



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 06:17 AM GMT

PDB ID : 2WL5
Title : BIOSYNTHETIC THIOLASE FROM Z. RAMIGERA. COMPLEX OF THE
H348N 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
<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) : 1.9-1692
EDS : rb-20026688
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)
Refmac : 5.8.0135
CCP4 : 6.5.0
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : trunk26865

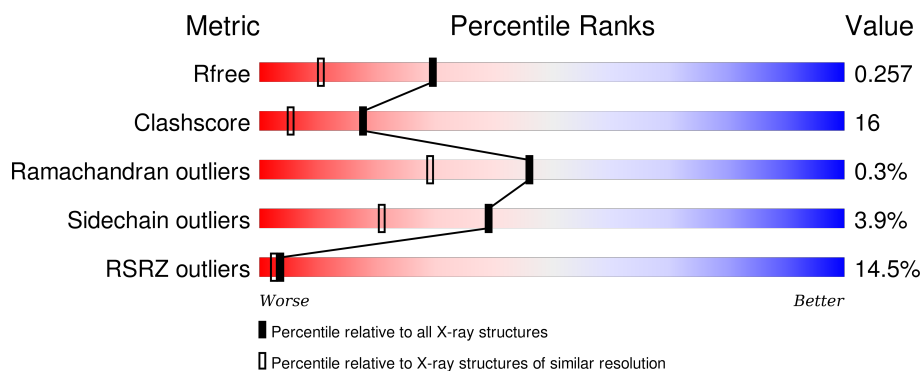
1 Overall quality at a glance ⓘ

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 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}	91344	4533 (1.80-1.80)
Clashscore	102246	5383 (1.80-1.80)
Ramachandran outliers	100387	5320 (1.80-1.80)
Sidechain outliers	100360	5319 (1.80-1.80)
RSRZ outliers	91569	4547 (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 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.

Mol	Chain	Length	Quality of chain
1	A	392	<div> <div>83%</div> <div>15%</div> <div>..</div> </div>
1	B	392	<div> <div>85%</div> <div>12%</div> <div>..</div> </div>
2	C	392	<div> <div>24%</div> <div>59%</div> <div>39%</div> <div>..</div> </div>
2	D	392	<div> <div>31%</div> <div>65%</div> <div>33%</div> <div>..</div> </div>

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 crite-

ria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
3	SO4	B	1397	-	-	-	X
4	DNO	A	1398	X	-	-	-
4	DNO	C	1397	X	-	-	X
4	DNO	C	1398	X	-	-	-
4	DNO	C	1399	X	-	-	-
6	NA	B	1398	-	-	-	X

2 Entry composition

There are 8 unique types of molecules in this entry. The entry contains 12780 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	8	0
			2856	1783	513	539	21			
1	B	389	Total	C	N	O	S	0	7	0
			2850	1775	511	541	23			

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	129	ARG	ALA	SEE REMARK 999	UNP P07097
A	348	ASN	HIS	ENGINEERED MUTATION	UNP P07097
B	129	ARG	ALA	SEE REMARK 999	UNP P07097
B	348	ASN	HIS	ENGINEERED MUTATION	UNP P07097

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	C	389	Total	C	N	O	S	0	1	0
			2815	1748	508	538	21			
2	D	389	Total	C	N	O	S	0	0	0
			2811	1744	508	538	21			

There are 4 discrepancies between the modelled and reference sequences:

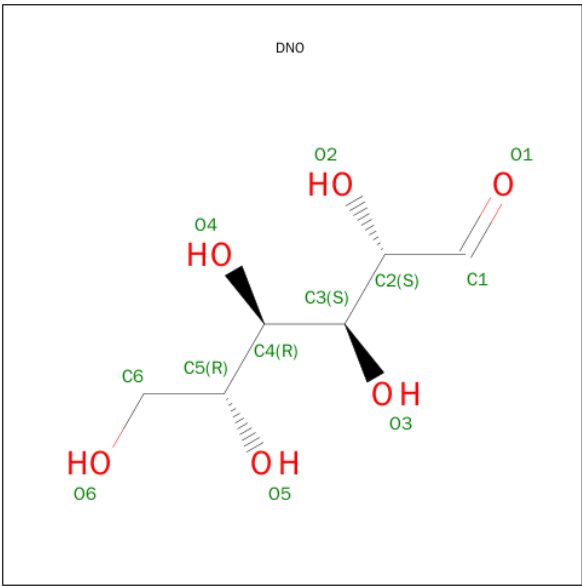
Chain	Residue	Modelled	Actual	Comment	Reference
C	129	ARG	ALA	SEE REMARK 999	UNP P07097
C	348	ASN	HIS	ENGINEERED MUTATION	UNP P07097
D	129	ARG	ALA	SEE REMARK 999	UNP P07097
D	348	ASN	HIS	ENGINEERED MUTATION	UNP P07097

- Molecule 3 is SULFATE ION (three-letter code: SO4) (formula: O₄S).



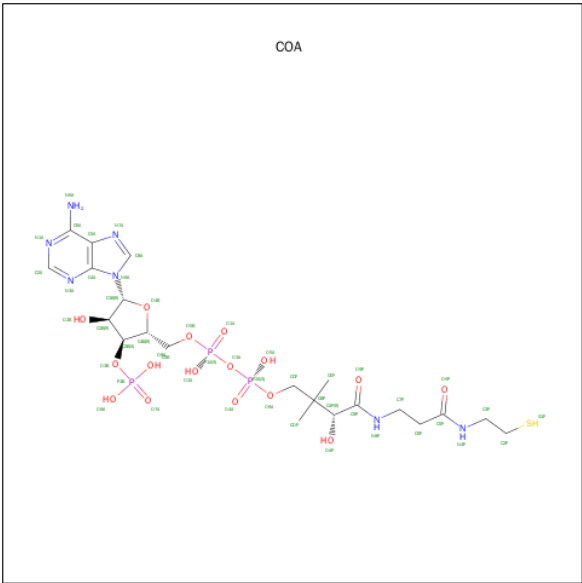
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	O	S	0	0
			5	4	1		
3	A	1	Total	O	S	0	0
			5	4	1		
3	A	1	Total	O	S	0	0
			5	4	1		
3	A	1	Total	O	S	0	0
			5	4	1		
3	B	1	Total	O	S	0	0
			5	4	1		
3	B	1	Total	O	S	0	0
			5	4	1		
3	B	1	Total	O	S	0	0
			5	4	1		
3	B	1	Total	O	S	0	0
			5	4	1		
3	C	1	Total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

- Molecule 4 is SUGAR (D-MANNOSE) (three-letter code: DNO) (formula: C₆H₁₂O₆).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	A	1	Total	C	O	0	0
			12	6	6		
4	C	1	Total	C	O	0	0
			12	6	6		
4	C	1	Total	C	O	0	0
			12	6	6		
4	C	1	Total	C	O	0	0
			12	6	6		

- Molecule 5 is COENZYME A (three-letter code: COA) (formula: C₂₁H₃₆N₇O₁₆P₃S).



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

- Molecule 6 is SODIUM ION (three-letter code: NA) (formula: Na).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	B	1	Total	Na		
			1	1	0	0

- Molecule 7 is CHLORIDE ION (three-letter code: CL) (formula: Cl).

