



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 6, 2026 – 06:14 AM UTC

PDB ID : 2WL4 / pdb_00002wl4
Title : BIOSYNTHETIC THIOLASE FROM Z. RAMIGERA. COMPLEX OF THE
H348A MUTANT WITH COENZYME A.
Authors : Merilainen, G.; Poikela, V.; Kursula, P.; Wierenga, R.K.
Deposited on : 2009-06-22
Resolution : 1.80 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) : 2.0
EDS : 3.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4 : 9.0.010 (Gargrove)
Density-Fitness : 1.0.12
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

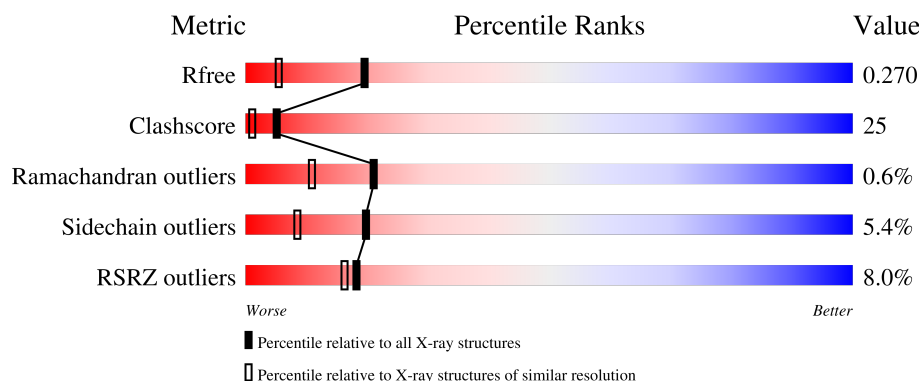
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.80 Å.

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



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	180053	7662 (1.80-1.80)
Clashscore	190562	8479 (1.80-1.80)
Ramachandran outliers	187476	8391 (1.80-1.80)
Sidechain outliers	187428	8390 (1.80-1.80)
RSRZ outliers	180081	7663 (1.80-1.80)

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

Mol	Chain	Length	Quality of chain
1	A	392	 83% 14% ..
2	B	392	 81% 16% ..
3	C	392	 17% 52% 43% . .
4	D	392	 15% 48% 46% 5% ..

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
5	SO4	A	1401	-	-	X	-
5	SO4	B	1398	-	-	X	-
5	SO4	D	1394	-	-	X	-
7	CL	C	1396	-	-	X	-
7	CL	D	1399	-	-	X	-

2 Entry composition

There are 9 unique types of molecules in this entry. The entry contains 12721 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 ACETYL-COA ACETYLTRANSFERASE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	389	Total	C	N	O	S	0	5	0
			2837	1765	511	539	22			

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	129	ARG	ALA	SEE REMARK 999	UNP P07097
A	348	ALA	HIS	engineered mutation	UNP P07097

- Molecule 2 is a protein called ACETYL-COA ACETYLTRANSFERASE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	389	Total	C	N	O	S	0	7	0
			2843	1770	509	543	21			

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	129	ARG	ALA	SEE REMARK 999	UNP P07097
B	348	ALA	HIS	engineered mutation	UNP P07097

- Molecule 3 is a protein called ACETYL-COA ACETYLTRANSFERASE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	C	389	Total	C	N	O	S	0	1	0
			2816	1747	509	539	21			

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
C	129	ARG	ALA	SEE REMARK 999	UNP P07097
C	348	ALA	HIS	engineered mutation	UNP P07097

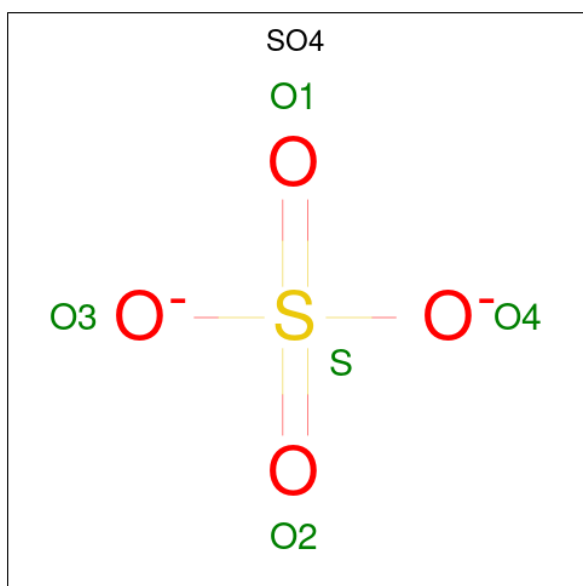
- Molecule 4 is a protein called ACETYL-COA ACETYLTRANSFERASE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
4	D	389	Total	C	N	O	S	0	3	0
			2828	1755	513	539	21			

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
D	129	ARG	ALA	SEE REMARK 999	UNP P07097
D	348	ALA	HIS	engineered mutation	UNP P07097

- Molecule 5 is SULFATE ION (CCD ID: SO4) (formula: O₄S).



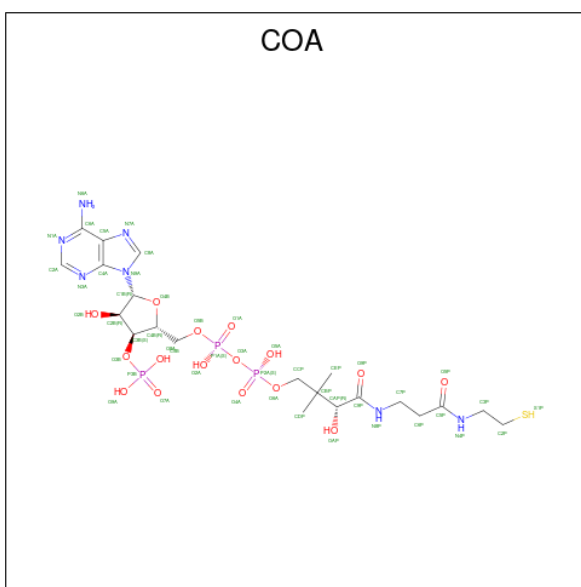
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	A	1	Total	O	S	0	0
			5	4	1		
5	A	1	Total	O	S	0	0
			5	4	1		
5	A	1	Total	O	S	0	0
			5	4	1		
5	A	1	Total	O	S	0	0
			5	4	1		
5	A	1	Total	O	S	0	0
			5	4	1		
5	A	1	Total	O	S	0	0
			5	4	1		

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

- Molecule 6 is COENZYME A (CCD ID: COA) (formula: $C_{21}H_{36}N_7O_{16}P_3S$).



Mol	Chain	Residues	Atoms						ZeroOcc	AltConf
6	A	1	Total 48	C 21	N 7	O 16	P 3	S 1	0	0
6	B	1	Total 48	C 21	N 7	O 16	P 3	S 1	0	0

- Molecule 7 is CHLORIDE ION (CCD ID: CL) (formula: Cl).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	B	1	Total	Cl	0	0
			1	1		
7	C	1	Total	Cl	0	0
			1	1		
7	D	1	Total	Cl	0	0
			1	1		

- Molecule 8 is SODIUM ION (CCD ID: NA) (formula: Na).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
8	C	2	Total	Na	0	0
			2	2		
8	D	1	Total	Na	0	0
			1	1		

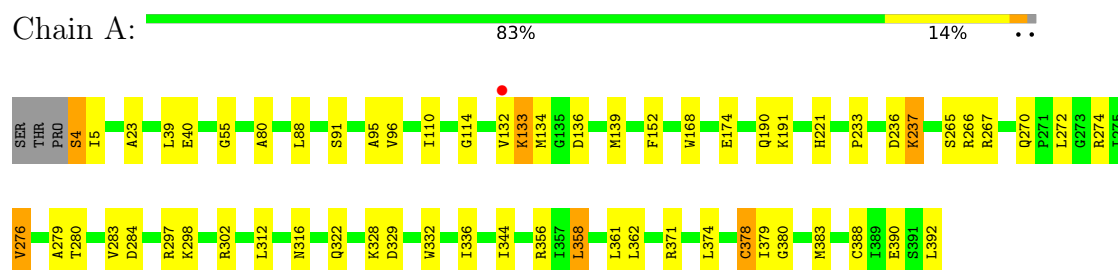
- Molecule 9 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
9	A	426	Total 426	O 426	0	0
9	B	407	Total 407	O 407	0	0
9	C	149	Total 149	O 149	0	0
9	D	188	Total 188	O 188	0	0

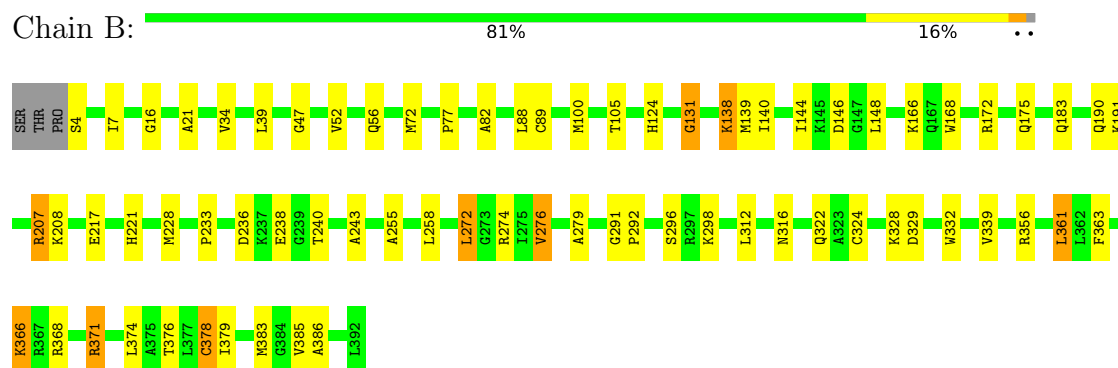
3 Residue-property plots

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 and electron density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red dot above a residue indicates a poor fit to the electron density ($RSRZ > 2$). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

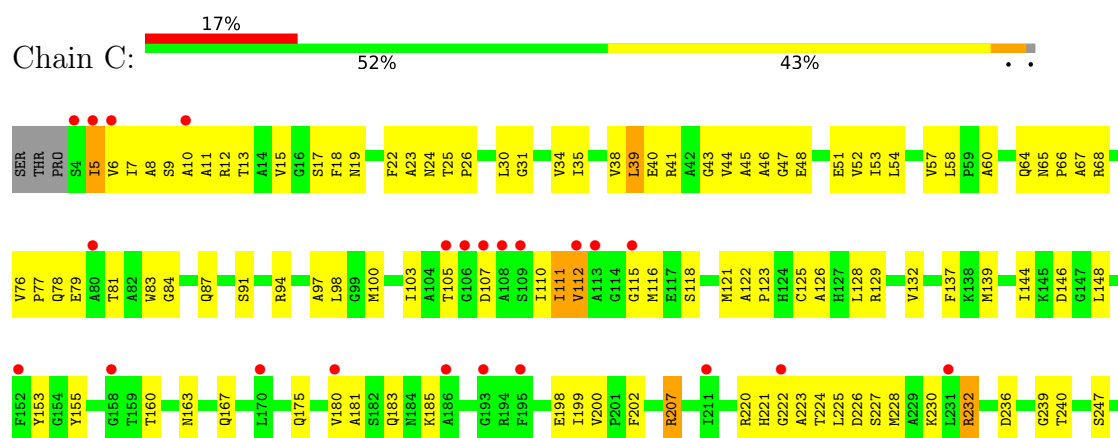
• Molecule 1: ACETYL-COA ACETYLTRANSFERASE

