



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 01:38 AM GMT

PDB ID : 2DQY
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
<http://wwpdb.org/validation/2016/XrayValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

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

MolProbity : 4.02b-467
Mogul : 1.7 (RC4), CSD as536be (2015)
Xtriage (Phenix) : **NOT EXECUTED**
EDS : **NOT EXECUTED**
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : trunk26865

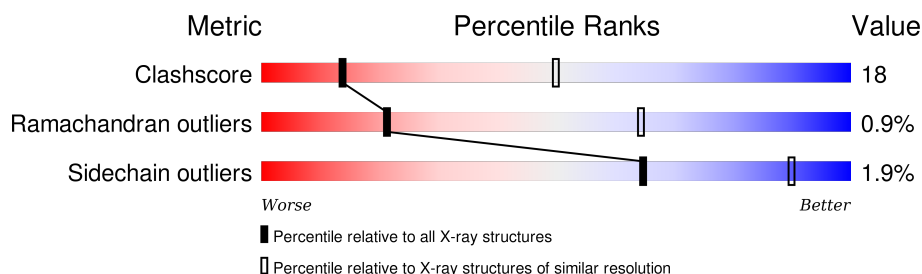
1 Overall quality at a glance

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	102246	1912 (3.00-3.00)
Ramachandran outliers	100387	1853 (3.00-3.00)
Sidechain outliers	100360	1856 (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 on the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	A	542	
1	B	542	
1	C	542	

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	-	-	-

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Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
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.

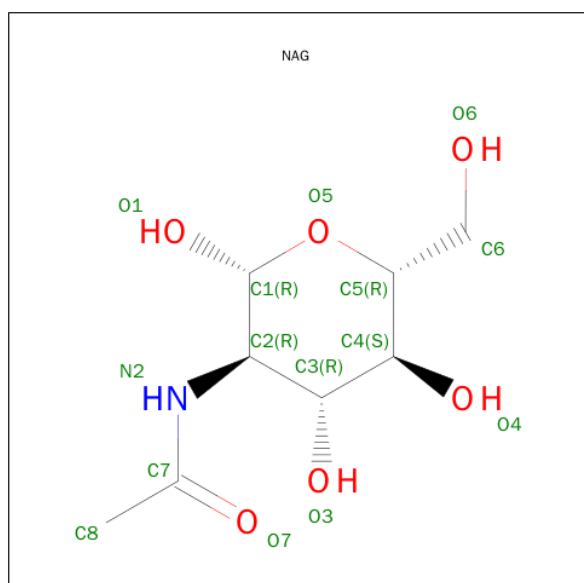
- Molecule 1 is a protein called Liver carboxylesterase 1.

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:

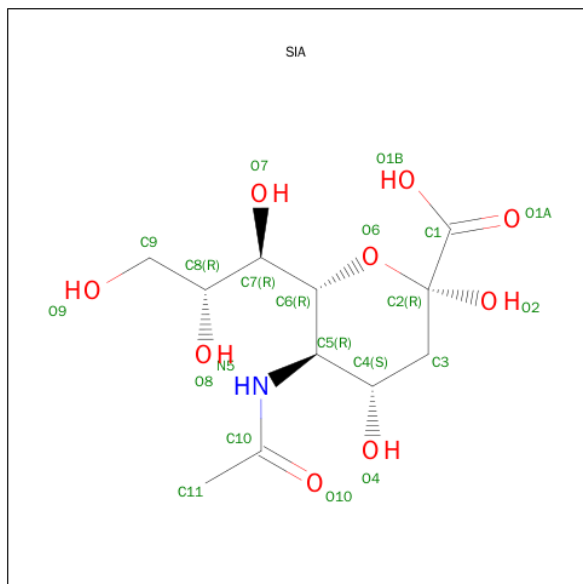
Chain	Residue	Modelled	Actual	Comment	Reference
A	?	-	GLN	DELETION	UNP P23141
B	?	-	GLN	DELETION	UNP P23141
C	?	-	GLN	DELETION	UNP P23141

- Molecule 2 is SUGAR (N-ACETYL-D-GLUCOSAMINE) (three-letter code: 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 SUGAR (O-SIALIC ACID) (three-letter code: SIA) (formula: $C_{11}H_{19}NO_9$).



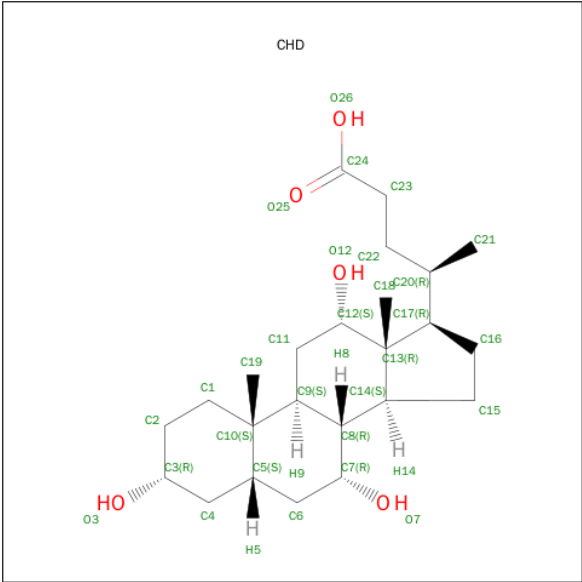
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	A	1	Total	C	N	O	0	0
			21	11	1	9		
3	B	1	Total	C	N	O	0	0
			21	11	1	9		
3	C	1	Total	C	N	O	0	0
			21	11	1	9		

- Molecule 4 is SULFATE ION (three-letter code: SO4) (formula: O_4S).