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

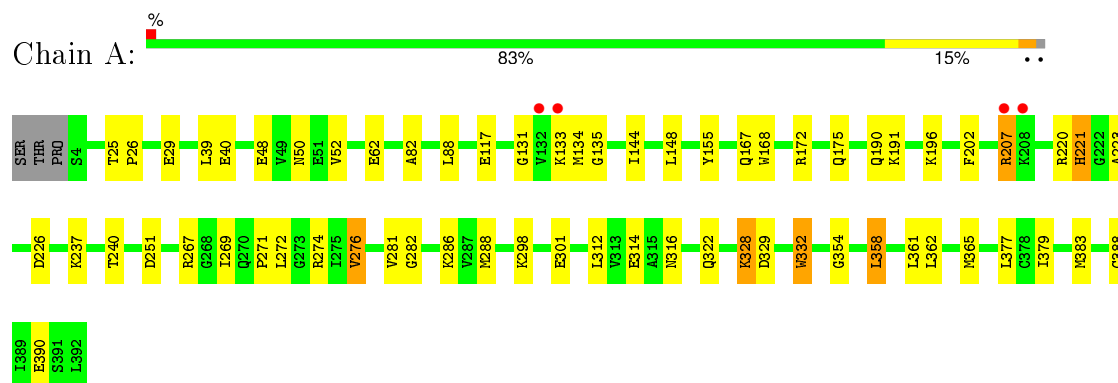
- Molecule 8 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
8	A	453	Total	O		
			453	453	0	0
8	B	479	Total	O		
			479	479	0	0
8	C	171	Total	O		
			171	171	0	0
8	D	129	Total	O		
			129	129	0	0

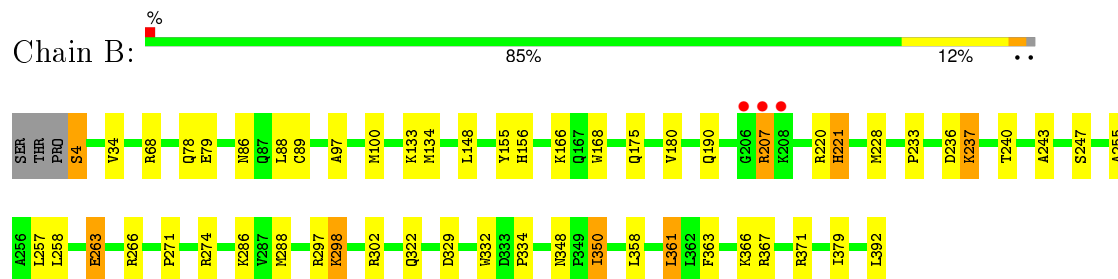
3 Residue-property plots

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 ($\text{RSRZ} > 2$). 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.

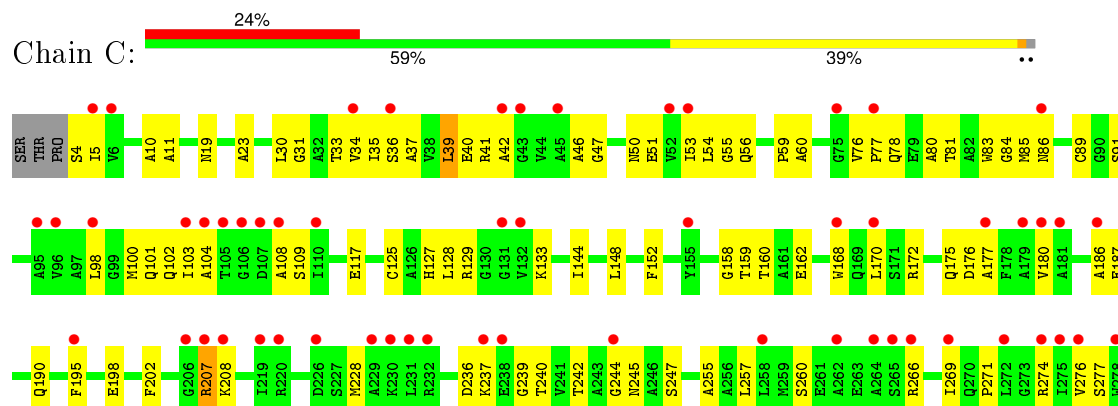
• Molecule 1: ACETYL-COA ACETYLTRANSFERASE

