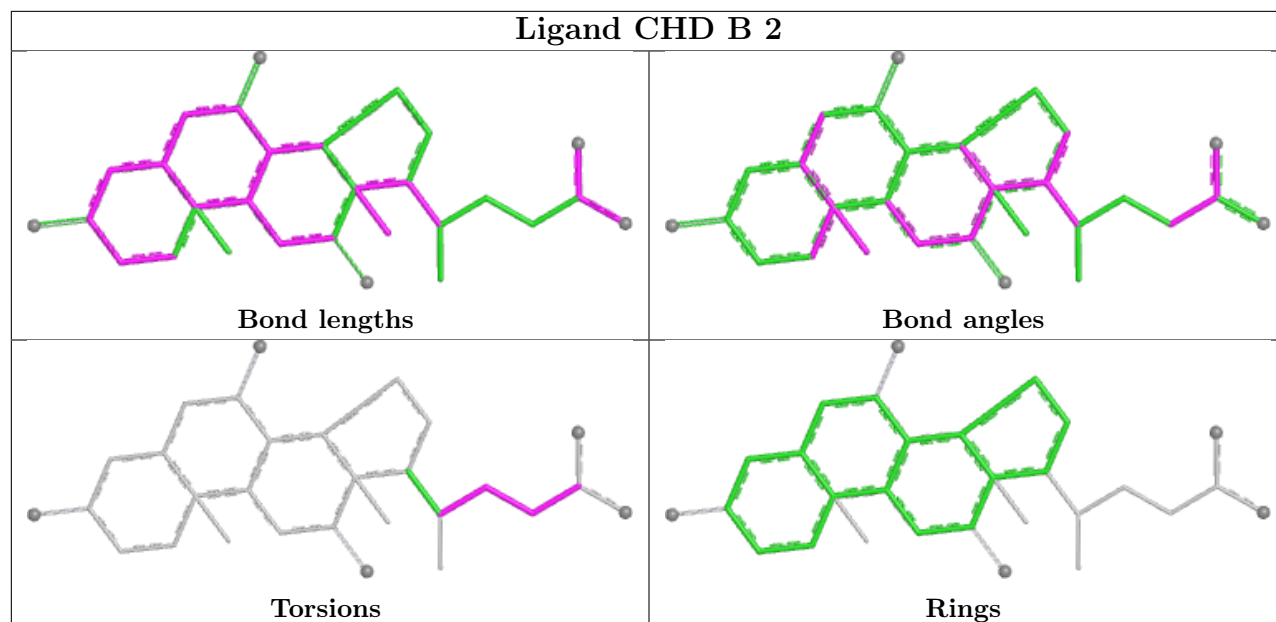
Ligand SIA C 382



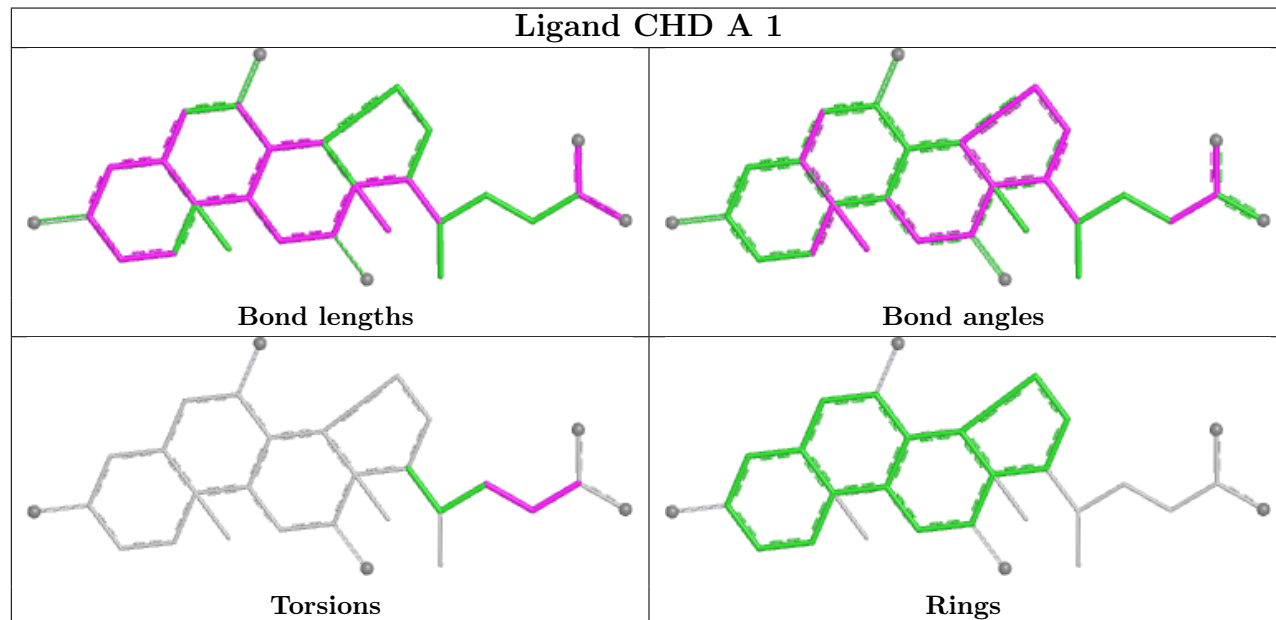