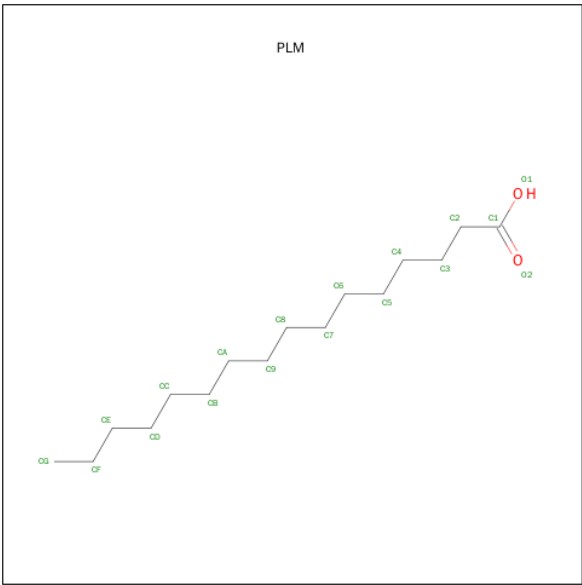
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	A	1	Total	O	S	0	0
			5	4	1		
4	A	1	Total	O	S	0	0
			5	4	1		
4	B	1	Total	O	S	0	0
			5	4	1		
4	A	1	Total	O	S	0	0
			5	4	1		
4	C	1	Total	O	S	0	0
			5	4	1		
4	C	1	Total	O	S	0	0
			5	4	1		

- Molecule 5 is CHOLIC ACID (three-letter code: 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 (three-letter code: PLM) (formula: C₁₆H₃₂O₂).



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

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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.

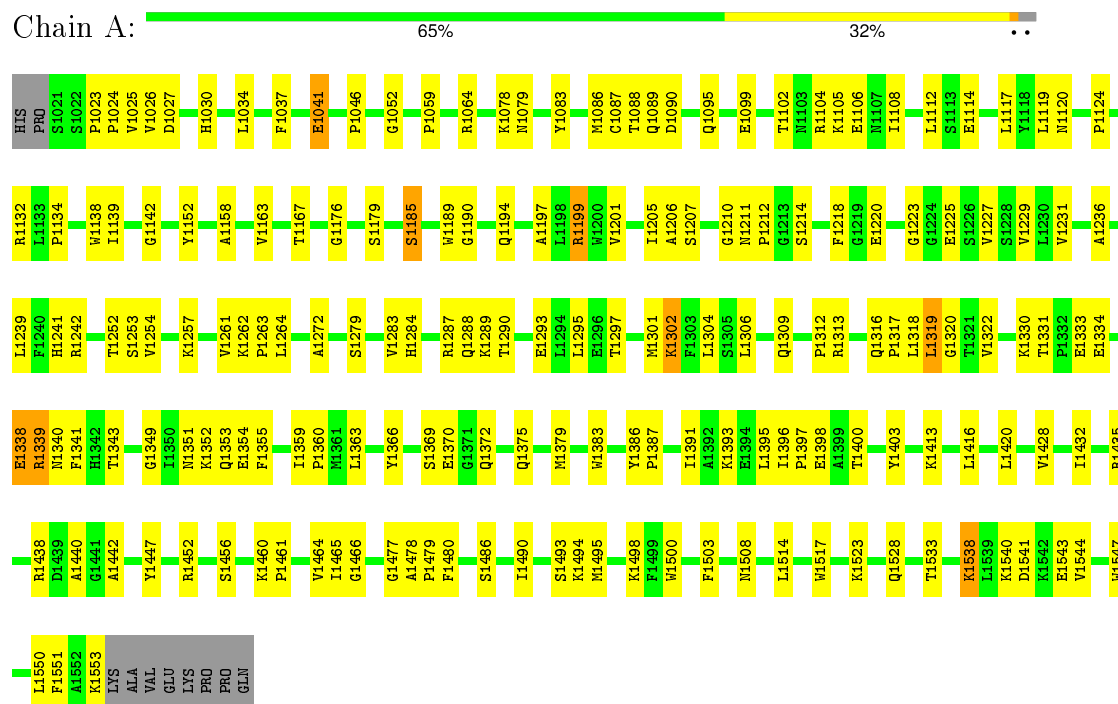
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	A	108	Total	O	0	0
			108	108		
7	B	87	Total	O	0	0
			87	87		
7	C	106	Total	O	0	0
			106	106		

3 Residue-property plots

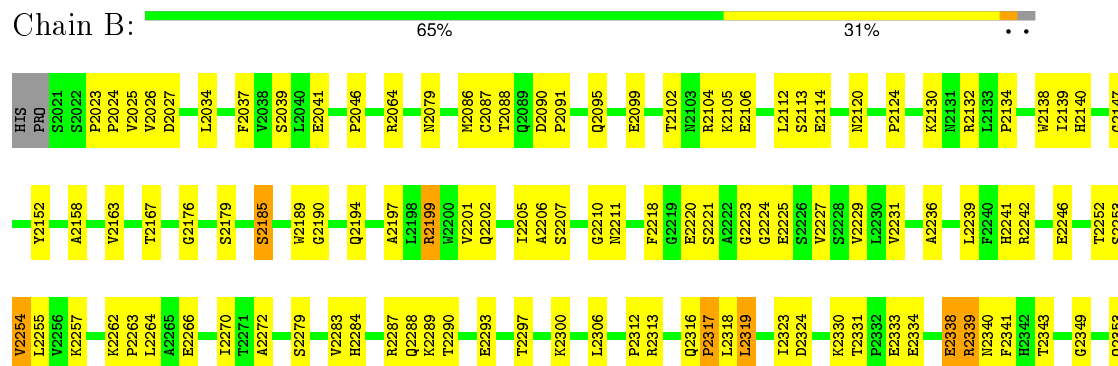
These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according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

Note EDS was not executed.