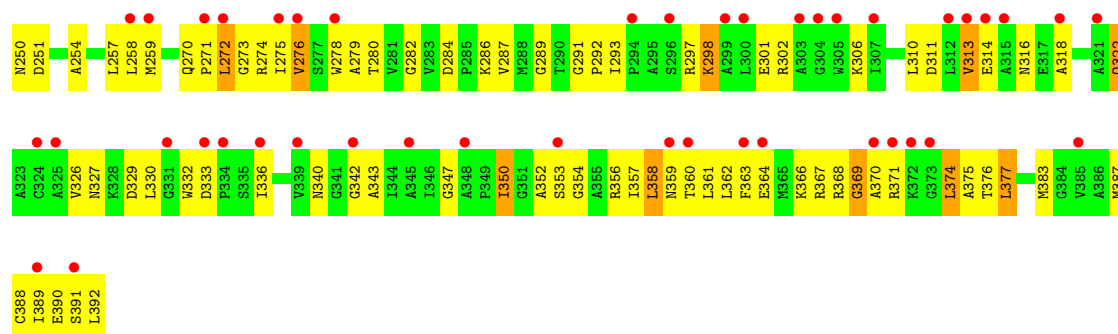


• Molecule 2: ACETYL-COA ACETYLTRANSFERASE

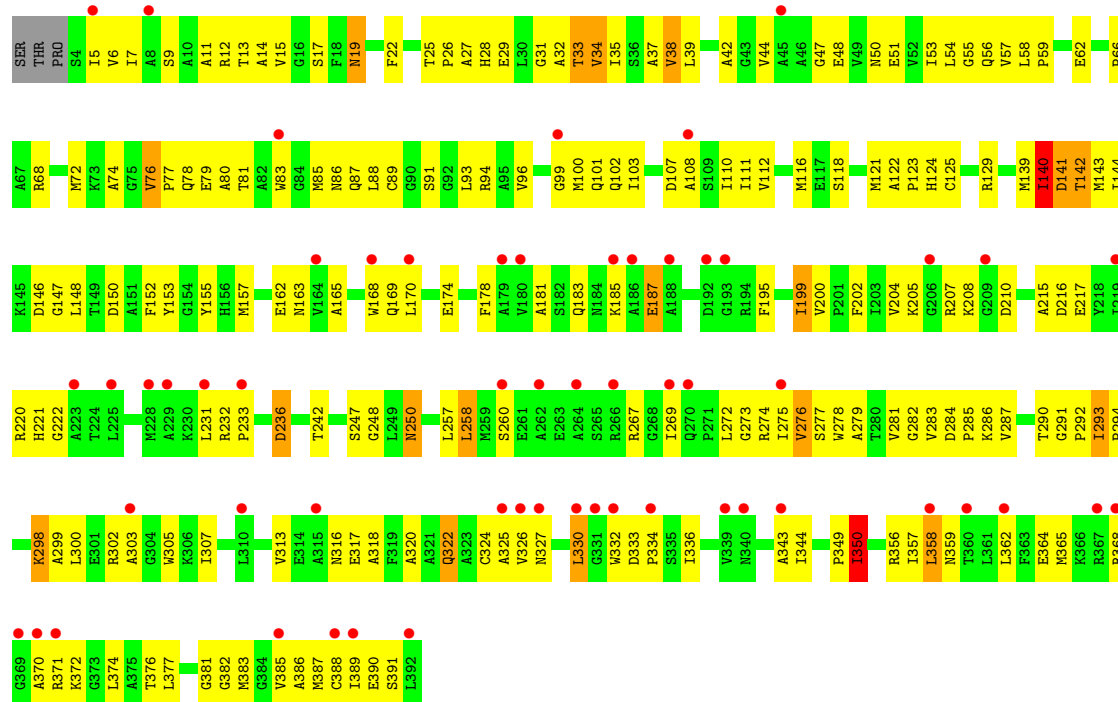


• Molecule 3: ACETYL-COA ACETYLTRANSFERASE





● Molecule 4: ACETYL-COA ACETYLTRANSFERASE



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	84.31Å 79.14Å 149.41Å 90.00° 92.68° 90.00°	Depositor
Resolution (Å)	19.61 – 1.80 19.61 – 1.80	Depositor EDS
% Data completeness (in resolution range)	99.6 (19.61-1.80) 86.6 (19.61-1.80)	Depositor EDS
R_{merge}	0.10	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.75 (at 1.80Å)	Xtriage
Refinement program	PHENIX (PHENIX.REFINE)	Depositor
R, R_{free}	0.231 , 0.270 0.232 , 0.270	Depositor DCC
R_{free} test set	9051 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å ²)	13.7	Xtriage
Anisotropy	0.115	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.44 , 81.4	EDS
L-test for twinning ²	$\langle L \rangle = 0.37$, $\langle L^2 \rangle = 0.19$	Xtriage
Estimated twinning fraction	0.159 for h,-k,-l	Xtriage
F_o, F_c correlation	0.90	EDS
Total number of atoms	12721	wwPDB-VP
Average B, all atoms (Å ²)	41.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.09% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

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

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: NA, SO4, CL, COA, CSO, CSD

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	0.65	0/2884	0.88	0/3892
2	B	0.64	0/2888	0.89	0/3896
3	C	0.34	0/2864	0.80	2/3867 (0.1%)
4	D	0.37	0/2869	0.79	2/3870 (0.1%)
All	All	0.52	0/11505	0.84	4/15525 (0.0%)

There are no bond length outliers.

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	D	140	ILE	N-CA-C	6.08	121.98	109.34
3	C	313	VAL	N-CA-C	5.64	115.99	108.27
4	D	250	ASN	N-CA-C	5.13	116.88	109.07
3	C	250	ASN	N-CA-C	5.04	116.85	109.24

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	2837	0	2870	58	0
2	B	2843	0	2882	77	0
3	C	2816	0	2825	212	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	D	2828	0	2848	239	0
5	A	45	0	0	9	0
5	B	40	0	0	2	0
5	C	20	0	0	0	0
5	D	20	0	0	5	0
6	A	48	0	32	1	0
6	B	48	0	32	6	0
7	B	1	0	0	0	0
7	C	1	0	0	7	0
7	D	1	0	0	7	0
8	C	2	0	0	0	0
8	D	1	0	0	0	0
9	A	426	0	0	22	0
9	B	407	0	0	25	0
9	C	149	0	0	40	0
9	D	188	0	0	78	0
All	All	12721	0	11489	569	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 25.

All (569) 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)
3:C:64:GLN:HG2	4:D:88:LEU:HD11	1.42	1.00
2:B:296:SER:OG	2:B:376[B]:THR:HG21	1.62	0.99
3:C:298:LYS:HE2	3:C:302:ARG:HE	1.24	0.99
4:D:140:ILE:CD1	4:D:141:ASP:H	1.76	0.98
3:C:356:ARG:HH21	3:C:357:ILE:HG22	1.25	0.97
2:B:374:LEU:HD21	2:B:376[B]:THR:HG23	1.46	0.95
4:D:357:ILE:HD11	4:D:377:LEU:HD11	1.51	0.93
3:C:374:LEU:HD22	3:C:375:ALA:H	1.37	0.90
3:C:38:VAL:HA	3:C:41:ARG:HD2	1.56	0.87
2:B:56:GLN:HB2	9:B:2073:HOH:O	1.75	0.86
3:C:146:ASP:HB2	9:C:2063:HOH:O	1.76	0.86
4:D:35:ILE:HG23	4:D:112:VAL:HG11	1.58	0.85
2:B:124:HIS:HD2	9:B:2164:HOH:O	1.60	0.85
4:D:125:CYS:SG	4:D:140:ILE:HD11	2.18	0.84
3:C:207:ARG:H	3:C:207:ARG:HD3	1.42	0.84
2:B:376[B]:THR:HG22	2:B:386:ALA:CB	2.06	0.84
1:A:279:ALA:HA	5:A:1401:SO4:O1	1.77	0.84

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:354:GLY:HA2	3:C:377:LEU:HD21	1.57	0.83
2:B:279:ALA:HB1	9:B:2310:HOH:O	1.78	0.82
3:C:207:ARG:HG2	3:C:207:ARG:HH11	1.40	0.82
2:B:376[B]:THR:HG22	2:B:386:ALA:HB2	1.62	0.81
2:B:374:LEU:HD21	2:B:376[B]:THR:CG2	2.10	0.81
1:A:95:ALA:HB3	9:A:2127:HOH:O	1.79	0.81
3:C:7:ILE:HD12	3:C:362:LEU:HD21	1.62	0.81
4:D:344:ILE:HB	9:D:2103:HOH:O	1.81	0.80
1:A:4:SER:HA	9:A:2295:HOH:O	1.81	0.80
2:B:207:ARG:HD3	2:B:207:ARG:H	1.47	0.80
4:D:62:GLU:HB3	9:D:2043:HOH:O	1.81	0.80
4:D:231:LEU:HB3	9:D:2129:HOH:O	1.81	0.80
1:A:23:ALA:HB1	9:A:2023:HOH:O	1.82	0.80
4:D:140:ILE:HD12	4:D:141:ASP:H	1.47	0.80
3:C:100:MET:HG3	3:C:275:ILE:HG21	1.62	0.79
4:D:125:CYS:HB3	7:D:1399:CL:CL	2.20	0.79
3:C:58:LEU:HD22	9:C:2063:HOH:O	1.80	0.79
4:D:140:ILE:HD13	4:D:141:ASP:H	1.47	0.78
4:D:207:ARG:H	4:D:207:ARG:HD3	1.47	0.78
1:A:267:ARG:NH1	9:A:2304:HOH:O	2.16	0.78
3:C:38:VAL:CG1	3:C:257:LEU:HB2	2.13	0.78
3:C:364:GLU:HA	3:C:367:ARG:HG2	1.64	0.78
3:C:298:LYS:HE2	3:C:302:ARG:NE	1.99	0.77
3:C:180:VAL:HG21	3:C:225:LEU:HA	1.65	0.77
3:C:374:LEU:HD22	3:C:375:ALA:N	2.00	0.76
3:C:356:ARG:NH2	3:C:357:ILE:HG22	1.98	0.76
4:D:276:VAL:HG11	4:D:305:TRP:CH2	2.19	0.76
1:A:280:THR:HG22	5:A:1401:SO4:O4	1.84	0.75
4:D:14:ALA:HB1	9:D:2121:HOH:O	1.86	0.75
4:D:316:ASN:OD1	4:D:357:ILE:HD13	1.85	0.75
4:D:273:GLY:HA2	4:D:391:SER:HB3	1.67	0.75
1:A:270:GLN:HG3	9:A:2306:HOH:O	1.86	0.75
3:C:54:LEU:HB3	9:C:2025:HOH:O	1.85	0.75
3:C:105:THR:HG21	4:D:101:GLN:HG2	1.68	0.75
4:D:140:ILE:HD13	4:D:142:THR:H	1.51	0.74
2:B:339:VAL:HG11	2:B:368:ARG:NH2	2.04	0.73
2:B:228:MET:HE1	9:B:2404:HOH:O	1.87	0.73
4:D:15:VAL:HG13	9:D:2142:HOH:O	1.88	0.73
3:C:47:GLY:HA2	3:C:77:PRO:HG3	1.69	0.72
4:D:216:ASP:HA	9:D:2121:HOH:O	1.88	0.72
2:B:374:LEU:CD2	2:B:376[B]:THR:HG23	2.18	0.72