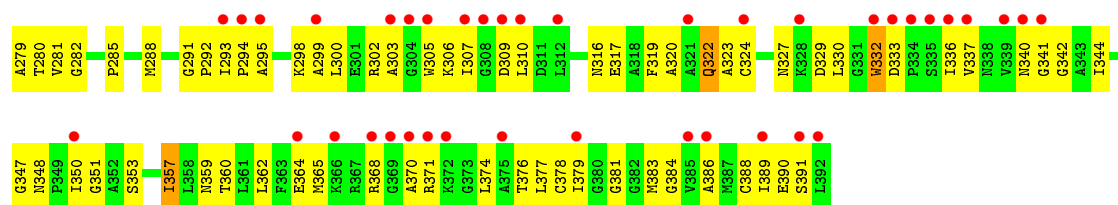


• Molecule 1: ACETYL-COA ACETYLTRANSFERASE

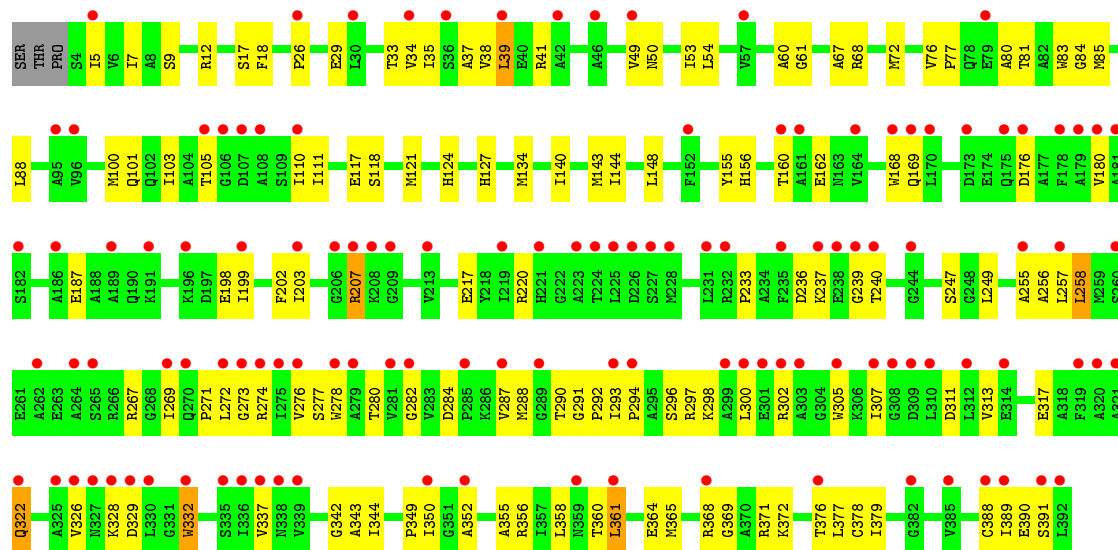


• Molecule 2: ACETYL-COA ACETYLTRANSFERASE





● Molecule 2: 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	84.70 Å 79.20 Å 153.00 Å 90.00° 92.50° 90.00°	Depositor
Resolution (Å)	19.39 – 1.80 19.39 – 1.80	Depositor EDS
% Data completeness (in resolution range)	98.6 (19.39-1.80) 86.6 (19.39-1.80)	Depositor EDS
R_{merge}	0.12	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.46 (at 1.80 Å)	Xtriage
Refinement program	PHENIX (PHENIX.REFINE)	Depositor
R, R_{free}	0.221 , 0.257 0.221 , 0.257	Depositor DCC
R_{free} test set	9226 reflections (5.26%)	DCC
Wilson B-factor (Å ²)	12.6	Xtriage
Anisotropy	0.115	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	(Not available) , (Not available)	EDS
Estimated twinning fraction	0.176 for h,-k,-l	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.36$, $\langle L^2 \rangle = 0.18$	Xtriage
Outliers	0 of 184510 reflections	Xtriage
F_o, F_c correlation	0.91	EDS
Total number of atoms	12780	wwPDB-VP
Average B, all atoms (Å ²)	36.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.88% 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, 0.375 respectively for untwinned datasets, and 0.333, 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: CSO, CL, NA, DNO, COA, 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	0.54	0/2912	0.67	0/3928
1	B	0.54	0/2900	0.69	3/3910 (0.1%)
2	C	0.27	0/2858	0.46	0/3859
2	D	0.26	0/2851	0.46	0/3849
All	All	0.43	0/11521	0.58	3/15546 (0.0%)

There are no bond length outliers.

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	367	ARG	NE-CZ-NH2	-7.13	116.73	120.30
1	B	361	LEU	CA-CB-CG	5.37	127.65	115.30
1	B	367	ARG	NE-CZ-NH1	5.27	122.93	120.30

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	2856	0	2910	73	0
1	B	2850	0	2888	51	0
2	C	2815	0	2827	143	0
2	D	2811	0	2818	113	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	A	20	0	0	0	0
3	B	25	0	0	0	0
3	C	20	0	0	0	0
3	D	5	0	0	0	0
4	A	12	0	12	0	0
4	C	36	0	36	2	0
5	A	48	0	32	5	0
5	B	48	0	32	3	0
6	B	1	0	0	0	0
7	B	1	0	0	0	0
8	A	453	0	0	28	0
8	B	479	0	0	16	0
8	C	171	0	0	45	0
8	D	129	0	0	24	0
All	All	12780	0	11555	367	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 16.

All (367) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:207:ARG:HG2	1:A:207:ARG:HH11	1.10	1.14
1:A:207:ARG:H	1:A:207:ARG:HD3	1.29	0.97
2:C:274:ARG:HE	2:C:390:GLU:HG2	1.33	0.93
2:D:207:ARG:H	2:D:207:ARG:HD3	1.36	0.90
1:A:226:ASP:HB3	8:A:2448:HOH:O	1.74	0.88
2:C:388:CYS:HB2	8:C:2120:HOH:O	1.74	0.88
2:C:207:ARG:HD3	2:C:207:ARG:H	1.36	0.88
2:C:160:THR:HG21	8:C:2125:HOH:O	1.74	0.87
2:D:389:ILE:HG23	8:D:2095:HOH:O	1.75	0.86
2:C:125:CYS:SG	8:D:2021:HOH:O	2.30	0.83
2:C:305:TRP:CZ3	2:C:388:CYS:HB3	2.14	0.82
1:A:207:ARG:HG2	1:A:207:ARG:NH1	1.90	0.82
1:A:202:PHE:HZ	8:A:2049:HOH:O	1.63	0.82
2:C:5:ILE:HD13	2:C:100:MET:HG2	1.61	0.81
2:D:61:GLY:HA3	8:D:2021:HOH:O	1.83	0.79
2:C:168:TRP:HA	8:C:2078:HOH:O	1.83	0.79
1:B:207:ARG:HH11	1:B:207:ARG:HG2	1.46	0.79
2:C:247:SER:OG	2:C:348:ASN:HB2	1.83	0.78
2:C:293:ILE:HB	2:C:294:PRO:HD3	1.66	0.78