- Molecule 1: Liver carboxylesterase 1



- Molecule 1: Liver carboxylesterase 1



4 Data and refinement statistics

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

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	55.29 Å 179.88 Å 201.32 Å 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: PLM, SIA, CHD, 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	0.43	0/4236	0.60	1/5754 (0.0%)
1	B	0.42	0/4236	0.58	0/5754
1	C	0.42	0/4236	0.58	0/5754
All	All	0.42	0/12708	0.59	1/17262 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	1319	LEU	N-CA-C	-7.63	90.40	111.00

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	165	0
1	B	4130	0	4131	143	0
1	C	4130	0	4131	153	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

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	B	21	0	18	2	0
3	C	21	0	18	8	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	468	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 18.

All (468) 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:HB3	1:C:3199:ARG:HH11	1.31	0.95
1:B:2199:ARG:HB3	1:B:2199:ARG:HH11	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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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:O	1:B:2318:LEU:HD12	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
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:B:2105:LYS:HG3	1:B:2106:GLU:H	1.55	0.69
1:B:2025:VAL:HG22	1:B:2034:LEU:HD23	1.74	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: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:C:3414:LYS:NZ	5:C:3:CHD:H42	2.09	0.67
1:A:1396:ILE:HB	1:A:1397:PRO:HD3	1.76	0.67
1:A:1241:HIS:O	1:A:1242:ARG:HG3	1.93	0.67
1:A:1025:VAL:HG22	1:A:1034:LEU:HD23	1.73	0.67
1:C:3304:LEU:HD13	6:C:13:PLM:H91	1.76	0.67
1:B:2262:LYS:HB3	1:B:2263:PRO:HD3	1.77	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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:3262:LYS:HB3	1:C:3263:PRO:HD3	1.77	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:1078:LYS:HG3	3:A:182:SIA:O1B	1.96	0.65
1:A:1024:PRO:HG3	1:A:1037:PHE:CZ	2.32	0.65
1:A:1290:THR:OG1	1:A:1293:GLU:HG3	1.97	0.65
3:B:282:SIA:H6	3:B:282:SIA:H113	1.79	0.65
1:A:1331:THR:OG1	1:A:1334:GLU:HG3	1.97	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:A:1333:GLU:H	1:A:1333:GLU:CD	2.01	0.64
1:B:2370:GLU:HB3	1:B:2372:GLN:NE2	2.12	0.64
1:C:3396:ILE:HB	1:C:3397:PRO:HD3	1.79	0.63
1:B:2341:PHE:HB3	7:B:7221:HOH:O	1.99	0.63
1:B:2333:GLU:H	1:B:2333:GLU:CD	2.01	0.63
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: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:B:2363:LEU:HB3	6:B:12:PLM:HA1	1.81	0.62
1:A:1306:LEU:HD22	1:A:1366:TYR:CE1	2.35	0.62
1:B:2538:LYS:HB3	1:B:2541:ASP:HB2	1.81	0.62
1:C:3333:GLU:H	1:C:3333:GLU:CD	2.03	0.61
1:A:1079:ASN:HB2	3:A:182:SIA:O2	2.01	0.61
1:C:3300:LYS:O	1:C:3302:LYS:HG3	2.00	0.61
1:B:2498:LYS:HB3	1:B:2514:LEU:HD11	1.81	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:C:3538:LYS:HB3	1:C:3541:ASP:HB2	1.81	0.61
1:B:2227:VAL:O	1:B:2231:VAL:HG23	2.00	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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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:1370:GLU:HB3	1:A:1372:GLN:NE2	2.17	0.58
1:A:1225:GLU:O	1:A:1229:VAL:HG23	2.04	0.58
1:C:3428:VAL:O	1:C:3432:ILE:HG13	2.03	0.58
1:A:1318:LEU:HG	1:A:1319:LEU:N	2.18	0.58
1:B:2428:VAL:O	1:B:2432:ILE:HG13	2.03	0.58
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: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:A:1236:ALA:HA	1:A:1239:LEU:HD12	1.85	0.56
1:B:2242:ARG:HH11	1:B:2242:ARG:HG2	1.69	0.56
1:B:2551:PHE:C	1:B:2553:LYS:H	2.07	0.56
1:B:2359:ILE:HB	1:B:2360:PRO:HD3	1.86	0.56
1:C:3242:ARG:NH2	7:C:7118:HOH:O	2.39	0.56
1:C:3227:VAL:O	1:C:3231:VAL:HG23	2.06	0.56
1:B:2086:MET:HG3	1:B:2112:LEU:HD23	1.88	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:CG	1:B:2242:ARG:HH11	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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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:A:1428:VAL:HG12	1:A:1432:ILE:HD11	1.89	0.55