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:64:GLN:HG2	4:D:88:LEU:CD1	2.18	0.72
3:C:374:LEU:CD2	3:C:375:ALA:H	2.01	0.72
4:D:140:ILE:HD12	4:D:141:ASP:N	2.05	0.72
4:D:282:GLY:HA2	4:D:383:MET:HA	1.72	0.72
2:B:207:ARG:HG2	2:B:208:LYS:H	1.55	0.72
4:D:174:GLU:HB2	9:D:2100:HOH:O	1.88	0.72
4:D:123:PRO:HB2	7:D:1399:CL:CL	2.27	0.72
3:C:125:CYS:HB2	7:D:1399:CL:CL	2.26	0.71
4:D:368:ARG:HG3	9:D:2182:HOH:O	1.89	0.71
3:C:128:LEU:HD21	3:C:137:PHE:CE2	2.25	0.71
2:B:371:ARG:HG3	9:B:2373:HOH:O	1.90	0.71
3:C:97:ALA:HA	3:C:387:MET:HE1	1.72	0.71
4:D:42:ALA:HB1	9:D:2031:HOH:O	1.89	0.71
4:D:47:GLY:HA2	4:D:77:PRO:HG2	1.71	0.71
2:B:139:MET:O	9:B:2164:HOH:O	2.08	0.71
2:B:124:HIS:CD2	9:B:2164:HOH:O	2.38	0.70
4:D:162:GLU:HG3	9:D:2132:HOH:O	1.91	0.70
4:D:207:ARG:HD3	4:D:207:ARG:N	2.06	0.70
3:C:279:ALA:HA	9:C:2112:HOH:O	1.92	0.70
3:C:280:THR:HG23	4:D:81:THR:HG21	1.73	0.70
1:A:133:LYS:HB2	9:D:2013:HOH:O	1.91	0.69
4:D:35:ILE:HD12	9:D:2023:HOH:O	1.92	0.69
2:B:339:VAL:HG11	2:B:368:ARG:HH22	1.56	0.69
3:C:310:LEU:HG	9:C:2113:HOH:O	1.93	0.68
3:C:8:ALA:HB3	9:C:2095:HOH:O	1.91	0.68
3:C:18:PHE:CZ	4:D:129:ARG:HD3	2.29	0.68
4:D:326:VAL:HG13	9:D:2150:HOH:O	1.93	0.68
4:D:222:GLY:N	9:D:2127:HOH:O	2.27	0.68
4:D:292:PRO:HB2	9:D:2150:HOH:O	1.94	0.68
3:C:121:MET:HE2	9:C:2004:HOH:O	1.93	0.67
4:D:76:VAL:HG23	5:D:1397:SO4:O1	1.94	0.67
9:A:2138:HOH:O	2:B:105:THR:HG22	1.93	0.67
4:D:371:ARG:O	4:D:390:GLU:HA	1.94	0.67
3:C:259:MET:HB2	9:C:2097:HOH:O	1.94	0.67
4:D:207:ARG:HG2	4:D:208:LYS:HG3	1.76	0.67
4:D:299:ALA:HB2	9:D:2152:HOH:O	1.94	0.66
3:C:65:ASN:OD1	9:C:2035:HOH:O	2.13	0.66
3:C:83:TRP:HH2	3:C:98:LEU:HD13	1.59	0.66
4:D:365:MET:HE2	4:D:370:ALA:O	1.95	0.66
4:D:100:MET:HB2	9:D:2061:HOH:O	1.94	0.66
3:C:43:GLY:HA3	9:C:2021:HOH:O	1.95	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:C:2029:HOH:O	4:D:125:CYS:SG	2.54	0.66
1:A:378:CSD:SG	9:A:2343:HOH:O	2.53	0.66
3:C:139:MET:HE1	4:D:139:MET:HE2	1.78	0.65
4:D:35:ILE:HB	9:D:2023:HOH:O	1.96	0.65
3:C:68:ARG:CB	7:C:1396:CL:CL	2.81	0.65
1:A:283:VAL:HA	5:A:1400:SO4:O4	1.96	0.65
1:A:280:THR:N	5:A:1401:SO4:O3	2.30	0.65
3:C:302:ARG:NH1	4:D:107:ASP:HA	2.11	0.65
1:A:371:ARG:HG2	9:A:2387:HOH:O	1.95	0.65
3:C:6:VAL:HG13	9:C:2098:HOH:O	1.96	0.65
3:C:274:ARG:HH21	3:C:392:LEU:HD21	1.62	0.65
4:D:140:ILE:N	9:D:2083:HOH:O	2.29	0.65
3:C:228:MET:HG3	9:C:2093:HOH:O	1.96	0.64
1:A:302:ARG:NH1	5:A:1401:SO4:O1	2.30	0.64
6:B:1401:COA:H31	9:B:2172:HOH:O	1.95	0.64
3:C:31:GLY:O	3:C:35:ILE:HG13	1.98	0.64
3:C:65:ASN:HB3	7:C:1396:CL:CL	2.35	0.64
2:B:175:GLN:HE22	2:B:240:THR:CG2	2.10	0.64
3:C:60:ALA:HB1	9:C:2029:HOH:O	1.97	0.64
4:D:57:VAL:C	4:D:59:PRO:HD3	2.23	0.64
3:C:38:VAL:HG12	3:C:257:LEU:HB2	1.80	0.64
3:C:371:ARG:HA	9:C:2141:HOH:O	1.96	0.64
4:D:298:LYS:HE3	9:D:2153:HOH:O	1.97	0.64
3:C:183:GLN:OE1	3:C:220:ARG:HG2	1.96	0.64
1:A:265:SER:HA	9:A:2298:HOH:O	1.98	0.63
4:D:150:ASP:HB2	9:D:2086:HOH:O	1.98	0.63
4:D:178:PHE:HB2	5:D:1396:SO4:O1	1.98	0.63
4:D:247:SER:HB3	4:D:318:ALA:HA	1.79	0.63
1:A:168:TRP:CH2	1:A:329:ASP:HB2	2.33	0.63
3:C:53:ILE:HG12	3:C:83:TRP:CE2	2.34	0.62
4:D:183:GLN:NE2	4:D:220:ARG:HD3	2.15	0.62
2:B:339:VAL:HG13	9:B:2357:HOH:O	1.99	0.62
3:C:65:ASN:ND2	7:C:1396:CL:CL	2.70	0.62
1:A:316:ASN:HB3	9:A:2343:HOH:O	2.00	0.61
4:D:199:ILE:HD12	9:D:2120:HOH:O	1.99	0.61
3:C:374:LEU:HD21	3:C:387:MET:O	1.99	0.61
3:C:362:LEU:HD12	9:C:2132:HOH:O	2.00	0.61
1:A:279:ALA:HB1	1:A:298:LYS:HD3	1.83	0.61
3:C:333:ASP:O	3:C:336:ILE:HG12	2.01	0.61
4:D:51:GLU:HB3	4:D:111:ILE:CD1	2.30	0.61
2:B:207:ARG:HG2	2:B:208:LYS:N	2.14	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:51:GLU:HA	3:C:81:THR:O	2.01	0.61
4:D:142:THR:O	4:D:146:ASP:HB2	2.00	0.61
4:D:232:ARG:HH11	4:D:232:ARG:HB2	1.66	0.61
4:D:305:TRP:CZ3	4:D:388:CYS:HB3	2.36	0.61
2:B:166:LYS:HG3	9:B:2187:HOH:O	2.00	0.61
4:D:232:ARG:HB2	4:D:232:ARG:NH1	2.15	0.60
4:D:110:ILE:HG23	4:D:257:LEU:HD21	1.84	0.60
3:C:232:ARG:H	3:C:232:ARG:NE	1.99	0.60
3:C:5:ILE:HG13	3:C:100:MET:HG2	1.83	0.60
3:C:52:VAL:HG13	3:C:112:VAL:HG12	1.82	0.60
4:D:269:ILE:HD13	9:D:2031:HOH:O	2.02	0.60
4:D:279:ALA:HB3	9:D:2152:HOH:O	2.01	0.60
3:C:293:ILE:HA	3:C:330:LEU:HD21	1.83	0.60
2:B:376[A]:THR:HG23	2:B:385:VAL:O	2.01	0.59
3:C:358:LEU:HD22	3:C:362:LEU:HG	1.83	0.59
3:C:144:ILE:HD13	3:C:148:LEU:HD12	1.81	0.59
4:D:168:TRP:HB3	9:D:2099:HOH:O	2.01	0.59
3:C:200:VAL:HG13	9:C:2080:HOH:O	2.00	0.59
4:D:250:ASN:HB3	9:D:2142:HOH:O	2.02	0.59
1:A:312:LEU:HD23	1:A:361:LEU:HD12	1.84	0.59
2:B:207:ARG:HD3	2:B:207:ARG:N	2.15	0.59
4:D:12:ARG:HH22	4:D:199:ILE:HD11	1.68	0.59
3:C:316:ASN:ND2	3:C:377:LEU:HD23	2.18	0.59
4:D:140:ILE:CD1	4:D:141:ASP:N	2.54	0.58
1:A:284:ASP:OD2	9:A:2312:HOH:O	2.17	0.58
3:C:57:VAL:HG12	3:C:58:LEU:HD23	1.86	0.58
4:D:140:ILE:HD12	9:D:2083:HOH:O	2.02	0.58
1:A:371:ARG:HD2	9:A:2381:HOH:O	2.03	0.58
4:D:94:ARG:NH2	9:D:2059:HOH:O	2.36	0.58
4:D:275:ILE:CD1	9:D:2061:HOH:O	2.52	0.58
4:D:277:SER:HB3	4:D:303:ALA:HB2	1.85	0.58
3:C:153:TYR:HB3	3:C:155:TYR:CE2	2.38	0.58
2:B:221:HIS:HD2	9:B:2220:HOH:O	1.86	0.58
2:B:374:LEU:HD21	2:B:376[A]:THR:OG1	2.04	0.58
4:D:56:GLN:OE1	4:D:116:MET:HE3	2.02	0.58
4:D:274:ARG:HB3	4:D:390:GLU:O	2.02	0.58
2:B:16:GLY:HA2	9:B:2261:HOH:O	2.04	0.58
4:D:178:PHE:HE1	4:D:317:GLU:CD	2.12	0.58
4:D:258:LEU:HD12	9:D:2007:HOH:O	2.04	0.57
3:C:274:ARG:NH2	3:C:392:LEU:HD21	2.19	0.57
3:C:87:GLN:N	3:C:91:SER:OG	2.37	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:D:50:ASN:HB2	4:D:110:ILE:O	2.04	0.57
4:D:242:THR:HB	9:D:2129:HOH:O	2.04	0.57
3:C:83:TRP:CH2	3:C:98:LEU:HD13	2.40	0.57
4:D:96:VAL:HG12	9:D:2061:HOH:O	2.04	0.57
3:C:68:ARG:HG3	4:D:152:PHE:HZ	1.70	0.57
2:B:363:PHE:CD1	2:B:366[A]:LYS:NZ	2.72	0.57
3:C:116:MET:HG2	9:C:2025:HOH:O	2.04	0.57
3:C:125:CYS:CB	7:D:1399:CL:CL	2.90	0.57
3:C:272:LEU:HD12	3:C:366:LYS:HD2	1.87	0.57
4:D:96:VAL:O	9:D:2061:HOH:O	2.18	0.57
2:B:243:ALA:HB1	6:B:1401:COA:O2A	2.05	0.56
4:D:9:SER:OG	4:D:42:ALA:HB2	2.05	0.56
4:D:141:ASP:O	4:D:143:MET:N	2.31	0.56
4:D:80:ALA:HB2	9:D:2033:HOH:O	2.05	0.56
4:D:287:VAL:HB	4:D:290:THR:HG23	1.87	0.56
4:D:349:PRO:O	4:D:350:ILE:C	2.48	0.56
3:C:342:GLY:HA3	9:C:2116:HOH:O	2.03	0.56
2:B:356:ARG:C	2:B:356:ARG:HD2	2.31	0.56
3:C:180:VAL:HG13	3:C:223:ALA:O	2.06	0.56
3:C:353:SER:O	3:C:357:ILE:HG23	2.06	0.56
2:B:183:GLN:HG3	9:B:2404:HOH:O	2.06	0.56
3:C:316:ASN:HB2	3:C:377:LEU:HA	1.88	0.56
4:D:349:PRO:HG3	9:D:2142:HOH:O	2.06	0.56
2:B:100:MET:SD	5:B:1398:SO4:O4	2.64	0.56
4:D:44:VAL:HG13	4:D:48:GLU:OE1	2.06	0.56
4:D:51:GLU:HB3	4:D:111:ILE:HD12	1.88	0.56
2:B:175:GLN:HE22	2:B:240:THR:HG21	1.71	0.56
3:C:276:VAL:HG22	3:C:388:CYS:HB3	1.88	0.56
4:D:165:ALA:HA	4:D:170:LEU:HD12	1.88	0.56
4:D:305:TRP:CE2	4:D:372:LYS:HD3	2.40	0.56
1:A:114:GLY:HA2	9:A:2127:HOH:O	2.05	0.55
3:C:110:ILE:HG23	3:C:257:LEU:HD21	1.89	0.55
3:C:330:LEU:HD13	3:C:332:TRP:CZ2	2.42	0.55
4:D:35:ILE:HG23	4:D:112:VAL:HG21	1.89	0.55
4:D:298:LYS:HB3	9:D:2153:HOH:O	2.06	0.55
2:B:316:ASN:HB3	9:B:2381:HOH:O	2.05	0.55
3:C:146:ASP:HB3	5:D:1394:SO4:O1	2.07	0.55
4:D:327:ASN:HB3	9:D:2165:HOH:O	2.05	0.55
3:C:272:LEU:CD1	3:C:366:LYS:HD2	2.37	0.55
3:C:314:GLU:O	3:C:375:ALA:HA	2.07	0.54
2:B:34:VAL:HG12	2:B:255:ALA:HB3	1.90	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:D:85:MET:HG3	9:D:2039:HOH:O	2.06	0.54
4:D:283:VAL:HG11	4:D:290:THR:O	2.06	0.54
3:C:306:LYS:HB3	9:C:2114:HOH:O	2.07	0.54
3:C:340[C]:ASN:HD21	3:C:360:THR:HG23	1.73	0.54
3:C:100:MET:HG3	3:C:275:ILE:CG2	2.36	0.54
1:A:174:GLU:HG3	9:A:2210:HOH:O	2.07	0.54
4:D:34:VAL:O	4:D:38:VAL:HG13	2.07	0.54