Ligand CHD C 3



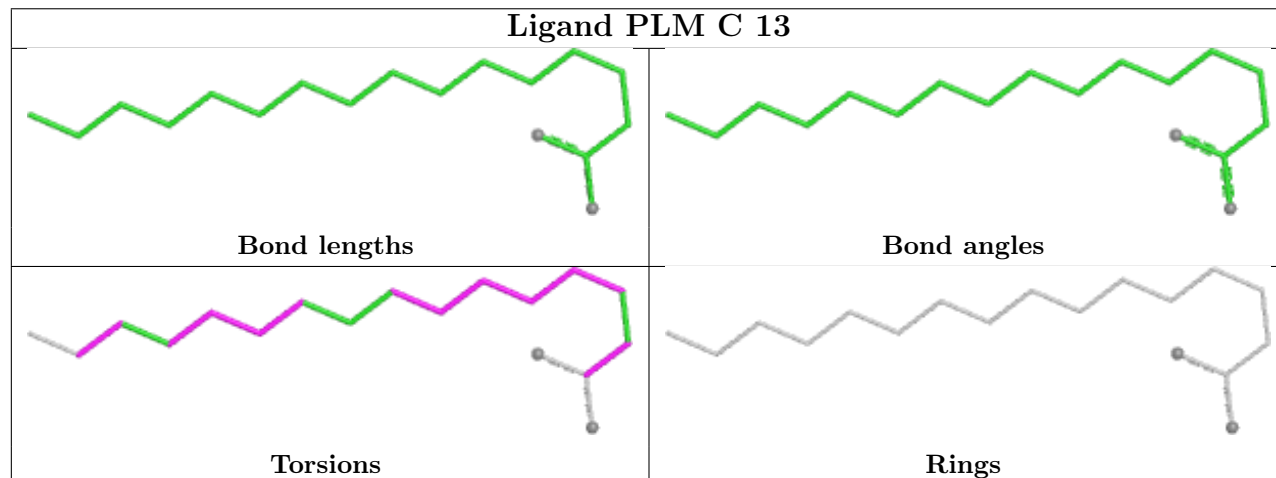
Ligand CHD B 2

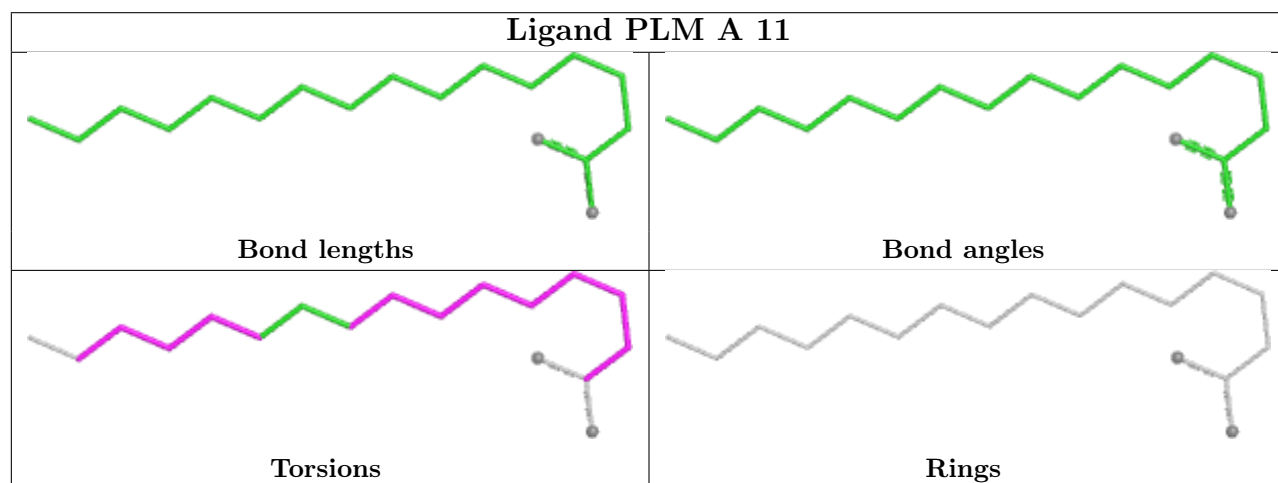