1:C:3242:ARG:HH11	1:C:3242:ARG:HG2	1.72	0.55
1:C:3540:LYS:O	1:C:3544:VAL:HG23	2.07	0.55
1:C:3393:LYS:HA	1:C:3396:ILE:HG12	1.89	0.55
1:B:2403:TYR:CG	1:B:2420:LEU:HD23	2.42	0.55
1:A:1375:GLN:HE21	1:A:1413:LYS:HZ2	1.55	0.54
1:A:1304:LEU:HD13	6:A:11:PLM:HA2	1.89	0.54
1:C:3275:LYS:HD3	7:C:7176:HOH:O	2.06	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
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:HH11	1:A:1242:ARG:HG2	1.73	0.54
1:C:3102:THR:OG1	1:C:3104:ARG:HG2	2.07	0.54
1:A:1272:ALA:O	1:A:1289:LYS:HE3	2.08	0.54
3:C:382:SIA:H111	7:C:7211:HOH:O	2.07	0.53
1:C:3316:GLN:HA	1:C:3316:GLN:NE2	2.23	0.53
1:C:3505:ARG:HB3	7:C:7115:HOH:O	2.08	0.53
1:B:2338:GLU:CG	1:B:2340:ASN:H	2.20	0.53
1:A:1403:TYR:CG	1:A:1420:LEU:HD23	2.42	0.53
1:B:2105:LYS:HE2	1:B:2106:GLU:CG	2.33	0.53
1:A:1242:ARG:CG	1:A:1242:ARG:HH11	2.21	0.53
1:B:2393:LYS:HA	1:B:2396:ILE:HG12	1.91	0.53
1:A:1262:LYS:HZ1	3:C:382:SIA:H112	1.72	0.52
1:B:2284:HIS:O	1:B:2288:GLN:HG2	2.08	0.52
1:A:1284:HIS:O	1:A:1288:GLN:HG2	2.09	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:C:3316:GLN:HA	1:C:3316:GLN:HE21	1.75	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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:2355:PHE:CE1	1:B:2360:PRO:HG3	2.45	0.52
1:A:1261:VAL:HG22	7:A:7108:HOH:O	2.08	0.52
1:C:3063:LEU:HD11	7:C:7196:HOH:O	2.09	0.52
1:C:3242:ARG:HH11	1:C:3242:ARG:CG	2.23	0.51
1:A:1461:PRO:HD3	5:A:1:CHD:O12	2.10	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:1316:GLN:HA	1:A:1316:GLN:NE2	2.25	0.51
1:B:2428:VAL:HG12	1:B:2432:ILE:HD11	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:HE21	1.75	0.51
1:A:1338:GLU:CG	1:A:1340:ASN:H	2.21	0.51
1:C:3079:ASN:HB2	3:C:382:SIA:O2	2.10	0.51
1:A:1452:ARG:HG2	1:A:1452:ARG:HH11	1.75	0.51
1:A:1349:GLY:HA3	1:A:1447:TYR:CE1	2.46	0.51
1:C:3403:TYR:CG	1:C:3420:LEU:HD23	2.45	0.51
1:A:1478:ALA:N	1:A:1479:PRO:CD	2.74	0.51
1:A:1304:LEU:HB2	6:A:11:PLM:HA2	1.93	0.51
1:A:1262:LYS:HZ3	3:C:382:SIA:H112	1.75	0.51
1:C:3338:GLU:CG	1:C:3340:ASN:H	2.23	0.51
1:B:2487:GLU:N	7:B:7191:HOH:O	2.39	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:C:3241:HIS:C	1:C:3242:ARG:HG3	2.30	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:C:3428:VAL:HG12	1:C:3432:ILE:HD11	1.92	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: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:NH1	1:B:2242:ARG:CG	2.76	0.49
1:C:3477:GLY:HA2	1:C:3493:SER:OG	2.13	0.49
1:C:3398:GLU:HB2	7:C:7244:HOH:O	2.12	0.49
1:C:3152:TYR:CD1	1:C:3152:TYR:N	2.80	0.49
1:C:3257:LYS:HE2	1:C:3318:LEU:O	2.13	0.49
1:A:1369:SER:HA	5:A:1:CHD:H191	1.95	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:3423:ASP:HA	7:C:7003:HOH:O	2.13	0.49
1:B:2543:GLU:N	1:B:2543:GLU:OE2	2.37	0.49
1:C:3206:ALA:HA	1:C:3210:GLY:O	2.13	0.49
1:B:2132:ARG:HB3	1:B:2211:ASN:HB2	1.95	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: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:1354:GLU:HG2	7:A:7101:HOH:O	2.13	0.49
1:C:3543:GLU:N	1:C:3543:GLU:OE2	2.38	0.49
1:A:1152:TYR:CD1	1:A:1152:TYR:N	2.80	0.49
1:A:1142:GLY:HA2	6:A:11:PLM:H62	1.94	0.49
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: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:B:2206:ALA:HA	1:B:2210:GLY:O	2.14	0.48
1:C:3363:LEU:HB3	6:C:13:PLM:HA1	1.95	0.48
1:C:3026:VAL:HG12	1:C:3027:ASP:N	2.29	0.48
1:A:1477:GLY:HA2	1:A:1493:SER:OG	2.12	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:3303:PHE:CD2	1:C:3318:LEU:HA	2.49	0.48
1:C:3283:VAL:HG12	1:C:3287:ARG:NH1	2.28	0.48
1:C:3224:GLY:HA3	7:C:7279:HOH:O	2.14	0.48
1:B:2435:ARG:O	1:B:2438:ARG:HB3	2.14	0.48
1:C:3357:TRP:O	1:C:3360:PRO:HD2	2.14	0.48
1:C:3109:PRO:HA	7:C:7068:HOH:O	2.13	0.48
1:C:3420:LEU:HD22	1:C:3547:TRP:HZ2	1.79	0.48
1:A:1551:PHE:C	1:A:1553:LYS:H	2.15	0.48
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:A:1138:TRP:HH2	1:A:1220:GLU:HB2	1.79	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:B:2495:MET:HE3	1:B:2533:THR:HG21	1.95	0.47