2:B:21:ALA:HB3	9:B:2261:HOH:O	2.08	0.54
4:D:357:ILE:HD11	4:D:377:LEU:CD1	2.31	0.54
1:A:298:LYS:HE2	1:A:302:ARG:NH2	2.23	0.53
3:C:230:LYS:HA	9:C:2094:HOH:O	2.07	0.53
4:D:187:GLU:HG3	9:D:2127:HOH:O	2.07	0.53
4:D:204:VAL:HB	9:D:2119:HOH:O	2.07	0.53
3:C:183:GLN:CD	3:C:220:ARG:HG2	2.33	0.53
4:D:7:ILE:HD13	4:D:362:LEU:HD11	1.89	0.53
4:D:236:ASP:HB2	9:D:2132:HOH:O	2.09	0.53
1:A:266:ARG:NH2	5:A:1394:SO4:O1	2.39	0.53
6:A:1402:COA:H141	6:A:1402:COA:O9P	2.07	0.53
3:C:11:ALA:HB3	3:C:38:VAL:HG23	1.89	0.53
1:A:4:SER:C	1:A:5:ILE:HD12	2.33	0.53
4:D:215:ALA:HA	9:D:2120:HOH:O	2.08	0.53
4:D:316:ASN:OD1	4:D:357:ILE:HG21	2.07	0.53
6:B:1401:COA:O2A	6:B:1401:COA:H122	2.09	0.53
2:B:207:ARG:N	2:B:207:ARG:HH11	2.06	0.53
3:C:68:ARG:HB3	7:C:1396:CL:CL	2.46	0.53
4:D:93:LEU:HD23	4:D:385:VAL:HG13	1.91	0.53
4:D:300:LEU:HD13	4:D:307:ILE:HG13	1.90	0.53
4:D:169:GLN:HG3	9:D:2095:HOH:O	2.09	0.52
3:C:207:ARG:HH11	3:C:207:ARG:CG	2.15	0.52
4:D:35:ILE:HG12	4:D:112:VAL:HG11	1.91	0.52
4:D:103:ILE:HG23	4:D:108:ALA:O	2.09	0.52
2:B:324:CYS:O	2:B:328:LYS:HG3	2.09	0.52
4:D:35:ILE:O	4:D:39:LEU:HD23	2.09	0.52
1:A:297:ARG:NE	9:A:2319:HOH:O	2.43	0.52
2:B:316:ASN:ND2	9:B:2335:HOH:O	2.42	0.52
3:C:25:THR:HG21	3:C:30:LEU:HD21	1.91	0.52
3:C:302:ARG:NH1	9:C:2112:HOH:O	2.42	0.52
3:C:316:ASN:CG	3:C:377:LEU:HD23	2.34	0.52
4:D:281:VAL:HG13	9:D:2151:HOH:O	2.09	0.52
4:D:274:ARG:H	4:D:389:ILE:HG23	1.74	0.52
4:D:300:LEU:HD13	4:D:307:ILE:CD1	2.40	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:146:ASP:HB3	9:B:2076:HOH:O	2.09	0.52
3:C:284:ASP:HA	9:D:2055:HOH:O	2.10	0.52
3:C:322:GLN:O	3:C:326:VAL:HG23	2.10	0.52
4:D:163:ASN:HD22	4:D:286:LYS:HB3	1.75	0.52
2:B:274:ARG:NH2	9:B:2307:HOH:O	2.43	0.52
3:C:44:VAL:HG13	3:C:48:GLU:HB2	1.92	0.52
3:C:247:SER:HB2	3:C:318:ALA:O	2.10	0.52
3:C:232:ARG:H	3:C:232:ARG:HE	1.57	0.51
4:D:44:VAL:HG23	9:D:2031:HOH:O	2.10	0.51
4:D:216:ASP:CA	9:D:2121:HOH:O	2.53	0.51
2:B:312:LEU:HD23	2:B:361:LEU:HD22	1.91	0.51
3:C:377:LEU:HD22	9:C:2044:HOH:O	2.09	0.51
4:D:293:ILE:HB	4:D:294:PRO:HD3	1.91	0.51
3:C:39:LEU:HD21	3:C:46:ALA:HA	1.92	0.51
4:D:381:GLY:N	9:D:2088:HOH:O	2.43	0.51
1:A:96:VAL:HG23	9:A:2127:HOH:O	2.10	0.51
1:A:134:MET:HE1	9:D:2028:HOH:O	2.11	0.51
4:D:200:VAL:HG22	9:D:2114:HOH:O	2.10	0.51
4:D:388:CYS:C	4:D:389:ILE:HD12	2.35	0.51
3:C:19:ASN:C	3:C:23:ALA:HB2	2.36	0.51
4:D:247:SER:HA	4:D:344:ILE:HA	1.92	0.51
4:D:93:LEU:HD11	4:D:387:MET:HB3	1.93	0.51
4:D:144:ILE:HA	4:D:148:LEU:HB2	1.93	0.51
4:D:33:THR:HG21	4:D:202:PHE:HD1	1.76	0.51
3:C:163:ASN:O	3:C:167:GLN:HB2	2.10	0.50
3:C:330:LEU:HD13	3:C:332:TRP:CH2	2.46	0.50
4:D:47:GLY:HA2	4:D:77:PRO:CG	2.38	0.50
4:D:99:GLY:O	4:D:103:ILE:HD12	2.11	0.50
4:D:275:ILE:HD12	9:D:2004:HOH:O	2.11	0.50
4:D:364:GLU:OE2	4:D:368:ARG:HG2	2.11	0.50
4:D:123:PRO:C	7:D:1399:CL:CL	2.91	0.50
2:B:190:GLN:OE1	2:B:221:HIS:HE1	1.94	0.50
3:C:51:GLU:OE2	3:C:83:TRP:CD1	2.65	0.50
4:D:55:GLY:HA3	4:D:91[B]:SER:OG	2.11	0.50
1:A:133:LYS:HD3	1:A:133:LYS:H	1.77	0.50
3:C:94:ARG:HH22	4:D:51:GLU:CD	2.20	0.50
4:D:153:TYR:HB3	4:D:155:TYR:CE2	2.47	0.50
3:C:12:ARG:HB2	3:C:254:ALA:HB2	1.94	0.50
3:C:81:THR:HG23	4:D:383:MET:SD	2.51	0.50
4:D:87:GLN:OE1	4:D:94:ARG:HG2	2.12	0.50
3:C:128:LEU:HD12	4:D:124:HIS:HB2	1.94	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:D:32:ALA:HA	9:D:2023:HOH:O	2.12	0.49
4:D:371:ARG:HD3	4:D:371:ARG:N	2.27	0.49
4:D:386:ALA:HB3	9:D:2152:HOH:O	2.11	0.49
3:C:374:LEU:CD2	3:C:375:ALA:N	2.69	0.49
4:D:140:ILE:O	4:D:141:ASP:HB2	2.12	0.49
1:A:274:ARG:NH2	1:A:390:GLU:OE1	2.45	0.49
2:B:47:GLY:HA2	2:B:77:PRO:CG	2.42	0.49
3:C:227:SER:HA	3:C:230:LYS:HE3	1.94	0.49
4:D:317:GLU:O	4:D:344:ILE:HG13	2.12	0.49
4:D:124:HIS:C	7:D:1399:CL:CL	2.92	0.49
4:D:305:TRP:HZ3	4:D:388:CYS:HB3	1.75	0.49
1:A:80:ALA:HB2	9:A:2064:HOH:O	2.13	0.49
3:C:6:VAL:HB	3:C:271:PRO:HB3	1.94	0.49
3:C:153:TYR:CE1	3:C:286:LYS:HG3	2.48	0.49
3:C:207:ARG:HG2	3:C:207:ARG:NH1	2.18	0.49
2:B:148:LEU:HD23	9:B:2172:HOH:O	2.12	0.49
3:C:84:GLY:N	9:C:2035:HOH:O	2.41	0.49
4:D:387:MET:HG2	4:D:389:ILE:HD11	1.94	0.49
3:C:9:SER:OG	3:C:38:VAL:HG13	2.12	0.49
4:D:26:PRO:HD2	4:D:29:GLU:OE1	2.13	0.49
4:D:140:ILE:C	9:D:2083:HOH:O	2.55	0.49
4:D:248:GLY:HA2	9:D:2138:HOH:O	2.12	0.49
3:C:7:ILE:HD13	3:C:362:LEU:HD11	1.93	0.49
1:A:40:GLU:HG3	9:A:2045:HOH:O	2.13	0.48
1:A:298:LYS:NZ	5:A:1401:SO4:O2	2.46	0.48
3:C:22:PHE:HB3	3:C:25:THR:HB	1.95	0.48
3:C:387:MET:CG	3:C:388:CYS:N	2.76	0.48
4:D:343:ALA:O	4:D:344:ILE:C	2.55	0.48
1:A:139:MET:HE1	2:B:139:MET:HE1	1.95	0.48
2:B:379:ILE:HB	2:B:383:MET:HB2	1.95	0.48
4:D:183:GLN:OE1	4:D:220:ARG:HG2	2.13	0.48
1:A:276:VAL:HG22	1:A:388:CYS:HB2	1.96	0.48
3:C:78:GLN:HG3	3:C:79:GLU:OE2	2.14	0.48
3:C:358:LEU:CD2	3:C:362:LEU:HG	2.44	0.48
3:C:387:MET:CG	3:C:388:CYS:H	2.25	0.48
2:B:191[A]:LYS:NZ	2:B:191[A]:LYS:HB3	2.29	0.48
3:C:17:SER:HB3	9:C:2008:HOH:O	2.13	0.48
3:C:313:VAL:HA	3:C:374:LEU:O	2.14	0.48
4:D:283:VAL:CG1	4:D:294:PRO:HG2	2.43	0.48
2:B:376[B]:THR:HG22	2:B:386:ALA:HB1	1.91	0.48
3:C:78:GLN:NE2	4:D:285:PRO:HD3	2.28	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:369:GLY:HA3	9:C:2138:HOH:O	2.13	0.48
1:A:168:TRP:HH2	1:A:329:ASP:HB2	1.77	0.47
3:C:7:ILE:HG12	3:C:258:LEU:HD11	1.96	0.47
3:C:278:TRP:HA	3:C:387:MET:HA	1.94	0.47
4:D:12:ARG:NH1	4:D:13:THR:O	2.47	0.47
4:D:207:ARG:NH1	4:D:208:LYS:H	2.11	0.47
3:C:284:ASP:HB3	3:C:287:VAL:HG22	1.96	0.47
4:D:284:ASP:OD1	4:D:286:LYS:HB2	2.14	0.47
1:A:374:LEU:C	1:A:374:LEU:HD23	2.39	0.47
3:C:68:ARG:HB2	7:C:1396:CL:CL	2.52	0.47
3:C:291:GLY:HA3	3:C:383:MET:O	2.14	0.47
3:C:354:GLY:HA3	9:C:2044:HOH:O	2.15	0.47
4:D:35:ILE:CG2	4:D:112:VAL:HG11	2.38	0.47
4:D:53:ILE:HD13	4:D:83:TRP:CZ2	2.50	0.47
4:D:326:VAL:O	4:D:330:LEU:HB2	2.14	0.47
3:C:123:PRO:HD2	9:C:2026:HOH:O	2.15	0.47
4:D:19:ASN:HD22	4:D:19:ASN:N	2.13	0.47
3:C:132:VAL:HG21	3:C:137:PHE:CD1	2.50	0.47
3:C:236:ASP:HB3	3:C:239:GLY:HA3	1.97	0.47
3:C:257:LEU:HD22	9:C:2095:HOH:O	2.14	0.47
3:C:97:ALA:HA	3:C:387:MET:CE	2.41	0.47
1:A:328:LYS:HB2	1:A:328:LYS:HE3	1.58	0.46
3:C:115:GLY:HA3	3:C:352:ALA:HA	1.96	0.46
3:C:289:GLY:O	3:C:292:PRO:HD2	2.16	0.46
2:B:190:GLN:OE1	2:B:221:HIS:CE1	2.68	0.46
3:C:357:ILE:CD1	3:C:375:ALA:HB1	2.45	0.46
4:D:125:CYS:HG	4:D:140:ILE:HD11	1.78	0.46
4:D:170:LEU:HD21	9:D:2099:HOH:O	2.15	0.46
1:A:237:LYS:HE2	9:A:2282:HOH:O	2.14	0.46
2:B:172:ARG:HA	2:B:240:THR:OG1	2.15	0.46
4:D:385:VAL:HB	9:D:2056:HOH:O	2.16	0.46
4:D:74:ALA:HB2	9:D:2023:HOH:O	2.15	0.46
4:D:358:LEU:HD22	4:D:362:LEU:HG	1.98	0.46
1:A:298:LYS:HE2	1:A:302:ARG:CZ	2.46	0.46
3:C:129:ARG:CZ	9:C:2056:HOH:O	2.62	0.46
3:C:371:ARG:O	3:C:390:GLU:HA	2.15	0.46
4:D:178:PHE:CE1	4:D:317:GLU:CD	2.92	0.46
4:D:283:VAL:N	4:D:382:GLY:O	2.46	0.46
1:A:133:LYS:H	1:A:133:LYS:CD	2.28	0.46
2:B:168:TRP:CH2	2:B:329:ASP:HB2	2.51	0.46
3:C:198:GLU:HG3	3:C:199:ILE:N	2.31	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:D:302:ARG:HG3	9:D:2153:HOH:O	2.15	0.46
4:D:141:ASP:OD1	4:D:143:MET:HB3	2.16	0.46
4:D:181:ALA:O	4:D:185:LYS:HG3	2.16	0.46
1:A:237:LYS:HA	1:A:237:LYS:HD3	1.70	0.45
2:B:276:VAL:O	5:B:1398:SO4:O2	2.33	0.45
2:B:298:LYS:HG2	9:B:2310:HOH:O	2.16	0.45
2:B:374:LEU:HD23	2:B:374:LEU:C	2.40	0.45
3:C:13:THR:HA	9:C:2080:HOH:O	2.16	0.45
3:C:103:ILE:HD13	3:C:259:MET:HA	1.98	0.45
4:D:368:ARG:HB3	9:D:2179:HOH:O	2.16	0.45
3:C:45:ALA:HB3	3:C:48:GLU:OE1	2.16	0.45
3:C:202:PHE:HD1	9:C:2014:HOH:O	2.00	0.45
3:C:57:VAL:C	3:C:58:LEU:HD23	2.42	0.45
3:C:129:ARG:HD2	9:D:2068:HOH:O	2.17	0.45
4:D:66:PRO:CG	9:D:2043:HOH:O	2.64	0.45