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:C:279:ALA:HB2	8:C:2121:HOH:O	1.83	0.77
2:C:379:ILE:HG12	8:C:2152:HOH:O	1.84	0.77
2:C:302:ARG:HD2	8:C:2121:HOH:O	1.83	0.77
2:D:49:VAL:HG13	8:D:2016:HOH:O	1.83	0.76
1:B:207:ARG:H	1:B:207:ARG:HH11	1.31	0.76
2:C:187:GLU:HA	8:C:2085:HOH:O	1.85	0.75
1:A:168:TRP:CH2	1:A:329:ASP:HB2	2.21	0.75
1:B:168:TRP:HH2	1:B:329:ASP:HB2	1.52	0.74
1:B:168:TRP:CH2	1:B:329:ASP:HB2	2.24	0.73
2:C:31:GLY:O	2:C:34[B]:VAL:HG12	1.88	0.73
1:A:196[A]:LYS:HD3	8:A:2121:HOH:O	1.89	0.73
2:C:180:VAL:HG22	8:C:2100:HOH:O	1.89	0.72
1:B:237:LYS:HD2	1:B:237:LYS:N	2.03	0.71
2:D:291:GLY:O	2:D:294:PRO:HD2	1.90	0.71
1:B:134:MET:HE2	2:C:144:ILE:HD11	1.73	0.71
1:A:301:GLU:HG3	8:A:2366:HOH:O	1.91	0.71
2:C:47:GLY:HA2	2:C:77:PRO:HG3	1.73	0.70
2:C:320:ALA:HA	8:C:2138:HOH:O	1.90	0.70
1:B:79:GLU:HB3	8:B:2139:HOH:O	1.91	0.69
1:A:175:GLN:HE22	1:A:240:THR:HG21	1.58	0.69
1:A:26:PRO:HB3	8:A:2085:HOH:O	1.91	0.69
1:A:207:ARG:CG	1:A:207:ARG:HH11	1.95	0.68
1:A:168:TRP:HH2	1:A:329:ASP:HB2	1.57	0.68
2:C:379:ILE:HB	2:C:383:MET:HB2	1.77	0.67
1:A:220[B]:ARG:NH1	8:A:2300:HOH:O	2.27	0.67
2:D:236:ASP:HB3	2:D:239:GLY:HA3	1.75	0.67
1:A:175:GLN:HE22	1:A:240:THR:CG2	2.08	0.67
1:B:243:ALA:HB1	8:B:2470:HOH:O	1.94	0.66
2:D:88:LEU:HB2	2:D:379:ILE:HG23	1.78	0.66
2:C:144:ILE:HD13	2:C:148:LEU:HD12	1.76	0.66
2:C:282:GLY:HA2	8:C:2155:HOH:O	1.96	0.65
2:C:317:GLU:CD	2:C:342:GLY:HA3	2.16	0.65
1:B:134:MET:CE	2:C:144:ILE:HD11	2.26	0.65
1:B:207:ARG:HG2	1:B:207:ARG:NH1	2.08	0.65
1:A:148:LEU:HD23	8:A:2198:HOH:O	1.96	0.65
2:D:35:ILE:O	2:D:38:VAL:HG22	1.96	0.65
2:C:128:LEU:O	8:C:2065:HOH:O	2.14	0.65
1:A:362:LEU:HD22	8:A:2344:HOH:O	1.97	0.64
2:C:91:SER:HB2	8:C:2029:HOH:O	1.96	0.64
2:C:81:THR:HG21	2:D:280:THR:HG23	1.77	0.64
2:C:330:LEU:HD12	2:C:332:TRP:CH2	2.33	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:C:236:ASP:HB3	2:C:239:GLY:HA3	1.79	0.64
2:D:207:ARG:HD3	2:D:207:ARG:N	2.12	0.63
5:A:1399:COA:H32	8:A:2198:HOH:O	1.96	0.63
2:C:383:MET:HG2	8:C:2155:HOH:O	1.96	0.62
1:A:358[B]:LEU:HD21	1:A:362:LEU:HD11	1.80	0.62
2:D:292:PRO:HD3	2:D:378:CYS:HB3	1.82	0.62
2:C:299:ALA:HA	8:C:2121:HOH:O	1.98	0.62
2:D:293:ILE:HB	2:D:294:PRO:HD3	1.81	0.62
2:D:33:THR:HG1	2:D:202:PHE:HD1	1.48	0.62
1:B:175:GLN:HE22	1:B:240:THR:CG2	2.13	0.62
2:C:5:ILE:HD11	2:C:104:ALA:HB2	1.82	0.61
2:C:293:ILE:HG23	2:C:330:LEU:HD21	1.83	0.61
1:B:371:ARG:HD2	8:B:2437:HOH:O	2.00	0.61
2:D:313:VAL:HB	2:D:337:VAL:HG22	1.82	0.61
2:D:34:VAL:CG1	2:D:255:ALA:HB3	2.31	0.61
2:C:228:MET:HB2	8:C:2100:HOH:O	2.01	0.60
2:C:292:PRO:HD3	8:C:2156:HOH:O	2.00	0.60
1:A:25:THR:HG23	8:A:2049:HOH:O	2.00	0.60
1:A:251:ASP:HA	8:A:2158:HOH:O	2.00	0.60
2:C:274:ARG:NE	2:C:390:GLU:HG2	2.13	0.60
1:A:196[A]:LYS:NZ	8:A:2268:HOH:O	2.33	0.60
2:D:290:THR:HB	8:D:2098:HOH:O	2.00	0.60
1:A:362:LEU:CD2	8:A:2344:HOH:O	2.50	0.60
1:B:156:HIS:HD2	4:C:1397:DNO:O2	1.84	0.60
1:B:263:GLU:OE1	1:B:266:ARG:NH2	2.35	0.60
1:B:220:ARG:HD2	8:B:2310:HOH:O	2.00	0.60
2:D:317:GLU:CD	2:D:342:GLY:HA3	2.22	0.59
1:B:297:ARG:NE	8:B:2379:HOH:O	2.34	0.59
1:A:62:GLU:CD	8:A:2085:HOH:O	2.40	0.59
1:A:117:GLU:HB3	8:A:2158:HOH:O	2.02	0.59
2:C:53:ILE:HD13	2:C:83:TRP:CZ2	2.38	0.59
1:A:281:VAL:HG13	8:B:2139:HOH:O	2.01	0.59
2:C:327:ASN:HD21	2:C:337:VAL:HG11	1.67	0.59
5:B:1399:COA:H8A	8:B:2470:HOH:O	2.03	0.58
2:C:277:SER:N	8:C:2120:HOH:O	2.35	0.58
2:C:364:GLU:O	2:C:368:ARG:HG2	2.03	0.58
2:C:152:PHE:CZ	2:D:72:MET:HG3	2.39	0.58
2:C:77:PRO:HA	4:C:1398:DNO:H5	1.86	0.58
2:D:356:ARG:NE	8:D:2115:HOH:O	2.36	0.57
2:D:198:GLU:OE1	2:D:360:THR:HA	2.03	0.57
2:D:276:VAL:CG1	2:D:388:CYS:HB2	2.34	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:D:100:MET:HE2	2:D:101:GLN:HG3	1.85	0.57
2:C:35:ILE:O	2:C:39:LEU:HD13	2.04	0.57
1:B:175:GLN:HE22	1:B:240:THR:HG21	1.70	0.57
1:B:298:LYS:HE2	1:B:302:ARG:HG3	1.87	0.57
2:C:362:LEU:HD21	2:C:389:ILE:HG21	1.87	0.57
2:D:257:LEU:HD23	2:D:258:LEU:N	2.20	0.57
2:D:35:ILE:O	2:D:39:LEU:HD22	2.05	0.57
2:C:276:VAL:O	2:C:277:SER:HB3	2.05	0.56
2:D:269:ILE:O	2:D:271:PRO:HD3	2.04	0.56
2:C:281:VAL:N	8:C:2123:HOH:O	2.38	0.56
2:C:291:GLY:O	2:C:294:PRO:HD2	2.06	0.56
2:D:148:LEU:HD13	2:D:156:HIS:HE2	1.71	0.56
1:A:269:ILE:O	1:A:271:PRO:HD3	2.05	0.56
2:D:12:ARG:O	2:D:199:ILE:HA	2.06	0.55
1:A:312:LEU:HD23	1:A:361[B]:LEU:HD12	1.88	0.55
2:C:198:GLU:OE1	2:C:360:THR:HA	2.05	0.55
2:D:34:VAL:HG11	2:D:255:ALA:HB3	1.88	0.55
2:D:344:ILE:HG23	8:D:2078:HOH:O	2.05	0.55
1:A:358[B]:LEU:CD2	1:A:362:LEU:HD11	2.37	0.54
1:A:191:LYS:HG3	8:A:2250:HOH:O	2.07	0.54
2:C:98:LEU:O	2:C:102:GLN:HG2	2.07	0.54
2:C:378:CYS:HB2	8:C:2156:HOH:O	2.07	0.54
2:D:7:ILE:HG12	2:D:258:LEU:CD1	2.37	0.54
2:D:237:LYS:HB3	8:D:2075:HOH:O	2.08	0.54
1:A:207:ARG:H	1:A:207:ARG:CD	2.10	0.54
2:C:282:GLY:CA	8:C:2155:HOH:O	2.54	0.54
1:B:133:LYS:HD2	2:C:19:ASN:ND2	2.22	0.54
1:B:190:GLN:OE1	1:B:221:HIS:HE1	1.90	0.54
1:B:286:LYS:HD3	8:B:2216:HOH:O	2.07	0.54
1:B:271:PRO:HG2	1:B:392:LEU:HD12	1.89	0.54
2:D:9:SER:HA	2:D:272:LEU:HD23	1.90	0.54
5:A:1399:COA:H21	5:A:1399:COA:O5P	2.06	0.54
1:A:220[A]:ARG:NH2	8:A:2298:HOH:O	2.41	0.53
1:A:298:LYS:HA	1:A:298:LYS:NZ	2.22	0.53