1:A:1312:PRO:HG2	1:A:1383:TRP:NE1	2.29	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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:2241:HIS:C	1:B:2242:ARG:HG3	2.34	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:C:3368:LEU:O	5:C:3:CHD:H62	2.15	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:B:2395:LEU:HD22	1:B:2550:LEU:CD1	2.45	0.47
1:A:1543:GLU:N	1:A:1543:GLU:OE2	2.40	0.47
1:A:1139:ILE:HG22	1:A:1223:GLY:HA2	1.95	0.47
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:B:2138:TRP:HH2	1:B:2220:GLU:HB2	1.79	0.46
1:A:1241:HIS:C	1:A:1242:ARG:HG3	2.34	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:B:2318:LEU:O	1:B:2319:LEU:C	2.53	0.46
1:C:3478:ALA:N	1:C:3479:PRO:CD	2.78	0.46
1:A:1391:ILE:HB	7:A:7219:HOH:O	2.15	0.46
1:B:2134:PRO:CG	1:B:2163:VAL:HG12	2.38	0.46
1:A:1359:ILE:HB	1:A:1360:PRO:CD	2.43	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:C:3242:ARG:NH1	1:C:3242:ARG:CG	2.78	0.46
1:C:3304:LEU:HB3	6:C:13:PLM:H91	1.97	0.46
1:B:2316:GLN:HA	1:B:2316:GLN:HE21	1.80	0.46
1:B:2221:SER:O	1:B:2224:GLY:N	2.47	0.46
1:B:2139:ILE:HG22	1:B:2223:GLY:HA2	1.97	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:B:2272:ALA:O	1:B:2289:LYS:HE3	2.16	0.46
1:A:1030:HIS:HD2	7:A:7089:HOH:O	1.99	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:C:3105:LYS:HE2	1:C:3106:GLU:CG	2.38	0.46
1:A:1318:LEU:HD23	1:A:1318:LEU:H	1.81	0.46
1:C:3414:LYS:HZ2	5:C:3:CHD:H42	1.81	0.46
1:B:2266:GLU:O	1:B:2270:ILE:HG13	2.16	0.46
1:C:3304:LEU:HD22	6:C:13:PLM:H91	1.98	0.45
1:B:2370:GLU:HB3	1:B:2372:GLN:HE21	1.81	0.45
1:A:1395:LEU:HD22	1:A:1550:LEU:CD1	2.46	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:3119:LEU:HD12	1:C:3119:LEU:C	2.37	0.45
1:C:3283:VAL:O	1:C:3287:ARG:HG3	2.16	0.45
1:A:1495:MET:HE3	1:A:1533:THR:HG21	1.98	0.45
1:B:2312:PRO:HG2	1:B:2383:TRP:NE1	2.32	0.45
1:A:1351:ASN:HB3	1:A:1466:GLY:O	2.17	0.45
1:C:3486:SER:O	1:C:3490:ILE:HG13	2.16	0.45
1:A:1242:ARG:HD3	1:A:1503:PHE:O	2.17	0.45
1:A:1026:VAL:CG1	1:A:1207:SER:HB3	2.46	0.45
1:C:3538:LYS:HE2	7:C:7024:HOH:O	2.16	0.45
1:B:2477:GLY:HA2	1:B:2493:SER:OG	2.17	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:C:3395:LEU:HD22	1:C:3550:LEU:HD12	1.97	0.45
1:B:2306:LEU:HD22	1:B:2366:TYR:CE1	2.52	0.45
1:C:3262:LYS:HE3	1:C:3279:SER:OG	2.17	0.44
1:B:2026:VAL:CG1	1:B:2207:SER:HB3	2.47	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:A:1370:GLU:HB3	1:A:1372:GLN:HE21	1.82	0.44
1:A:1120:ASN:HB2	1:A:1167:THR:OG1	2.18	0.44
1:B:2039:SER:OG	1:B:2046:PRO:HB3	2.17	0.44
1:C:3272:ALA:O	1:C:3289:LYS:HE3	2.17	0.44
1:B:2095:GLN:O	1:B:2099:GLU:HG3	2.18	0.44
1:C:3088:THR:HG22	1:C:3295:LEU:HD13	2.00	0.44
1:A:1088:THR:HG22	1:A:1295:LEU:HD13	1.99	0.44
1:C:3355:PHE:CE1	1:C:3360:PRO:HG3	2.52	0.44
1:B:2349:GLY:HA3	1:B:2447:TYR:CE1	2.52	0.44
1:B:2283:VAL:HG12	1:B:2287:ARG:NH1	2.31	0.44
1:C:3120:ASN:HB2	1:C:3167:THR:OG1	2.18	0.44
1:C:3205:ILE:HA	1:C:3205:ILE:HD12	1.88	0.44
1:C:3266:GLU:O	1:C:3270:ILE:HG13	2.16	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:3357:TRP:HA	5:C:3:CHD:H22	1.99	0.44
1:B:2323:ILE:HG21	1:B:2330:LYS:HA	1.99	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: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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1508:ASN:HB3	7:A:7128:HOH:O	2.16	0.44
1:A:1395:LEU:HD22	1:A:1550:LEU:HD12	1.98	0.44
1:C:3041:GLU:O	1:C:3041:GLU:HG3	2.18	0.44
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:C:3304:LEU:HD22	6:C:13:PLM:C7	2.49	0.43
1:A:1283:VAL:HG12	1:A:1287:ARG:NH1	2.34	0.43
1:A:1197:ALA:O	1:A:1201:VAL:HG23	2.18	0.43
1:C:3329:LEU:HD23	7:C:7174:HOH:O	2.19	0.43
1:B:2330:LYS:HB2	1:B:2334:GLU:OE2	2.18	0.43
1:A:1034:LEU:C	1:A:1034:LEU:HD13	2.39	0.43
1:C:3059:PRO:HD3	1:C:3117:LEU:HD12	2.00	0.43
1:C:3034:LEU:C	1:C:3034:LEU:HD13	2.38	0.43
1:A:1025:VAL:HG22	1:A:1034:LEU:CD2	2.46	0.43
1:C:3330:LYS:HB2	1:C:3334:GLU:OE2	2.18	0.43
1:B:2528:GLN:O	1:B:2533:THR:HA	2.19	0.43
1:B:2379:MET:HG2	1:B:2400:THR:OG1	2.17	0.43
1:A:1041:GLU:HG3	1:A:1041:GLU:O	2.18	0.43
1:A:1124:PRO:HD3	1:A:1158:ALA:HB1	2.00	0.43
1:A:1105:LYS:HG3	1:A:1106:GLU:N	2.30	0.43
1:C:3023:PRO:HB2	1:C:3034:LEU:HD21	2.01	0.43