4:D:140:ILE:HD13	4:D:142:THR:N	2.28	0.45
2:B:131:GLY:C	9:B:2158:HOH:O	2.60	0.45
3:C:316:ASN:OD1	3:C:357:ILE:HG21	2.17	0.45
2:B:236:ASP:OD1	2:B:238:GLU:HG2	2.17	0.45
2:B:296:SER:HG	2:B:376[B]:THR:HG21	1.77	0.45
3:C:316:ASN:OD1	3:C:377:LEU:HD23	2.17	0.45
4:D:59:PRO:HB2	5:D:1394:SO4:O3	2.17	0.45
4:D:292:PRO:HB3	4:D:376:THR:OG1	2.16	0.45
3:C:87:GLN:HG3	9:D:2046:HOH:O	2.17	0.45
3:C:122:ALA:HA	9:C:2026:HOH:O	2.15	0.45
3:C:146:ASP:HB3	5:D:1394:SO4:S	2.57	0.45
3:C:356:ARG:NH1	9:C:2133:HOH:O	2.49	0.45
2:B:89:CSO:OD	6:B:1401:COA:H22	2.17	0.45
3:C:38:VAL:HG11	3:C:257:LEU:N	2.30	0.45
3:C:83:TRP:HA	9:C:2035:HOH:O	2.17	0.45
4:D:233:PRO:HB2	4:D:236:ASP:O	2.16	0.45
2:B:4:SER:HB3	9:B:2394:HOH:O	2.17	0.45
2:B:378:CSD:OD1	6:B:1401:COA:S1P	2.71	0.45
3:C:54:LEU:N	9:C:2024:HOH:O	2.49	0.45
3:C:298:LYS:HE3	3:C:301:GLU:OE1	2.17	0.45
3:C:364:GLU:OE1	3:C:367:ARG:HD2	2.17	0.45
4:D:278:TRP:HH2	9:D:2059:HOH:O	1.99	0.45
1:A:356:ARG:HD2	1:A:356:ARG:C	2.42	0.45
3:C:207:ARG:HG2	9:C:2086:HOH:O	2.17	0.45
2:B:89:CSO:SG	9:B:2376:HOH:O	2.62	0.44
3:C:79:GLU:O	4:D:281:VAL:HG23	2.17	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:D:293:ILE:CB	4:D:294:PRO:HD3	2.47	0.44
3:C:10:ALA:HB3	3:C:363:PHE:CE2	2.52	0.44
3:C:76:VAL:HG13	3:C:77:PRO:HD2	1.98	0.44
3:C:311:ASP:HB2	3:C:370:ALA:HB1	1.99	0.44
2:B:144:ILE:HD13	2:B:148:LEU:HD12	1.98	0.44
4:D:275:ILE:HD13	9:D:2061:HOH:O	2.15	0.44
1:A:280:THR:O	5:A:1401:SO4:O3	2.34	0.44
3:C:48:GLU:OE1	3:C:48:GLU:N	2.51	0.44
3:C:207:ARG:CG	3:C:207:ARG:NH1	2.77	0.44
3:C:273:GLY:HA2	3:C:391:SER:HA	2.00	0.44
3:C:316:ASN:HD21	3:C:377:LEU:HD23	1.82	0.44
4:D:88:LEU:HD23	4:D:88:LEU:HA	1.86	0.44
4:D:96:VAL:HG21	4:D:358:LEU:HD12	2.00	0.44
4:D:147:GLY:O	4:D:148:LEU:HD23	2.17	0.44
4:D:334:PRO:HD3	9:D:2165:HOH:O	2.16	0.44
1:A:379:ILE:HB	1:A:383:MET:HB2	2.00	0.44
3:C:274:ARG:O	3:C:389:ILE:HA	2.18	0.44
4:D:140:ILE:CA	9:D:2083:HOH:O	2.66	0.44
4:D:58:LEU:N	4:D:59:PRO:HD3	2.31	0.44
4:D:298:LYS:HD2	9:D:2154:HOH:O	2.17	0.44
3:C:107:ASP:CG	4:D:278:TRP:HE1	2.24	0.44
3:C:374:LEU:CD2	3:C:387:MET:O	2.66	0.44
4:D:287:VAL:HB	4:D:290:THR:CG2	2.48	0.44
4:D:291:GLY:N	4:D:292:PRO:CD	2.81	0.44
3:C:118:SER:HB2	9:C:2050:HOH:O	2.17	0.44
3:C:207:ARG:HD3	3:C:207:ARG:N	2.21	0.44
4:D:123:PRO:CB	7:D:1399:CL:CL	3.00	0.44
4:D:370:ALA:N	9:D:2182:HOH:O	2.50	0.44
1:A:233:PRO:HB2	1:A:236:ASP:O	2.17	0.43
3:C:343:ALA:N	9:C:2116:HOH:O	2.50	0.43
1:A:136:ASP:OD1	4:D:140:ILE:HA	2.18	0.43
3:C:47:GLY:HA2	3:C:77:PRO:CG	2.45	0.43
3:C:57:VAL:HG21	3:C:350:ILE:CG2	2.47	0.43
4:D:66:PRO:HD2	9:D:2048:HOH:O	2.18	0.43
4:D:183:GLN:CD	4:D:220:ARG:HD3	2.43	0.43
1:A:134:MET:HE2	1:A:134:MET:HB3	1.85	0.43
3:C:126:ALA:O	3:C:128:LEU:HG	2.18	0.43
4:D:291:GLY:O	4:D:294:PRO:HD2	2.18	0.43
4:D:300:LEU:CD1	4:D:307:ILE:HG13	2.48	0.43
3:C:129:ARG:NH2	4:D:122:ALA:O	2.40	0.43
2:B:378:CSD:SG	9:B:2381:HOH:O	2.62	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:D:48:GLU:CD	4:D:267:ARG:HH12	2.25	0.43
2:B:207:ARG:HG2	2:B:208:LYS:HG2	2.00	0.43
3:C:364:GLU:O	3:C:368:ARG:HG2	2.19	0.43
4:D:33:THR:O	4:D:37:ALA:HB2	2.19	0.43
4:D:326:VAL:CG1	4:D:332:TRP:HZ2	2.32	0.43
3:C:64:GLN:O	3:C:65:ASN:C	2.61	0.43
3:C:270:GLN:HA	3:C:271:PRO:HD3	1.86	0.43
3:C:64:GLN:HE22	4:D:157:MET:HE3	1.84	0.43
3:C:220:ARG:O	3:C:222:GLY:N	2.52	0.43
4:D:293:ILE:O	4:D:330:LEU:HD21	2.18	0.43
2:B:291:GLY:N	2:B:292:PRO:CD	2.81	0.43
3:C:282:GLY:HA2	3:C:383:MET:HA	2.00	0.43
4:D:22:PHE:HB3	4:D:25:THR:HB	2.01	0.43
1:A:336:ILE:HA	9:A:2376:HOH:O	2.18	0.42
3:C:7:ILE:HG21	3:C:362:LEU:CD1	2.49	0.42
4:D:38:VAL:HG23	4:D:257:LEU:HB2	2.01	0.42
4:D:195:PHE:HB2	9:D:2110:HOH:O	2.19	0.42
1:A:152:PHE:CZ	2:B:72:MET:HG3	2.54	0.42
2:B:138:LYS:HD3	2:B:140:ILE:HD11	2.01	0.42
3:C:357:ILE:HD11	3:C:375:ALA:HB1	2.00	0.42
3:C:24:ASN:O	3:C:26:PRO:HD3	2.18	0.42
4:D:25:THR:HA	4:D:26:PRO:HD3	1.87	0.42
3:C:68:ARG:HG2	7:C:1396:CL:CL	2.57	0.42
3:C:327:ASN:C	3:C:329:ASP:H	2.28	0.42
7:C:1396:CL:CL	4:D:383:MET:HE2	2.57	0.42
4:D:383:MET:N	9:D:2184:HOH:O	2.52	0.42
1:A:88:LEU:HD12	1:A:380:GLY:O	2.19	0.42
4:D:78:GLN:NE2	9:D:2055:HOH:O	2.53	0.42
4:D:89:CSO:O	4:D:377:LEU:HD22	2.20	0.42
4:D:93:LEU:HD11	4:D:387:MET:CB	2.50	0.42
4:D:365:MET:HA	9:D:2182:HOH:O	2.19	0.42
4:D:207:ARG:HH11	4:D:208:LYS:H	1.66	0.42
1:A:344:ILE:HG22	9:A:2215:HOH:O	2.20	0.42
2:B:233:PRO:HB2	2:B:236:ASP:O	2.20	0.42
3:C:112:VAL:HG12	3:C:112:VAL:O	2.19	0.42
3:C:274:ARG:HH21	3:C:392:LEU:HD11	1.84	0.42
9:C:2035:HOH:O	4:D:86:ASN:O	2.21	0.42
4:D:28:HIS:HA	4:D:116:MET:SD	2.60	0.42
1:A:190:GLN:OE1	1:A:221:HIS:HE1	2.02	0.42
3:C:155:TYR:HE1	3:C:160:THR:HG22	1.85	0.42
2:B:124:HIS:HA	2:B:140:ILE:O	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:6:VAL:HG12	3:C:274:ARG:HD3	2.01	0.41
4:D:5:ILE:HD13	4:D:260:SER:HA	2.00	0.41
3:C:292:PRO:HB3	3:C:376:THR:OG1	2.20	0.41
4:D:325:ALA:HB2	9:D:2163:HOH:O	2.21	0.41
3:C:175:GLN:HE22	3:C:240:THR:CG2	2.33	0.41
3:C:224:THR:C	3:C:226:ASP:N	2.74	0.41
4:D:85:MET:HE2	4:D:85:MET:HB2	1.88	0.41
4:D:118:SER:OG	4:D:121:MET:HB2	2.21	0.41
4:D:333:ASP:HA	4:D:334:PRO:HD2	1.88	0.41
2:B:168:TRP:CD1	2:B:168:TRP:N	2.88	0.41
3:C:181:ALA:O	3:C:185:LYS:HG3	2.20	0.41
3:C:293:ILE:O	3:C:297:ARG:HG3	2.20	0.41
4:D:313:VAL:HA	4:D:374:LEU:O	2.20	0.41
2:B:7:ILE:HA	2:B:258[A]:LEU:HD13	2.02	0.41
2:B:272:LEU:HD12	2:B:366[A]:LYS:HD3	2.02	0.41
3:C:6:VAL:CG1	3:C:274:ARG:HD3	2.50	0.41
3:C:15:VAL:HG11	3:C:347:GLY:HA3	2.02	0.41
3:C:53:ILE:HD12	3:C:111:ILE:HG21	2.03	0.41
4:D:5:ILE:HD12	4:D:103:ILE:HB	2.02	0.41
4:D:389:ILE:HD12	4:D:389:ILE:N	2.35	0.41
3:C:78:GLN:HG3	3:C:79:GLU:CD	2.45	0.41
2:B:52:VAL:O	2:B:82:ALA:HA	2.21	0.41
3:C:282:GLY:O	4:D:79:GLU:HA	2.21	0.41
4:D:17:SER:OG	4:D:217:GLU:HG3	2.21	0.41
4:D:300:LEU:HD13	4:D:307:ILE:CG1	2.50	0.41
3:C:25:THR:HG21	3:C:30:LEU:CD2	2.50	0.41
3:C:51:GLU:HG3	3:C:81:THR:O	2.20	0.41
3:C:66:PRO:O	3:C:67:ALA:C	2.61	0.41
4:D:33:THR:HG21	4:D:202:PHE:CD1	2.54	0.41
4:D:102:GLN:NE2	9:D:2063:HOH:O	2.54	0.41
4:D:187:GLU:HG3	4:D:221:HIS:HA	2.02	0.41
4:D:205:LYS:HA	4:D:210:ASP:OD1	2.20	0.41
4:D:320:ALA:O	4:D:324:CYS:SG	2.75	0.41
4:D:220:ARG:HG2	4:D:220:ARG:H	1.74	0.41
4:D:322:GLN:HE21	4:D:322:GLN:HB2	1.68	0.41
1:A:55:GLY:HA3	1:A:91:SER:HB3	2.03	0.40
1:A:358:LEU:HD22	1:A:362:LEU:HG	2.03	0.40
3:C:374:LEU:HD23	3:C:374:LEU:HA	1.74	0.40
4:D:26:PRO:O	4:D:27:ALA:C	2.64	0.40
4:D:35:ILE:HD11	4:D:54:LEU:HD11	2.04	0.40
4:D:38:VAL:CG2	4:D:257:LEU:HB2	2.50	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:D:356:ARG:NH1	9:D:2173:HOH:O	2.31	0.40
1:A:274:ARG:HD3	9:A:2310:HOH:O	2.21	0.40
1:A:298:LYS:HD3	5:A:1401:SO4:O3	2.20	0.40
3:C:7:ILE:HG21	3:C:362:LEU:HD13	2.02	0.40
3:C:64:GLN:HE22	4:D:157:MET:CE	2.35	0.40
4:D:31:GLY:O	4:D:35:ILE:HD12	2.21	0.40
1:A:276:VAL:HG22	1:A:388:CYS:CB	2.52	0.40
2:B:217:GLU:HG2	9:B:2261:HOH:O	2.21	0.40
3:C:10:ALA:C	3:C:38:VAL:HG22	2.46	0.40
3:C:340[C]:ASN:HD21	3:C:360:THR:CG2	2.35	0.40
4:D:11:ALA:HB3	4:D:38:VAL:HG12	2.02	0.40
4:D:285:PRO:HB2	9:D:2087:HOH:O	2.21	0.40
2:B:88:LEU:HB2	2:B:379:ILE:HG23	2.02	0.40
6:B:1401:COA:O9P	6:B:1401:COA:H141	2.22	0.40
3:C:7:ILE:HG12	3:C:258:LEU:CD1	2.51	0.40
3:C:387:MET:HG2	3:C:388:CYS:N	2.37	0.40
4:D:39:LEU:HD12	4:D:44:VAL:O	2.21	0.40
4:D:68:ARG:O	4:D:72:MET:HG2	2.21	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	391/392 (100%)	376 (96%)	15 (4%)	0	100	100
2	B	392/392 (100%)	378 (96%)	13 (3%)	1 (0%)	36	25
3	C	389/392 (99%)	350 (90%)	36 (9%)	3 (1%)	16	6
4	D	389/392 (99%)	352 (90%)	31 (8%)	6 (2%)	8	2
All	All	1561/1568 (100%)	1456 (93%)	95 (6%)	10 (1%)	21	11