1:A:332:TRP:HZ2	8:A:2391:HOH:O	1.90	0.53
2:C:127:HIS:HD2	8:D:2042:HOH:O	1.91	0.53
2:C:281:VAL:HG22	8:C:2122:HOH:O	2.08	0.53
1:B:4:SER:HB3	8:B:2366:HOH:O	2.09	0.53
2:D:276:VAL:HG13	2:D:388:CYS:HB2	1.89	0.53
2:D:305:TRP:CH2	2:D:372:LYS:HB3	2.44	0.53
1:B:334:PRO:HA	8:B:2403:HOH:O	2.08	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:276:VAL:HG22	1:A:388:CYS:HB2	1.91	0.53
2:C:109:SER:HB3	8:C:2111:HOH:O	2.09	0.53
2:C:365:MET:HA	2:C:370:ALA:HB3	1.91	0.53
1:A:274:ARG:NH2	1:A:390:GLU:OE1	2.42	0.52
2:C:300:LEU:HD13	2:C:307:ILE:HG12	1.91	0.52
2:C:376:THR:HB	8:C:2150:HOH:O	2.10	0.52
1:A:40:GLU:HG3	8:A:2059:HOH:O	2.09	0.52
2:C:274:ARG:HG2	2:C:390:GLU:O	2.09	0.52
2:D:7:ILE:HG23	2:D:256:ALA:HB1	1.92	0.52
1:A:361[A]:LEU:CD1	1:A:365:MET:SD	2.98	0.52
2:C:37:ALA:O	2:C:41:ARG:HG3	2.10	0.52
2:C:159:THR:O	2:C:162:GLU:HB2	2.09	0.52
2:D:26:PRO:HD2	2:D:29:GLU:OE1	2.09	0.52
2:D:111:ILE:HA	8:D:2016:HOH:O	2.10	0.52
2:D:292:PRO:HD3	2:D:378:CYS:CB	2.39	0.52
2:C:333:ASP:O	2:C:336:ILE:HG12	2.10	0.52
1:A:133:LYS:O	2:C:129:ARG:HG2	2.10	0.51
2:C:300:LEU:HD21	2:C:310:LEU:HD11	1.92	0.51
1:A:379:ILE:HB	1:A:383:MET:HB2	1.93	0.51
2:C:170:LEU:HD13	2:C:324:CYS:HB2	1.93	0.51
1:B:237:LYS:HD2	1:B:237:LYS:H	1.76	0.51
2:C:281:VAL:HG12	2:C:282:GLY:N	2.26	0.51
2:C:280:THR:HG23	2:D:81:THR:HG21	1.91	0.51
2:D:53:ILE:HD12	2:D:111:ILE:HG21	1.91	0.51
2:C:190:GLN:HB3	8:C:2085:HOH:O	2.11	0.51
2:D:5:ILE:HG21	2:D:100:MET:CG	2.41	0.51
2:D:371:ARG:O	2:D:390:GLU:HA	2.10	0.51
1:B:34:VAL:HG12	1:B:255:ALA:HB3	1.93	0.50
2:D:305:TRP:CZ3	2:D:372:LYS:HB3	2.46	0.50
2:D:124:HIS:HA	2:D:140:ILE:O	2.10	0.50
2:C:5:ILE:HG21	2:C:100:MET:HG2	1.93	0.50
2:D:203:ILE:HB	8:D:2068:HOH:O	2.11	0.50
1:B:166:LYS:HG3	8:B:2222:HOH:O	2.12	0.49
1:A:207:ARG:CG	1:A:207:ARG:NH1	2.63	0.49
1:A:301:GLU:CG	8:A:2366:HOH:O	2.55	0.49
1:B:68:ARG:NH2	8:B:2114:HOH:O	2.45	0.49
2:C:291:GLY:HA3	8:C:2156:HOH:O	2.12	0.49
2:D:292:PRO:HG3	2:D:377:LEU:C	2.32	0.49
1:A:190:GLN:OE1	1:A:221:HIS:HE1	1.95	0.49
2:C:371:ARG:HA	2:C:391:SER:OG	2.13	0.49
2:D:247:SER:HB3	2:D:317:GLU:O	2.12	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:134:MET:HG2	2:D:144:ILE:HD11	1.94	0.49
2:C:269:ILE:O	2:C:271:PRO:HD3	2.13	0.49
1:B:133:LYS:HD2	2:C:19:ASN:HD22	1.77	0.49
2:C:127:HIS:CD2	8:D:2042:HOH:O	2.64	0.49
2:C:281:VAL:HG22	8:C:2058:HOH:O	2.13	0.48
2:C:51:GLU:CD	2:C:83:TRP:HE1	2.16	0.48
2:C:175:GLN:HE22	2:C:240:THR:HG21	1.78	0.48
2:D:293:ILE:O	2:D:297:ARG:HG3	2.13	0.48
2:D:103:ILE:HD11	2:D:111:ILE:HG12	1.96	0.48
2:D:278:TRP:O	2:D:302:ARG:NH1	2.44	0.48
2:C:50:ASN:O	2:C:80:ALA:HB1	2.13	0.48
2:C:298:LYS:HD3	2:C:298:LYS:O	2.14	0.48
2:D:369:GLY:HA2	8:D:2117:HOH:O	2.13	0.48
2:D:155:TYR:HE1	2:D:160:THR:HG22	1.78	0.48
2:D:317:GLU:OE2	2:D:342:GLY:HA3	2.13	0.48
2:D:168:TRP:CH2	2:D:329:ASP:HB2	2.49	0.48
1:A:50:ASN:HB3	8:A:2037:HOH:O	2.13	0.48
2:C:285:PRO:HG3	2:C:381:GLY:O	2.13	0.48
2:C:374:LEU:C	2:C:374:LEU:HD23	2.33	0.47
2:C:19:ASN:C	2:C:23:ALA:HB2	2.34	0.47
2:D:361:LEU:O	2:D:365:MET:HG3	2.14	0.47
2:D:50:ASN:HB2	2:D:110:ILE:O	2.14	0.47
2:C:347:GLY:HA2	8:C:2141:HOH:O	2.14	0.47
2:D:68:ARG:N	8:D:2027:HOH:O	2.46	0.47
5:A:1399:COA:O7A	2:C:208:LYS:NZ	2.47	0.47
2:C:316:ASN:HB2	2:C:377:LEU:HG	1.96	0.47
2:C:186:ALA:HB2	2:C:341:GLY:HA3	1.96	0.47
1:B:86:ASN:HB2	8:B:2090:HOH:O	2.13	0.47
1:B:190:GLN:OE1	1:B:221:HIS:CE1	2.67	0.47
2:C:55:GLY:C	8:C:2029:HOH:O	2.52	0.47
1:B:298:LYS:HE2	1:B:302:ARG:CG	2.44	0.47
2:C:10:ALA:O	2:C:11:ALA:HB2	2.15	0.47
2:C:306:LYS:HB2	2:C:309:ASP:OD1	2.14	0.47
1:B:247[A]:SER:OG	1:B:348:ASN:HB2	2.15	0.47
1:A:202:PHE:CZ	8:A:2049:HOH:O	2.51	0.47
1:B:207:ARG:H	1:B:207:ARG:NH1	2.07	0.47
1:A:281:VAL:HG12	1:A:282:GLY:N	2.29	0.47
2:D:284:ASP:HB3	2:D:287:VAL:HG22	1.97	0.47
2:C:5:ILE:CD1	2:C:100:MET:HG2	2.40	0.47
2:C:362:LEU:CD2	2:C:389:ILE:HG21	2.45	0.47
2:C:34[A]:VAL:HG12	2:C:255:ALA:HB3	1.96	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:C:280:THR:OG1	2:D:81:THR:HG21	2.15	0.47
2:C:269:ILE:HG12	8:C:2023:HOH:O	2.14	0.46
1:A:167:GLN:NE2	8:A:2218:HOH:O	2.47	0.46
2:D:34:VAL:O	2:D:38:VAL:HG13	2.15	0.46
1:B:97:ALA:O	1:B:100[B]:MET:HG3	2.15	0.46
2:D:127:HIS:CG	8:D:2043:HOH:O	2.68	0.46
2:C:177:ALA:HB1	8:C:2080:HOH:O	2.14	0.46
2:C:168:TRP:CH2	2:C:329:ASP:HB2	2.51	0.46
2:C:295:ALA:HA	8:C:2123:HOH:O	2.16	0.46
2:C:54:LEU:O	2:C:84:GLY:HA2	2.16	0.46
1:A:207:ARG:N	1:A:207:ARG:HD3	2.11	0.46
2:C:378:CYS:HA	8:C:2156:HOH:O	2.16	0.46
2:D:233:PRO:HB2	2:D:236:ASP:O	2.15	0.46
2:C:101:GLN:HG2	2:D:105:THR:HG21	1.98	0.46
2:D:257:LEU:O	2:D:258:LEU:HD13	2.15	0.46
2:C:353:SER:O	2:C:357:ILE:HG23	2.16	0.46
1:B:89:CSO:SG	1:B:350:ILE:HG23	2.56	0.46
2:C:47:GLY:HA2	2:C:77:PRO:CG	2.45	0.46
2:C:245:ASN:HB2	2:C:320:ALA:CB	2.46	0.46
2:D:118:SER:OG	2:D:121:MET:HB2	2.16	0.46
1:A:286:LYS:NZ	8:A:2353:HOH:O	2.50	0.45
2:D:307:ILE:HG23	2:D:332:TRP:HB3	1.99	0.45
2:C:129:ARG:HD3	2:D:18:PHE:CZ	2.51	0.45
2:D:176:ASP:O	2:D:180:VAL:HG23	2.17	0.45
2:C:317:GLU:OE2	2:C:342:GLY:HA3	2.16	0.45
1:A:358[B]:LEU:CD2	1:A:362:LEU:CD1	2.94	0.45
1:B:34:VAL:CG1	1:B:255:ALA:HB3	2.47	0.45
2:C:86:ASN:HA	8:C:2031:HOH:O	2.16	0.45