1:A:1330:LYS:HB2	1:A:1334:GLU:OE2	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: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:A:1318:LEU:N	1:A:1318:LEU:HD23	2.33	0.42
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:B:2246:GLU:HG2	1:B:2447:TYR:OH	2.20	0.42
1:B:2113:SER:HB2	1:C:3277:THR:HG21	2.01	0.42
1:C:3495:MET:O	1:C:3498:LYS:HB2	2.19	0.42
1:C:3452:ARG:NE	1:C:3462:LYS:HA	2.33	0.42
1:B:2366:TYR:HA	1:B:2367:PRO:HD3	1.78	0.42
1:A:1176:GLY:HA2	1:A:1189:TRP:HB2	2.01	0.42
1:C:3306:LEU:HD22	1:C:3366:TYR:CE1	2.54	0.42
1:C:3242:ARG:HD3	1:C:3503:PHE:O	2.19	0.42
1:C:3323:ILE:HG21	1:C:3330:LYS:HA	2.02	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:3248:GLY:HA3	7:C:7279:HOH:O	2.18	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:3058:PRO:HA	1:C:3059:PRO:HD2	1.98	0.42
1:B:2290:THR:HG23	1:B:2293:GLU:OE2	2.19	0.42
1:A:1023:PRO:HB2	1:A:1034:LEU:HD21	2.02	0.42
1:C:3087:CYS:O	1:C:3088:THR:C	2.57	0.42
1:A:1214:SER:HA	7:A:7017:HOH:O	2.19	0.42
1:C:3513:GLY:N	7:C:7182:HOH:O	2.52	0.42
1:B:2087:CYS:O	1:B:2088:THR:C	2.58	0.42
1:B:2220:GLU:HB3	7:B:7149:HOH:O	2.20	0.42
1:B:2190:GLY:O	1:B:2194:GLN:HG3	2.19	0.42
1:A:1119:LEU:HD12	1:A:1119:LEU:C	2.40	0.42
1:B:2140:HIS:CE1	1:B:2147:GLY:HA3	2.55	0.42
1:B:2532:ASN:HB3	7:B:7015:HOH:O	2.19	0.42
1:B:2023:PRO:HB2	1:B:2034:LEU:HD21	2.02	0.42
1:A:1379:MET:HG2	1:A:1400:THR:OG1	2.19	0.42
1:C:3379:MET:HG2	1:C:3400:THR:OG1	2.20	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:C:3370:GLU:HB3	1:C:3372:GLN:HE21	1.83	0.42
1:B:2324:ASP:OD2	1:B:2324:ASP:N	2.53	0.42
1:B:2404:LEU:HD22	1:B:2413:LYS:O	2.20	0.42
1:A:1383:TRP:CZ3	1:A:1393:LYS:HB2	2.54	0.42
1:A:1352:LYS:HB3	1:A:1465:ILE:O	2.20	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:C:3124:PRO:HD3	1:C:3158:ALA:HB1	2.02	0.41
1:B:2205:ILE:HD12	1:B:2205:ILE:HA	1.87	0.41
1:C:3503:PHE:O	1:C:3507:GLY:N	2.49	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:A:1046:PRO:HA	7:A:7027:HOH:O	2.20	0.41
1:B:2297:THR:HA	1:B:2300:LYS:HE3	2.02	0.41
1:B:2257:LYS:HD3	1:B:2257:LYS:HA	1.92	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:1262:LYS:HZ3	3:C:382:SIA:C11	2.33	0.41
3:C:382:SIA:C11	3:C:382:SIA:H4	2.34	0.41
2:C:379:NAG:H83	2:C:379:NAG:H3	2.02	0.41
1:A:1179:SER:HA	1:A:1185:SER:O	2.21	0.41
1:C:3264:LEU:O	1:C:3268:ILE:HG13	2.19	0.41
1:C:3528:GLN:O	1:C:3533:THR:HA	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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: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:B:2034:LEU:HB3	1:B:2079:ASN:HA	2.03	0.41
1:A:1465:ILE:HD11	7:A:7255:HOH:O	2.21	0.41
1:B:2124:PRO:HD3	1:B:2158:ALA:HB1	2.03	0.41
1:B:2023:PRO:HA	1:B:2024:PRO:HD3	1.82	0.41
1:C:3304:LEU:O	1:C:3364:MET:HA	2.21	0.41
1:B:2254:VAL:CG2	1:B:2388:LEU:HD23	2.50	0.41
1:C:3349:GLY:HA3	1:C:3447:TYR:CZ	2.55	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:A:1205:ILE:HD12	1:A:1205:ILE:HA	1.90	0.41
1:A:1064:ARG:NH2	1:A:1114:GLU:OE2	2.54	0.41
1:B:2383:TRP:CZ3	1:B:2393:LYS:HB2	2.56	0.41
1:A:1528:GLN:O	1:A:1533:THR:HA	2.20	0.41
1:C:3495:MET:HE3	1:C:3533:THR:HG21	2.02	0.41
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:B:2176:GLY:HA2	1:B:2189:TRP:HB2	2.04	0.40
1:A:1318:LEU:CG	1:A:1319:LEU:N	2.77	0.40
1:B:2331:THR:HB	1:B:2333:GLU:OE1	2.20	0.40
1:A:1331:THR:HB	1:A:1333:GLU:OE1	2.21	0.40
1:B:2495:MET:O	1:B:2498:LYS:HB2	2.21	0.40
1:A:1087:CYS:O	1:A:1089:GLN:HG2	2.21	0.40
1:C:3480:PHE:HZ	1:C:3494:LYS:HG3	1.85	0.40
1:A:1486:SER:O	1:A:1490:ILE:HG13	2.22	0.40
1:C:3195:VAL:HG13	1:C:3239:LEU:CD1	2.51	0.40
1:B:2223:GLY:O	1:B:2227:VAL:HG23	2.21	0.40
1:A:1083:TYR:CD2	1:A:1108:ILE:HG21	2.57	0.40
1:B:2090:ASP:HA	1:B:2091:PRO:HD2	1.92	0.40
1:B:2034:LEU:HD13	1:B:2034:LEU:C	2.42	0.40
1:C:3257:LYS:CE	1:C:3316:GLN:OE1	2.70	0.40
1:A:1211:ASN:HA	1:A:1212:PRO:HD2	1.99	0.40
1:C:3404:LEU:HD22	1:C:3413:LYS:O	2.22	0.40
1:B:2179:SER:HA	1:B:2185:SER:O	2.22	0.40
1:A:1304:LEU:CB	6:A:11:PLM:HD2	2.51	0.40
1:A:1090:ASP:OD1	1:A:1090:ASP:C	2.60	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%)	24	66
1	B	530/542 (98%)	478 (90%)	44 (8%)	8 (2%)	13	50
1	C	530/542 (98%)	484 (91%)	43 (8%)	3 (1%)	30	72
All	All	1590/1626 (98%)	1443 (91%)	132 (8%)	15 (1%)	21	64