All (10) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
4	D	140	ILE
4	D	141	ASP
4	D	330	LEU
4	D	350	ILE
2	B	131	GLY
3	C	221	HIS
3	C	350	ILE
4	D	142	THR
4	D	236	ASP
3	C	369	GLY

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	279/277 (101%)	266 (95%)	13 (5%)	23	11
2	B	280/276 (101%)	269 (96%)	11 (4%)	28	16
3	C	277/278 (100%)	259 (94%)	18 (6%)	15	5
4	D	277/277 (100%)	259 (94%)	18 (6%)	15	5
All	All	1113/1108 (100%)	1053 (95%)	60 (5%)	20	8

All (60) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	4	SER
1	A	39	LEU
1	A	110	ILE
1	A	132	VAL
1	A	133	LYS
1	A	191	LYS
1	A	237	LYS
1	A	272	LEU
1	A	276	VAL
1	A	322	GLN
1	A	332	TRP
1	A	358	LEU

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Mol	Chain	Res	Type
1	A	392	LEU
2	B	39	LEU
2	B	138	LYS
2	B	207	ARG
2	B	272	LEU
2	B	276	VAL
2	B	322	GLN
2	B	332	TRP
2	B	361	LEU
2	B	366[A]	LYS
2	B	366[B]	LYS
2	B	371	ARG
3	C	5	ILE
3	C	34	VAL
3	C	39	LEU
3	C	40	GLU
3	C	111	ILE
3	C	112	VAL
3	C	207	ARG
3	C	232	ARG
3	C	251	ASP
3	C	272	LEU
3	C	276	VAL
3	C	298	LYS
3	C	322	GLN
3	C	358	LEU
3	C	359	ASN
3	C	361	LEU
3	C	374	LEU
3	C	377	LEU
4	D	6	VAL
4	D	19	ASN
4	D	33	THR
4	D	34	VAL
4	D	38	VAL
4	D	76	VAL
4	D	187	GLU
4	D	199	ILE
4	D	258	LEU
4	D	272	LEU
4	D	276	VAL
4	D	293	ILE

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Mol	Chain	Res	Type
4	D	298	LYS
4	D	322	GLN
4	D	336	ILE
4	D	350	ILE
4	D	358	LEU
4	D	359	ASN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (18) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	78	GLN
1	A	169	GLN
1	A	184	ASN
1	A	221	HIS
2	B	78	GLN
2	B	175	GLN
2	B	184	ASN
2	B	221	HIS
2	B	316	ASN
3	C	78	GLN
3	C	175	GLN
3	C	184	ASN
3	C	322	GLN
4	D	19	ASN
4	D	24	ASN
4	D	78	GLN
4	D	163	ASN
4	D	184	ASN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

4 non-standard protein/DNA/RNA residues 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	$\# Z > 2$
1	CSD	A	378	1	4,7,8	10.08	1 (25%)	1,8,10	1.97	0
2	CSD	B	378	2	4,7,8	9.80	1 (25%)	1,8,10	2.44	1 (100%)
2	CSO	B	89	2	3,6,7	0.60	0	1,6,8	1.65	0
4	CSO	D	89	4	3,6,7	0.62	0	1,6,8	0.18	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
1	CSD	A	378	1	-	0/2/6/8	-
2	CSD	B	378	2	-	0/2/6/8	-
2	CSO	B	89	2	-	0/1/5/7	-
4	CSO	D	89	4	-	1/1/5/7	-

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	378	CSD	OD1-SG	20.12	1.65	1.47
2	B	378	CSD	OD1-SG	19.56	1.65	1.47

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	378	CSD	OD1-SG-CB	2.44	110.10	105.60

There are no chirality outliers.