2:C:319:PHE:O	2:C:322:GLN:HG3	2.16	0.45
2:C:281:VAL:HG23	8:C:2123:HOH:O	2.16	0.45
2:D:276:VAL:O	2:D:277:SER:HB3	2.17	0.45
2:D:162:GLU:OE1	2:D:240:THR:HG22	2.16	0.45
2:C:5:ILE:CD1	2:C:104:ALA:HB2	2.45	0.45
2:C:344:ILE:HD11	8:C:2139:HOH:O	2.17	0.45
2:C:78:GLN:O	2:D:282:GLY:HA3	2.17	0.45
2:C:379:ILE:HD12	8:C:2157:HOH:O	2.17	0.45
2:C:11:ALA:N	2:C:359:ASN:OD1	2.50	0.44
1:B:228[B]:MET:HG2	8:B:2474:HOH:O	2.18	0.44
1:A:52:VAL:O	1:A:82:ALA:HA	2.17	0.44
2:D:292:PRO:HB3	2:D:376:THR:OG1	2.17	0.44
2:C:242:THR:C	2:C:244:GLY:H	2.20	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:C:176:ASP:O	2:C:180:VAL:HG23	2.17	0.44
2:C:36:SER:HA	2:C:39:LEU:HD22	1.98	0.44
2:D:144:ILE:HA	2:D:148:LEU:HB2	1.98	0.44
1:A:314:GLU:HG3	1:A:361[A]:LEU:HB2	1.98	0.44
1:A:88:LEU:HB2	1:A:379:ILE:HG23	2.00	0.44
2:D:76:VAL:HA	2:D:77:PRO:HD2	1.80	0.44
1:B:363:PHE:CD1	1:B:366[A]:LYS:NZ	2.86	0.43
2:D:368:ARG:HA	8:D:2120:HOH:O	2.18	0.43
1:A:354:GLY:HA2	1:A:377:LEU:HD11	2.00	0.43
1:A:134:MET:HG3	2:D:143:MET:HE1	2.00	0.43
1:A:135:GLY:HA2	2:D:144:ILE:HD12	2.00	0.43
2:D:53:ILE:HG12	2:D:83:TRP:CE2	2.53	0.43
2:D:7:ILE:HG12	2:D:258:LEU:HD12	2.00	0.43
2:C:89:CYS:O	2:C:377:LEU:HD22	2.18	0.43
2:C:133:LYS:HG2	8:C:2066:HOH:O	2.18	0.43
1:A:220[A]:ARG:CZ	5:A:1399:COA:N6A	2.81	0.43
2:D:12:ARG:HE	2:D:198:GLU:CD	2.21	0.43
1:A:361[A]:LEU:HD11	1:A:365:MET:SD	2.57	0.43
1:B:274:ARG:NH2	1:B:392:LEU:HD21	2.33	0.43
2:C:237:LYS:HD2	2:C:237:LYS:HA	1.74	0.43
2:D:37:ALA:O	2:D:41:ARG:HG3	2.18	0.43
2:C:158:GLY:HA2	2:C:319:PHE:CE1	2.54	0.43
2:D:17:SER:OG	2:D:217:GLU:HG3	2.17	0.43
1:A:316:ASN:HB3	8:A:2427:HOH:O	2.17	0.43
2:D:61:GLY:CA	8:D:2021:HOH:O	2.55	0.43
2:C:274:ARG:HE	2:C:390:GLU:CG	2.18	0.43
2:D:38:VAL:HG23	2:D:39:LEU:N	2.33	0.43
2:C:56:GLN:N	8:C:2029:HOH:O	2.52	0.43
2:C:386:ALA:HA	8:C:2150:HOH:O	2.18	0.43
2:C:298:LYS:HE2	2:C:302:ARG:HG3	2.01	0.42
2:D:293:ILE:HB	8:D:2098:HOH:O	2.18	0.42
2:C:4:SER:O	2:C:260:SER:HA	2.19	0.42
1:A:220[A]:ARG:HH12	1:A:223:ALA:CB	2.32	0.42
2:D:361:LEU:HD22	2:D:365:MET:SD	2.59	0.42
2:C:30:LEU:HD23	2:C:202:PHE:CE1	2.55	0.42
1:B:180:VAL:CG2	1:B:228[B]:MET:HG3	2.49	0.42
1:A:134:MET:SD	2:D:249:LEU:HD11	2.59	0.42
2:D:364:GLU:O	2:D:368:ARG:HG2	2.18	0.42
1:A:328:LYS:HB2	1:A:328:LYS:HE2	1.38	0.42
2:C:103:ILE:HG12	2:C:108:ALA:O	2.19	0.42
2:C:195:PHE:HZ	2:C:340:ASN:O	2.02	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:C:379:ILE:HG13	2:C:384:GLY:HA2	2.01	0.42
2:D:26:PRO:HD2	2:D:29:GLU:CD	2.40	0.42
2:D:33:THR:OG1	2:D:202:PHE:HD1	2.02	0.42
2:D:355:ALA:O	2:D:356:ARG:C	2.58	0.42
2:D:67:ALA:HB3	8:D:2027:HOH:O	2.20	0.42
2:D:54:LEU:O	2:D:84:GLY:HA2	2.19	0.42
2:D:311:ASP:HA	8:D:2103:HOH:O	2.19	0.42
2:D:349:PRO:HB2	2:D:352:ALA:HB3	2.02	0.42
2:D:60:ALA:C	8:D:2021:HOH:O	2.58	0.42
1:A:172:ARG:HA	1:A:240:THR:OG1	2.19	0.42
1:B:228[B]:MET:HE2	5:B:1399:COA:H61A	1.84	0.42
1:B:263:GLU:CD	8:B:2348:HOH:O	2.58	0.42
2:D:274:ARG:N	8:D:2095:HOH:O	2.53	0.42
2:D:328:LYS:HE3	2:D:328:LYS:HB2	1.84	0.42
2:C:85:MET:HA	2:D:85:MET:HA	2.01	0.42
2:C:276:VAL:HG23	2:C:303:ALA:HB2	2.02	0.41
1:B:207:ARG:HH11	1:B:207:ARG:CG	2.23	0.41
1:A:220[A]:ARG:NH2	8:A:2299:HOH:O	2.46	0.41
2:C:33:THR:HG1	2:C:202:PHE:HD1	1.68	0.41
2:D:322:GLN:O	2:D:326:VAL:HG23	2.20	0.41
2:C:266:ARG:HA	8:C:2165:HOH:O	2.20	0.41
1:B:233:PRO:HB2	1:B:236:ASP:O	2.18	0.41
2:C:172:ARG:HA	2:C:240:THR:OG1	2.20	0.41
2:D:273:GLY:HA2	2:D:391:SER:HA	2.01	0.41
2:C:323:ALA:CB	8:C:2138:HOH:O	2.67	0.41
2:D:307:ILE:HD12	2:D:307:ILE:H	1.85	0.41
1:A:29:GLU:OE1	8:A:2049:HOH:O	2.22	0.41
2:C:292:PRO:HA	2:C:295:ALA:HB3	2.01	0.41
2:D:88:LEU:HB2	2:D:379:ILE:CG2	2.48	0.41
1:A:131:GLY:CA	8:C:2065:HOH:O	2.68	0.41
2:C:46:ALA:HB1	2:C:76:VAL:HA	2.03	0.41
1:B:207:ARG:HH11	1:B:207:ARG:N	2.08	0.41
2:D:292:PRO:CD	2:D:378:CYS:HB3	2.51	0.41
2:D:317:GLU:O	2:D:343:ALA:HB3	2.20	0.41
2:C:42:ALA:HB3	2:C:257:LEU:HD13	2.03	0.41
2:D:267:ARG:NH2	8:D:2088:HOH:O	2.52	0.41
2:D:53:ILE:HD12	2:D:111:ILE:CG2	2.51	0.41
1:B:148:LEU:HD22	5:B:1399:COA:C5P	2.50	0.41
2:C:59:PRO:O	2:C:60:ALA:C	2.59	0.41
2:D:296:SER:O	2:D:300:LEU:HG	2.20	0.41
1:B:257[A]:LEU:HD23	1:B:258:LEU:N	2.35	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:D:117:GLU:HA	2:D:117:GLU:OE1	2.21	0.41
2:C:302:ARG:CZ	8:C:2132:HOH:O	2.69	0.41
1:A:144:ILE:HD13	1:A:148:LEU:HD12	2.03	0.41
2:D:68:ARG:NH1	2:D:80:ALA:O	2.51	0.41
2:C:117:GLU:OE1	2:C:351:GLY:HA3	2.21	0.41
1:A:131:GLY:HA2	8:C:2065:HOH:O	2.22	0.41
1:B:298:LYS:CE	8:B:2380:HOH:O	2.69	0.41
2:C:86:ASN:CB	8:C:2031:HOH:O	2.69	0.41
1:B:88:LEU:HB2	1:B:379:ILE:HG23	2.02	0.41
1:A:220[A]:ARG:NH1	1:A:223:ALA:HB2	2.36	0.40
2:D:293:ILE:HD12	8:D:2098:HOH:O	2.21	0.40
2:C:42:ALA:CB	2:C:257:LEU:HD13	2.52	0.40
5:A:1399:COA:O5A	2:D:134:MET:HE1	2.21	0.40
1:A:190:GLN:OE1	1:A:221:HIS:CE1	2.74	0.40
1:A:48:GLU:OE1	1:A:267:ARG:NH2	2.52	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	394/392 (100%)	378 (96%)	16 (4%)	0	100	100
1	B	393/392 (100%)	380 (97%)	12 (3%)	1 (0%)	46	29
2	C	388/392 (99%)	365 (94%)	22 (6%)	1 (0%)	46	29
2	D	387/392 (99%)	359 (93%)	26 (7%)	2 (0%)	34	17
All	All	1562/1568 (100%)	1482 (95%)	76 (5%)	4 (0%)	46	29