All (15) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	1185	SER
1	B	2185	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%)	440 (98%)	8 (2%)	66	91
1	B	448/457 (98%)	439 (98%)	9 (2%)	63	89
1	C	448/457 (98%)	439 (98%)	9 (2%)	63	89
All	All	1344/1371 (98%)	1318 (98%)	26 (2%)	65	90

All (26) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	1041	GLU
1	A	1199	ARG
1	A	1218	PHE
1	A	1264	LEU
1	A	1338	GLU
1	A	1339	ARG
1	A	1500	TRP
1	A	1523	LYS
1	B	2041	GLU
1	B	2199	ARG
1	B	2218	PHE
1	B	2264	LEU
1	B	2338	GLU
1	B	2339	ARG
1	B	2366	TYR
1	B	2500	TRP
1	B	2523	LYS
1	C	3041	GLU
1	C	3199	ARG
1	C	3218	PHE
1	C	3264	LEU
1	C	3338	GLU
1	C	3339	ARG
1	C	3463	THR
1	C	3500	TRP
1	C	3523	LYS

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (25) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	1030	HIS
1	A	1069	GLN
1	A	1160	HIS

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Mol	Chain	Res	Type
1	A	1238	ASN
1	A	1316	GLN
1	A	1372	GLN
1	A	1375	GLN
1	A	1549	ASN
1	B	2030	HIS
1	B	2045	GLN
1	B	2069	GLN
1	B	2131	ASN
1	B	2238	ASN
1	B	2316	GLN
1	B	2372	GLN
1	B	2375	GLN
1	B	2549	ASN
1	C	3030	HIS
1	C	3045	GLN
1	C	3069	GLN
1	C	3095	GLN
1	C	3131	ASN
1	C	3238	ASN
1	C	3372	GLN
1	C	3549	ASN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no carbohydrates in this entry.

5.6 Ligand geometry [i](#)

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	$\# Z > 2$
5	CHD	A	1	-	29,32,32	2.03	13 (44%)	48,51,51	1.31	6 (12%)
6	PLM	A	11	-	14,17,17	0.38	0	14,17,17	0.43	0
2	NAG	A	179	1	14,14,15	0.80	0	15,19,21	1.16	2 (13%)
3	SIA	A	182	-	17,21,21	1.05	2 (11%)	19,31,31	1.04	2 (10%)
4	SO4	A	184	-	4,4,4	0.27	0	6,6,6	0.08	0
4	SO4	A	185	-	4,4,4	0.35	0	6,6,6	0.14	0
4	SO4	A	285	-	4,4,4	0.28	0	6,6,6	0.11	0
6	PLM	B	12	-	14,17,17	0.44	0	14,17,17	0.43	0
5	CHD	B	2	-	29,32,32	2.16	15 (51%)	48,51,51	1.33	5 (10%)
2	NAG	B	279	1	14,14,15	0.53	0	15,19,21	1.13	1 (6%)
3	SIA	B	282	-	17,21,21	0.86	0	19,31,31	1.02	1 (5%)
4	SO4	B	284	-	4,4,4	0.20	0	6,6,6	0.16	0
6	PLM	C	13	-	14,17,17	0.42	0	14,17,17	0.43	0
5	CHD	C	3	-	29,32,32	2.06	11 (37%)	48,51,51	1.31	7 (14%)
2	NAG	C	379	1	14,14,15	0.63	0	15,19,21	1.13	2 (13%)
3	SIA	C	382	-	17,21,21	1.06	2 (11%)	19,31,31	1.19	2 (10%)
4	SO4	C	384	-	4,4,4	0.25	0	6,6,6	0.16	0
4	SO4	C	385	-	4,4,4	0.29	0	6,6,6	0.12	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
5	CHD	A	1	-	-	0/7/74/74	0/4/4/4
6	PLM	A	11	-	-	0/13/15/15	0/0/0/0
2	NAG	A	179	1	-	0/6/23/26	0/1/1/1
3	SIA	A	182	-	-	0/14/38/38	0/1/1/1
4	SO4	A	184	-	-	0/0/0/0	0/0/0/0
4	SO4	A	185	-	-	0/0/0/0	0/0/0/0
4	SO4	A	285	-	-	0/0/0/0	0/0/0/0
6	PLM	B	12	-	-	0/13/15/15	0/0/0/0
5	CHD	B	2	-	-	0/7/74/74	0/4/4/4
2	NAG	B	279	1	-	0/6/23/26	0/1/1/1

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	SIA	B	282	-	-	1/14/38/38	0/1/1/1
4	SO4	B	284	-	-	0/0/0/0	0/0/0/0
6	PLM	C	13	-	-	0/13/15/15	0/0/0/0
5	CHD	C	3	-	-	0/7/74/74	0/4/4/4
2	NAG	C	379	1	1/1/5/7	0/6/23/26	0/1/1/1
3	SIA	C	382	-	-	0/14/38/38	0/1/1/1
4	SO4	C	384	-	-	0/0/0/0	0/0/0/0
4	SO4	C	385	-	-	0/0/0/0	0/0/0/0