All (1) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	D	89	CSO	N-CA-CB-SG

There are no ring outliers.

4 monomers are involved in 6 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	A	378	CSD	1	0
2	B	378	CSD	2	0
2	B	89	CSO	2	0
4	D	89	CSO	1	0

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 33 ligands modelled in this entry, 6 are monoatomic - leaving 27 for Mogul analysis.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
5	SO4	C	1399	-	4,4,4	0.24	0	6,6,6	0.06	0
5	SO4	A	1394	-	4,4,4	0.26	0	6,6,6	0.17	0
5	SO4	D	1397	-	4,4,4	0.23	0	6,6,6	0.08	0
5	SO4	B	1402	-	4,4,4	0.23	0	6,6,6	0.10	0
5	SO4	D	1395	-	4,4,4	0.25	0	6,6,6	0.05	0
5	SO4	C	1398	-	4,4,4	0.24	0	6,6,6	0.08	0
5	SO4	B	1399	-	4,4,4	0.24	0	6,6,6	0.07	0
5	SO4	D	1396	-	4,4,4	0.22	0	6,6,6	0.13	0
5	SO4	B	1395	-	4,4,4	0.26	0	6,6,6	0.11	0
5	SO4	B	1396	-	4,4,4	0.24	0	6,6,6	0.11	0
5	SO4	B	1403	-	4,4,4	0.23	0	6,6,6	0.10	0
5	SO4	B	1398	-	4,4,4	0.25	0	6,6,6	0.18	0
5	SO4	A	1398	-	4,4,4	0.24	0	6,6,6	0.09	0
5	SO4	A	1401	-	4,4,4	0.23	0	6,6,6	0.23	0
5	SO4	B	1397	-	4,4,4	0.23	0	6,6,6	0.12	0
5	SO4	C	1393	-	4,4,4	0.23	0	6,6,6	0.06	0
5	SO4	C	1397	-	4,4,4	0.24	0	6,6,6	0.06	0
5	SO4	D	1394	-	4,4,4	0.24	0	6,6,6	0.08	0
6	COA	B	1401	-	47,50,50	1.68	8 (17%)	69,75,75	1.73	10 (14%)
5	SO4	B	1404	-	4,4,4	0.24	0	6,6,6	0.06	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
5	SO4	A	1399	-	4,4,4	0.24	0	6,6,6	0.07	0
5	SO4	A	1395	-	4,4,4	0.24	0	6,6,6	0.08	0
6	COA	A	1402	-	47,50,50	1.64	7 (14%)	69,75,75	1.59	10 (14%)
5	SO4	A	1400	-	4,4,4	0.26	0	6,6,6	0.14	0
5	SO4	A	1403	-	4,4,4	0.23	0	6,6,6	0.08	0
5	SO4	A	1396	-	4,4,4	0.30	0	6,6,6	0.11	0
5	SO4	A	1397	-	4,4,4	0.23	0	6,6,6	0.05	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
6	COA	B	1401	-	-	7/48/64/64	0/3/3/3
6	COA	A	1402	-	-	4/48/64/64	0/3/3/3

All (15) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
6	B	1401	COA	P3B-O7A	6.42	1.70	1.50
6	A	1402	COA	P3B-O7A	6.42	1.70	1.50
6	B	1401	COA	P3B-O8A	4.21	1.70	1.54
6	A	1402	COA	P3B-O8A	4.12	1.70	1.54
6	B	1401	COA	C5A-C4A	3.91	1.46	1.39
6	A	1402	COA	C5A-C4A	3.49	1.45	1.39
6	B	1401	COA	P2A-O5A	3.21	1.70	1.55
6	A	1402	COA	P2A-O5A	3.19	1.70	1.55
6	B	1401	COA	P1A-O2A	3.17	1.70	1.55
6	B	1401	COA	C5A-N7A	-3.06	1.33	1.39
6	A	1402	COA	P1A-O2A	3.04	1.69	1.55
6	A	1402	COA	C5A-N7A	-2.62	1.34	1.39
6	A	1402	COA	C5A-C6A	2.42	1.47	1.41
6	B	1401	COA	C5A-C6A	2.24	1.47	1.41
6	B	1401	COA	C4A-N9A	-2.13	1.33	1.37

All (20) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
6	B	1401	COA	C5A-C4A-N3A	-6.13	118.28	126.72
6	B	1401	COA	N3A-C4A-N9A	5.80	137.03	127.17

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
6	A	1402	COA	C5A-C4A-N3A	-5.72	118.84	126.72
6	A	1402	COA	N3A-C4A-N9A	5.62	136.73	127.17
6	B	1401	COA	C7P-C6P-C5P	-4.66	104.63	112.39
6	A	1402	COA	C4A-N9A-C8A	3.54	109.45	105.74
6	A	1402	COA	C2A-N3A-C4A	3.28	119.85	111.83
6	A	1402	COA	N3A-C2A-N1A	-3.22	123.71	128.58
6	B	1401	COA	C2A-N3A-C4A	3.17	119.58	111.83
6	B	1401	COA	C7P-N8P-C9P	-3.17	116.86	122.55
6	B	1401	COA	C6P-C7P-N8P	2.98	118.34	112.00
6	A	1402	COA	C7P-N8P-C9P	-2.98	117.20	122.55
6	B	1401	COA	C4A-N9A-C8A	2.93	108.81	105.74
6	B	1401	COA	C3P-N4P-C5P	-2.89	117.45	122.82
6	A	1402	COA	C7P-C6P-C5P	-2.63	108.02	112.39
6	B	1401	COA	N3A-C2A-N1A	-2.44	124.89	128.58
6	A	1402	COA	C6P-C7P-N8P	2.44	117.19	112.00
6	A	1402	COA	N9A-C8A-N7A	-2.30	110.67	113.94
6	A	1402	COA	C2A-N1A-C6A	2.30	122.51	118.73
6	B	1401	COA	C6P-C5P-N4P	2.18	120.31	116.34

There are no chirality outliers.

All (11) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
6	A	1402	COA	C2P-C3P-N4P-C5P
6	B	1401	COA	C5B-O5B-P1A-O1A
6	B	1401	COA	C5B-O5B-P1A-O2A
6	B	1401	COA	C5B-O5B-P1A-O3A
6	B	1401	COA	O4B-C4B-C5B-O5B
6	B	1401	COA	C3B-C4B-C5B-O5B
6	A	1402	COA	S1P-C2P-C3P-N4P
6	B	1401	COA	S1P-C2P-C3P-N4P
6	A	1402	COA	CCP-O6A-P2A-O4A
6	A	1402	COA	P1A-O3A-P2A-O4A
6	B	1401	COA	C3B-O3B-P3B-O7A

There are no ring outliers.

9 monomers are involved in 23 short contacts:

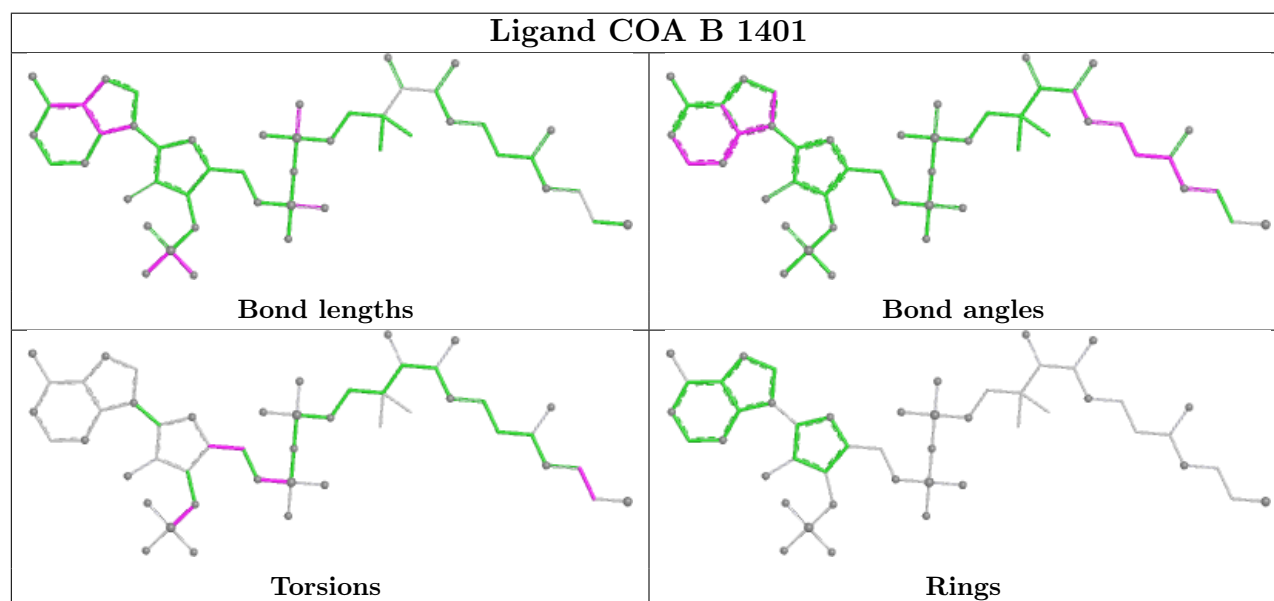
Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	A	1394	SO4	1	0
5	D	1397	SO4	1	0

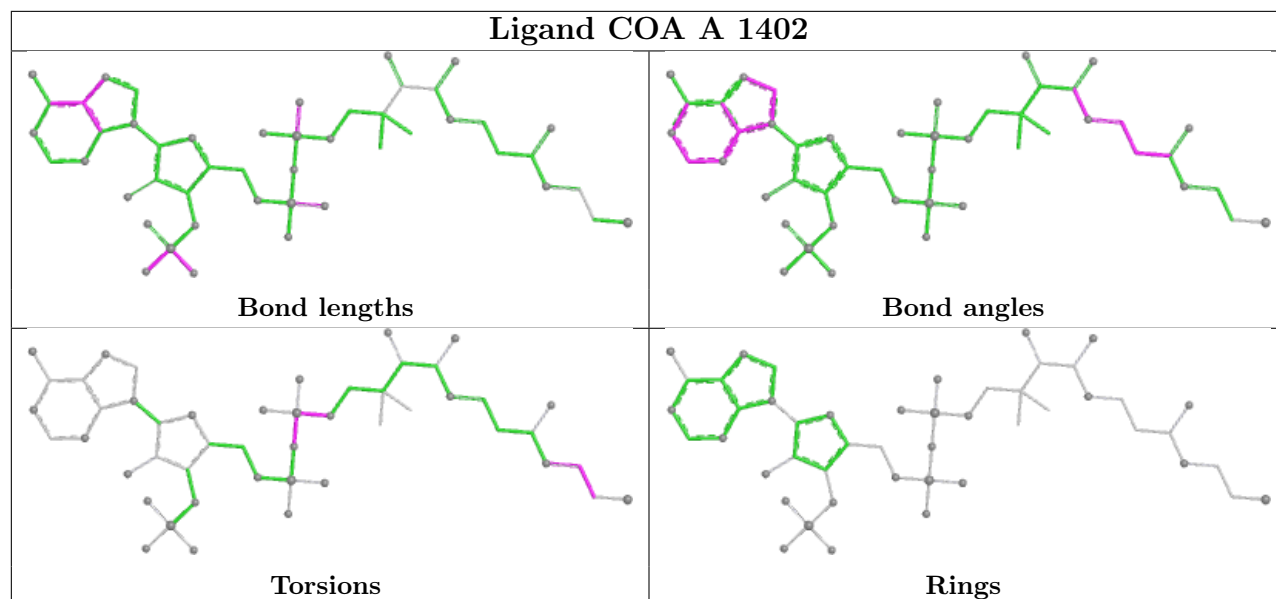
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Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	D	1396	SO4	1	0
5	B	1398	SO4	2	0
5	A	1401	SO4	7	0
5	D	1394	SO4	3	0
6	B	1401	COA	6	0
6	A	1402	COA	1	0
5	A	1400	SO4	1	0