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	C	350	ILE
2	D	350	ILE
2	D	169	GLN
1	B	350	ILE

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	283/278 (102%)	269 (95%)	14 (5%)	31	13
1	B	282/278 (101%)	268 (95%)	14 (5%)	30	13
2	C	277/279 (99%)	270 (98%)	7 (2%)	55	39
2	D	276/279 (99%)	265 (96%)	11 (4%)	38	20
All	All	1118/1114 (100%)	1072 (96%)	46 (4%)	39	19

All (46) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	39	LEU
1	A	155	TYR
1	A	207	ARG
1	A	221	HIS
1	A	237	LYS
1	A	272[A]	LEU
1	A	272[B]	LEU
1	A	276	VAL
1	A	288	MET
1	A	322	GLN
1	A	328	LYS
1	A	332	TRP
1	A	358[A]	LEU
1	A	358[B]	LEU
1	B	4	SER
1	B	78	GLN
1	B	155	TYR
1	B	207	ARG

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Mol	Chain	Res	Type
1	B	221	HIS
1	B	237	LYS
1	B	263	GLU
1	B	288	MET
1	B	298	LYS
1	B	322	GLN
1	B	332	TRP
1	B	358[A]	LEU
1	B	358[B]	LEU
1	B	361	LEU
2	C	39	LEU
2	C	40	GLU
2	C	207	ARG
2	C	288	MET
2	C	322	GLN
2	C	332	TRP
2	C	357	ILE
2	D	39	LEU
2	D	187	GLU
2	D	207	ARG
2	D	220	ARG
2	D	258	LEU
2	D	288	MET
2	D	298	LYS
2	D	322	GLN
2	D	332	TRP
2	D	358	LEU
2	D	361	LEU

Some 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	167	GLN
1	A	169	GLN
1	A	175	GLN
1	A	184	ASN
1	A	221	HIS
1	B	78	GLN
1	B	175	GLN
1	B	184	ASN
1	B	221	HIS

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Mol	Chain	Res	Type
2	C	78	GLN
2	C	127	HIS
2	C	175	GLN
2	C	184	ASN
2	C	270	GLN
2	D	175	GLN
2	D	184	ASN
2	D	190	GLN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

2 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	CSO	A	89	1	3,6,7	0.56	0	1,6,8	1.98	0
1	CSO	B	89	1	3,6,7	0.49	0	1,6,8	2.06	1 (100%)

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	CSO	A	89	1	-	0/1/5/7	0/0/0/0
1	CSO	B	89	1	-	0/1/5/7	0/0/0/0

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	89	CSO	O-C-CA	-2.06	120.11	125.49

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	B	89	CSO	1	0

5.5 Carbohydrates [i](#)

There are no carbohydrates in this entry.