All (43) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	B	2	CHD	C4-C3	2.05	1.55	1.51
5	A	1	CHD	C4-C3	2.09	1.55	1.51
5	B	2	CHD	C1-C2	2.16	1.58	1.53
5	A	1	CHD	C6-C7	2.19	1.56	1.52
3	C	382	SIA	C7-C6	2.19	1.55	1.52
5	B	2	CHD	C13-C17	2.21	1.59	1.55
5	C	3	CHD	C13-C12	2.27	1.58	1.54
5	A	1	CHD	C10-C9	2.27	1.60	1.56
5	C	3	CHD	C8-C7	2.28	1.57	1.53
5	A	1	CHD	C13-C17	2.28	1.59	1.55
5	C	3	CHD	C6-C5	2.34	1.57	1.53
5	C	3	CHD	C10-C5	2.34	1.59	1.55
5	B	2	CHD	C8-C14	2.37	1.58	1.53
5	B	2	CHD	C10-C5	2.38	1.59	1.55
5	A	1	CHD	C8-C7	2.43	1.57	1.53
3	A	182	SIA	C3-C2	2.44	1.55	1.51
5	B	2	CHD	C6-C7	2.48	1.56	1.52
3	A	182	SIA	O6-C2	2.50	1.45	1.42
5	B	2	CHD	C8-C9	2.51	1.58	1.53
5	A	1	CHD	C10-C5	2.52	1.59	1.55
5	C	3	CHD	C6-C7	2.60	1.57	1.52
5	B	2	CHD	C8-C7	2.62	1.57	1.53
5	B	2	CHD	C6-C5	2.62	1.58	1.53
5	C	3	CHD	C10-C9	2.67	1.61	1.56
5	A	1	CHD	C4-C5	2.70	1.58	1.53
3	C	382	SIA	O6-C2	2.70	1.45	1.42
5	A	1	CHD	C8-C9	2.73	1.59	1.53
5	C	3	CHD	C8-C9	2.77	1.59	1.53
5	A	1	CHD	C6-C5	2.84	1.58	1.53
5	B	2	CHD	C18-C13	2.90	1.59	1.54

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	A	1	CHD	C11-C9	2.99	1.58	1.53
5	A	1	CHD	C18-C13	3.03	1.59	1.54
5	B	2	CHD	C4-C5	3.03	1.59	1.53
5	A	1	CHD	C20-C17	3.16	1.60	1.54
5	B	2	CHD	C20-C17	3.18	1.60	1.54
5	C	3	CHD	C18-C13	3.28	1.59	1.54
5	A	1	CHD	C11-C12	3.30	1.59	1.53
5	C	3	CHD	C11-C12	3.31	1.59	1.53
5	B	2	CHD	C11-C9	3.39	1.59	1.53
5	B	2	CHD	C10-C9	3.45	1.62	1.56
5	C	3	CHD	C11-C9	3.54	1.59	1.53
5	B	2	CHD	C11-C12	3.56	1.59	1.53
5	C	3	CHD	C20-C17	4.42	1.62	1.54

All (28) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	B	2	CHD	C17-C13-C14	-4.11	95.90	100.05
2	B	279	NAG	C2-N2-C7	-3.98	117.92	123.04
5	C	3	CHD	C19-C10-C1	-3.59	102.16	108.20
5	A	1	CHD	C9-C11-C12	-3.38	110.09	114.36
5	A	1	CHD	C17-C13-C14	-3.23	96.79	100.05
5	B	2	CHD	C9-C11-C12	-3.04	110.52	114.36
2	A	179	NAG	C2-N2-C7	-2.65	119.64	123.04
5	B	2	CHD	C19-C10-C1	-2.64	103.75	108.20
5	C	3	CHD	C9-C11-C12	-2.59	111.08	114.36
5	A	1	CHD	C19-C10-C1	-2.53	103.95	108.20
5	A	1	CHD	C14-C13-C12	-2.42	105.22	107.39
3	C	382	SIA	C9-C8-C7	-2.38	106.88	112.48
5	B	2	CHD	C14-C13-C12	-2.36	105.28	107.39
5	C	3	CHD	C16-C15-C14	-2.32	100.44	105.12
3	A	182	SIA	C7-C6-C5	-2.32	110.81	114.32
2	C	379	NAG	C2-N2-C7	-2.28	120.11	123.04
5	C	3	CHD	C21-C20-C22	-2.26	106.57	110.35
3	B	282	SIA	C7-C6-C5	-2.25	110.92	114.32
5	B	2	CHD	C6-C5-C10	-2.23	110.19	112.66
3	C	382	SIA	C7-C6-C5	-2.18	111.03	114.32
5	A	1	CHD	C16-C15-C14	-2.13	100.84	105.12
5	A	1	CHD	C16-C17-C20	-2.12	108.28	112.05
3	A	182	SIA	C9-C8-C7	-2.07	107.62	112.48
5	C	3	CHD	C17-C13-C14	-2.06	97.97	100.05
5	C	3	CHD	C11-C9-C10	-2.02	111.69	113.79

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	C	3	CHD	C18-C13-C12	2.32	111.35	109.09
2	A	179	NAG	C3-C4-C5	2.53	114.61	110.20
2	C	379	NAG	C4-C3-C2	2.89	115.72	111.23

All (1) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
2	C	379	NAG	C1

All (1) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	B	282	SIA	O10-C10-N5-C5

There are no ring outliers.

9 monomers are involved in 42 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	A	1	CHD	2	0
6	A	11	PLM	9	0
3	A	182	SIA	3	0
6	B	12	PLM	2	0
3	B	282	SIA	2	0
6	C	13	PLM	7	0
5	C	3	CHD	7	0
2	C	379	NAG	2	0
3	C	382	SIA	8	0

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 will therefore be empty.

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

EDS was not executed - this section will therefore be empty.

6.3 Carbohydrates

EDS was not executed - this section will therefore be empty.

6.4 Ligands

EDS was not executed - this section will therefore be empty.

6.5 Other polymers

EDS was not executed - this section will therefore be empty.