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





5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Fit of model and data [i](#)

6.1 Protein, DNA and RNA chains [i](#)

In the following table, the column labelled ‘#RSRZ> 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95th percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q< 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	A	388/392 (98%)	-1.27	1 (0%) 90 90	5, 13, 33, 69	5 (1%)
2	B	387/392 (98%)	-1.27	0 100 100	4, 13, 31, 79	7 (1%)
3	C	389/392 (99%)	1.16	66 (16%) 4 3	23, 65, 100, 125	1 (0%)
4	D	388/392 (98%)	0.84	57 (14%) 6 4	20, 60, 118, 148	3 (0%)
All	All	1552/1568 (98%)	-0.13	124 (7%) 18 16	4, 37, 97, 148	16 (1%)

All (124) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
3	C	299	ALA	4.9
3	C	315	ALA	4.7
4	D	330	LEU	4.5
4	D	325	ALA	3.8
4	D	367	ARG	3.8
3	C	276	VAL	3.8
3	C	170	LEU	3.7
3	C	336	ILE	3.7
3	C	5	ILE	3.6
4	D	262	ALA	3.6
4	D	331	GLY	3.6
3	C	325	ALA	3.6
4	D	269	ILE	3.6
3	C	113	ALA	3.5
3	C	193	GLY	3.5
3	C	305	TRP	3.4
4	D	326	VAL	3.4
4	D	186	ALA	3.4
4	D	229	ALA	3.4
3	C	363	PHE	3.4
4	D	370	ALA	3.4

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Mol	Chain	Res	Type	RSRZ
3	C	389	ILE	3.3
4	D	179	ALA	3.3
4	D	362	LEU	3.2
3	C	345	ALA	3.2
3	C	6	VAL	3.2
3	C	107	ASP	3.2
1	A	132	VAL	3.1
4	D	310	LEU	3.1
4	D	358	LEU	3.1
3	C	307	ILE	3.1
3	C	275	ILE	3.0
3	C	108	ALA	3.0
4	D	188	ALA	3.0
4	D	170	LEU	3.0
4	D	168	TRP	3.0
4	D	392	LEU	2.9
3	C	318	ALA	2.9
4	D	209	GLY	2.9
3	C	353	SER	2.9
4	D	332	TRP	2.9
3	C	294	PRO	2.8
3	C	180	VAL	2.8
4	D	228	MET	2.8
3	C	312	LEU	2.8
4	D	233	PRO	2.8
3	C	303	ALA	2.8
4	D	8	ALA	2.7
4	D	206	GLY	2.7
4	D	388	CYS	2.7
4	D	334	PRO	2.6
3	C	259	MET	2.6
3	C	313	VAL	2.6
4	D	260	SER	2.6
3	C	371	ARG	2.6
3	C	112	VAL	2.6
4	D	315	ALA	2.6
4	D	339	VAL	2.6
4	D	327	ASN	2.6
3	C	304	GLY	2.5
3	C	186	ALA	2.5
3	C	272	LEU	2.5
4	D	83	TRP	2.5

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Mol	Chain	Res	Type	RSRZ
3	C	10	ALA	2.5
3	C	331	GLY	2.5
3	C	278	TRP	2.5
3	C	370	ALA	2.5
4	D	369	GLY	2.4
4	D	108	ALA	2.4
3	C	300	LEU	2.4
4	D	223	ALA	2.4
4	D	368	ARG	2.4
3	C	106	GLY	2.4
3	C	195	PHE	2.4
3	C	333	ASP	2.4
4	D	343	ALA	2.4
4	D	164	VAL	2.4
4	D	185	LYS	2.4
3	C	360	THR	2.3
4	D	219	ILE	2.3
3	C	158	GLY	2.3
3	C	314	GLU	2.3
4	D	303	ALA	2.3
4	D	275	ILE	2.3
4	D	389	ILE	2.3
4	D	192	ASP	2.3
4	D	270	GLN	2.3
4	D	231	LEU	2.3
3	C	321	ALA	2.3
3	C	348	ALA	2.3
4	D	371	ARG	2.3
4	D	180	VAL	2.3
3	C	4	SER	2.2
3	C	372	LYS	2.2
3	C	109	SER	2.2
3	C	296	SER	2.2
3	C	391	SER	2.2
4	D	193	GLY	2.2
3	C	334	PRO	2.2
3	C	80	ALA	2.2
4	D	385	VAL	2.2
4	D	360	THR	2.2
4	D	264	ALA	2.2
4	D	266	ARG	2.2
3	C	152	PHE	2.1

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Mol	Chain	Res	Type	RSRZ
3	C	211	ILE	2.1
4	D	5	ILE	2.1
4	D	99	GLY	2.1
3	C	364	GLU	2.1
4	D	340	ASN	2.1
3	C	222	GLY	2.1
3	C	339	VAL	2.1
3	C	231	LEU	2.1
4	D	225	LEU	2.1
3	C	342	GLY	2.1
3	C	258	LEU	2.1
3	C	324	CYS	2.1
4	D	45	ALA	2.1
3	C	105	THR	2.0
3	C	271	PRO	2.0
3	C	385	VAL	2.0
3	C	115	GLY	2.0
3	C	359	ASN	2.0
3	C	373	GLY	2.0

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

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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
4	CSO	D	89	7/8	0.97	0.08	36,42,63,77	0
2	CSO	B	89	7/8	0.99	0.04	4,10,34,73	0
2	CSD	B	378	8/9	1.00	0.04	4,9,24,109	0
1	CSD	A	378	8/9	1.00	0.03	7,13,23,32	0

6.3 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

6.4 Ligands [i](#)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum,

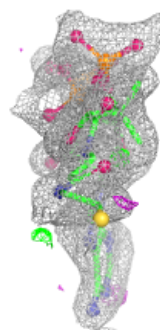
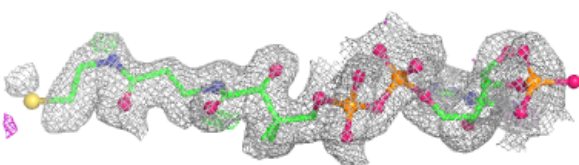
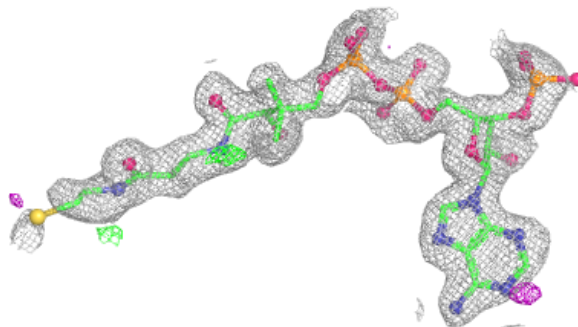
median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
5	SO4	D	1395	5/5	0.90	0.09	89,89,90,91	0
5	SO4	C	1398	5/5	0.93	0.09	96,97,97,98	0
5	SO4	B	1403	5/5	0.93	0.09	86,87,88,89	0
5	SO4	B	1404	5/5	0.94	0.10	77,77,79,82	0
5	SO4	A	1403	5/5	0.95	0.09	94,94,95,98	0
5	SO4	C	1393	5/5	0.95	0.11	108,108,109,109	0
5	SO4	C	1397	5/5	0.95	0.07	84,84,85,86	0
5	SO4	B	1402	5/5	0.95	0.07	75,75,76,76	0
5	SO4	D	1394	5/5	0.95	0.11	63,70,71,75	0
5	SO4	A	1398	5/5	0.95	0.09	71,78,79,81	0
5	SO4	D	1397	5/5	0.95	0.18	120,121,122,123	0
5	SO4	A	1400	5/5	0.96	0.09	60,60,69,75	0
5	SO4	B	1399	5/5	0.96	0.06	78,78,80,81	0
5	SO4	C	1399	5/5	0.96	0.08	90,91,94,94	0
8	NA	C	1395	1/1	0.96	0.09	60,60,60,60	0
5	SO4	A	1395	5/5	0.97	0.07	46,54,58,59	0
5	SO4	D	1396	5/5	0.97	0.06	52,59,70,71	0
5	SO4	A	1399	5/5	0.97	0.10	95,99,101,101	0
7	CL	D	1399	1/1	0.97	0.12	80,80,80,80	0
5	SO4	B	1397	5/5	0.97	0.07	66,66,71,73	0
5	SO4	A	1397	5/5	0.98	0.06	47,48,56,56	0
5	SO4	B	1398	5/5	0.98	0.05	45,51,56,57	0
6	COA	A	1402	48/48	0.98	0.06	21,32,63,131	0
6	COA	B	1401	48/48	0.98	0.05	20,36,80,112	0
5	SO4	B	1395	5/5	0.98	0.05	47,50,52,55	0
5	SO4	B	1396	5/5	0.98	0.06	45,49,57,63	0
8	NA	D	1398	1/1	0.98	0.04	38,38,38,38	0
7	CL	C	1396	1/1	0.99	0.05	58,58,58,58	0
5	SO4	A	1396	5/5	0.99	0.04	31,39,50,57	0
8	NA	C	1394	1/1	0.99	0.04	34,34,34,34	0
5	SO4	A	1401	5/5	0.99	0.07	28,44,49,50	0
5	SO4	A	1394	5/5	0.99	0.03	41,43,48,48	0
7	CL	B	1400	1/1	1.00	0.04	28,28,28,28	0

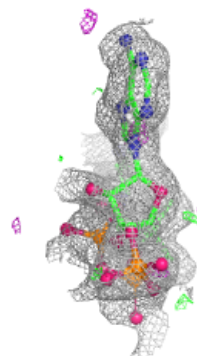
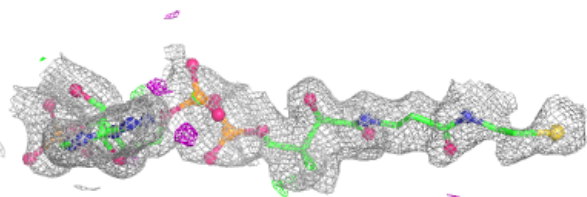
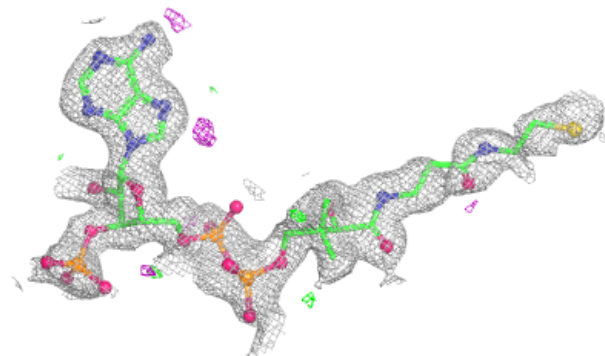
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation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

Electron density around COA A 1402:

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

**Electron density around COA B 1401:**

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



6.5 Other polymers [i](#)

There are no such residues in this entry.