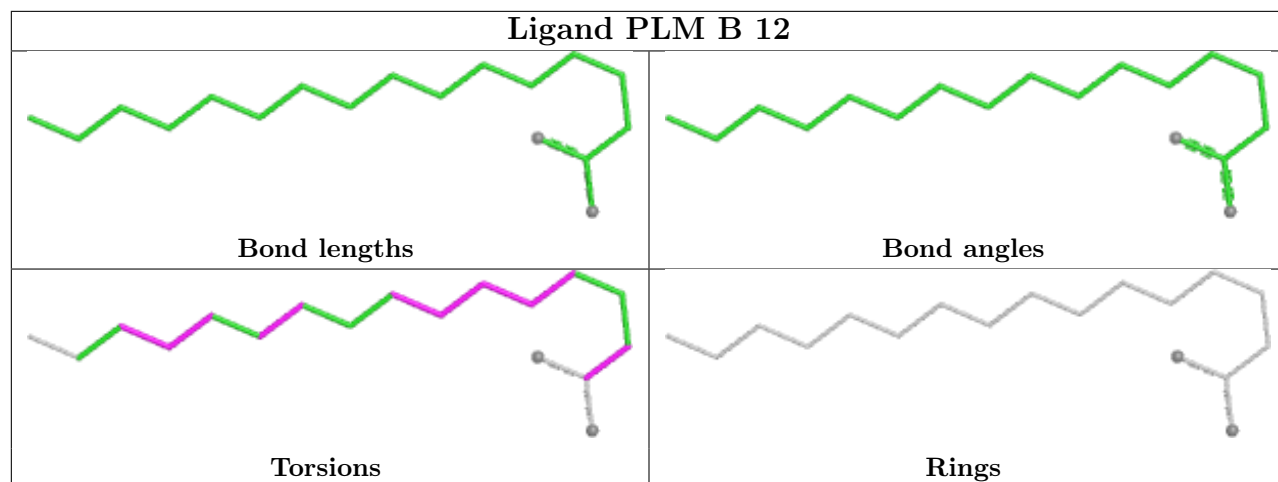


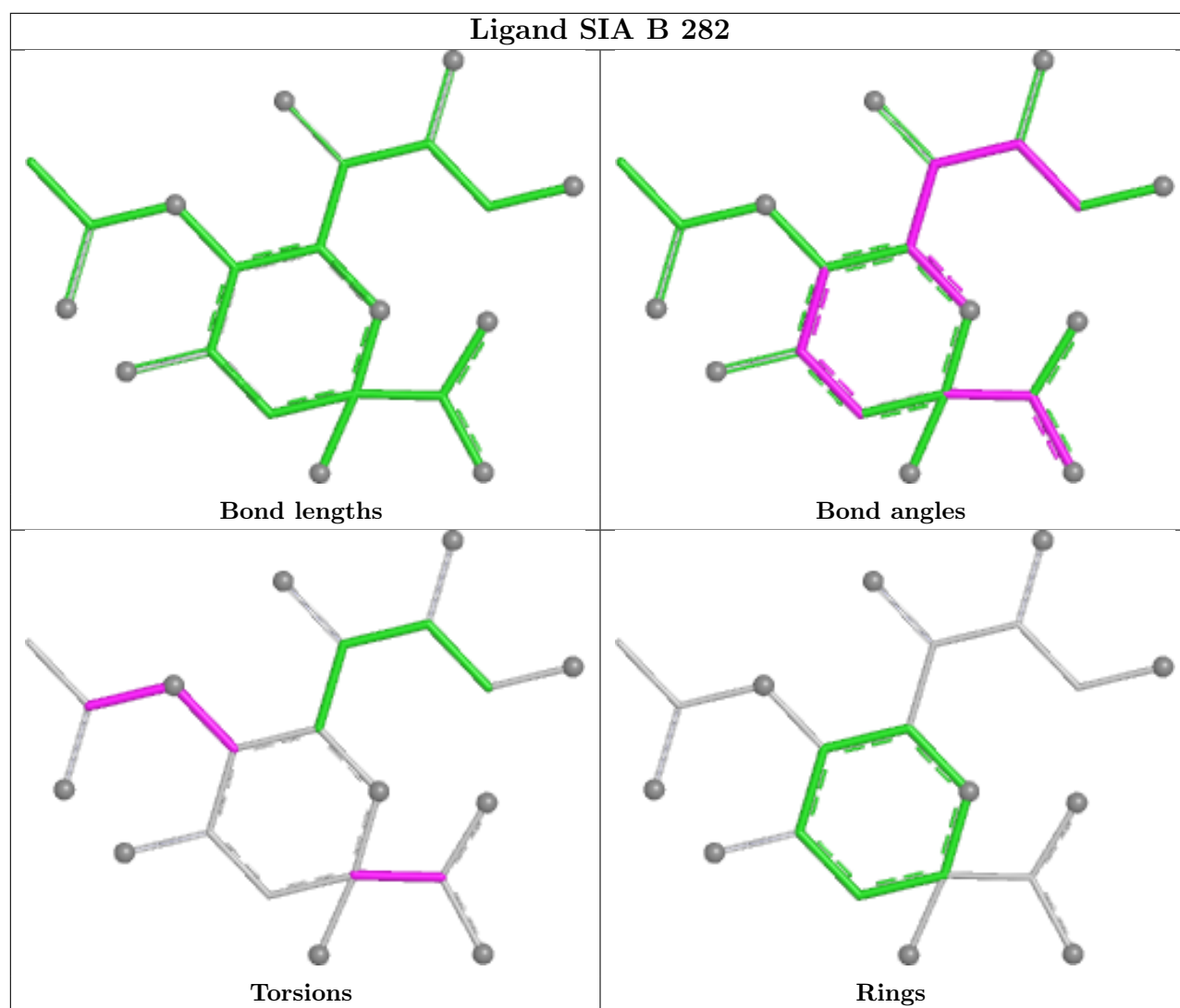
Ligand CHD A 1



Ligand PLM C 13







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.