5.6 Ligand geometry [i](#)

Of 22 ligands modelled in this entry, 2 are monoatomic - leaving 20 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	$\# Z > 2$
3	SO4	A	1394	-	4,4,4	0.20	0	6,6,6	0.07	0
3	SO4	A	1395	-	4,4,4	0.29	0	6,6,6	0.10	0
3	SO4	A	1396	-	4,4,4	0.18	0	6,6,6	0.13	0
3	SO4	A	1397	-	4,4,4	0.23	0	6,6,6	0.07	0
4	DNO	A	1398	-	11,11,11	2.08	4 (36%)	14,14,14	2.02	6 (42%)
5	COA	A	1399	-	40,50,50	2.46	12 (30%)	50,75,75	2.74	11 (22%)
3	SO4	B	1394	-	4,4,4	0.25	0	6,6,6	0.11	0
3	SO4	B	1395	-	4,4,4	0.28	0	6,6,6	0.12	0
3	SO4	B	1396	-	4,4,4	0.21	0	6,6,6	0.07	0
3	SO4	B	1397	-	4,4,4	0.25	0	6,6,6	0.08	0
5	COA	B	1399	-	40,50,50	2.47	11 (27%)	50,75,75	2.67	9 (18%)
3	SO4	B	1401	-	4,4,4	0.21	0	6,6,6	0.13	0
3	SO4	C	1393	-	4,4,4	0.22	0	6,6,6	0.06	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
3	SO4	C	1394	-	4,4,4	0.25	0	6,6,6	0.07	0
3	SO4	C	1395	-	4,4,4	0.23	0	6,6,6	0.11	0
3	SO4	C	1396	-	4,4,4	0.22	0	6,6,6	0.10	0
4	DNO	C	1397	-	11,11,11	1.93	2 (18%)	14,14,14	1.75	5 (35%)
4	DNO	C	1398	-	11,11,11	2.00	2 (18%)	14,14,14	1.98	7 (50%)
4	DNO	C	1399	-	11,11,11	2.07	4 (36%)	14,14,14	2.02	7 (50%)
3	SO4	D	1393	-	4,4,4	0.20	0	6,6,6	0.15	0

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	SO4	A	1394	-	-	0/0/0/0	0/0/0/0
3	SO4	A	1395	-	-	0/0/0/0	0/0/0/0
3	SO4	A	1396	-	-	0/0/0/0	0/0/0/0
3	SO4	A	1397	-	-	0/0/0/0	0/0/0/0
4	DNO	A	1398	-	2/2/4/5	0/14/16/16	0/0/0/0
5	COA	A	1399	-	-	0/44/64/64	0/3/3/3
3	SO4	B	1394	-	-	0/0/0/0	0/0/0/0
3	SO4	B	1395	-	-	0/0/0/0	0/0/0/0
3	SO4	B	1396	-	-	0/0/0/0	0/0/0/0
3	SO4	B	1397	-	-	0/0/0/0	0/0/0/0
5	COA	B	1399	-	-	0/44/64/64	0/3/3/3
3	SO4	B	1401	-	-	0/0/0/0	0/0/0/0
3	SO4	C	1393	-	-	0/0/0/0	0/0/0/0
3	SO4	C	1394	-	-	0/0/0/0	0/0/0/0
3	SO4	C	1395	-	-	0/0/0/0	0/0/0/0
3	SO4	C	1396	-	-	0/0/0/0	0/0/0/0
4	DNO	C	1397	-	2/2/4/5	0/14/16/16	0/0/0/0
4	DNO	C	1398	-	2/2/4/5	0/14/16/16	0/0/0/0
4	DNO	C	1399	-	2/2/4/5	0/14/16/16	0/0/0/0
3	SO4	D	1393	-	-	0/0/0/0	0/0/0/0

All (35) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	A	1399	COA	C5A-C4A	-2.60	1.34	1.40
5	A	1399	COA	C4A-N3A	-2.51	1.31	1.35
5	B	1399	COA	C5A-C4A	-2.47	1.34	1.40

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	A	1398	DNO	C2-C1	2.01	1.53	1.50
4	C	1399	DNO	C2-C1	2.04	1.53	1.50
4	C	1399	DNO	C3-C2	2.18	1.56	1.53
4	A	1398	DNO	C3-C2	2.21	1.56	1.53
5	A	1399	COA	P3B-O8A	2.90	1.65	1.54
5	B	1399	COA	P3B-O8A	2.94	1.65	1.54
5	B	1399	COA	C6A-N6A	3.31	1.45	1.34
5	A	1399	COA	C6A-N6A	3.34	1.45	1.34
5	A	1399	COA	C8A-N7A	3.81	1.41	1.34
5	B	1399	COA	P2A-O4A	3.91	1.65	1.51
4	A	1398	DNO	O1-C1	3.92	1.37	1.19
4	C	1399	DNO	O1-C1	3.93	1.38	1.19
4	C	1398	DNO	O1-C1	3.96	1.38	1.19
5	A	1399	COA	P1A-O1A	3.97	1.65	1.51
5	A	1399	COA	P2A-O4A	3.98	1.65	1.51
5	B	1399	COA	C8A-N7A	3.98	1.42	1.34
5	B	1399	COA	P1A-O1A	4.00	1.65	1.51
5	A	1399	COA	O4B-C1B	4.02	1.46	1.41
4	C	1397	DNO	O1-C1	4.03	1.38	1.19
4	C	1397	DNO	C4-C3	4.06	1.61	1.53
5	B	1399	COA	O4B-C1B	4.18	1.46	1.41
5	B	1399	COA	C2A-N3A	4.27	1.39	1.32
5	A	1399	COA	P3B-O7A	4.37	1.65	1.51
5	A	1399	COA	C2A-N3A	4.40	1.40	1.32
4	C	1398	DNO	C4-C3	4.43	1.62	1.53
5	B	1399	COA	P3B-O7A	4.47	1.65	1.51
4	C	1399	DNO	C4-C3	4.61	1.62	1.53
4	A	1398	DNO	C4-C3	4.69	1.63	1.53
5	A	1399	COA	C5P-N4P	5.63	1.46	1.33
5	B	1399	COA	C5P-N4P	5.66	1.46	1.33
5	A	1399	COA	C9P-N8P	6.75	1.47	1.33
5	B	1399	COA	C9P-N8P	6.88	1.48	1.33

All (45) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	B	1399	COA	N3A-C2A-N1A	-12.82	119.08	128.89
5	A	1399	COA	N3A-C2A-N1A	-11.80	119.86	128.89
5	B	1399	COA	P2A-O3A-P1A	-6.87	113.42	132.73
5	A	1399	COA	P2A-O3A-P1A	-5.49	117.33	132.73
5	A	1399	COA	C3P-N4P-C5P	-3.77	115.38	122.79
4	C	1398	DNO	O1-C1-C2	-3.09	116.60	125.60

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	C	1397	DNO	O1-C1-C2	-2.97	116.94	125.60
4	A	1398	DNO	O1-C1-C2	-2.80	117.44	125.60
4	C	1399	DNO	O1-C1-C2	-2.80	117.45	125.60
5	B	1399	COA	C4B-O4B-C1B	-2.61	106.85	109.72
4	C	1399	DNO	O2-C2-C3	2.01	114.06	109.45
4	C	1398	DNO	O2-C2-C3	2.05	114.14	109.45
4	A	1398	DNO	O2-C2-C3	2.08	114.21	109.45
5	A	1399	COA	O3A-P1A-O5B	2.08	108.45	102.94
4	C	1399	DNO	O3-C3-C2	2.13	112.69	108.93
4	C	1397	DNO	O5-C5-C6	2.15	114.22	109.22
4	C	1398	DNO	O4-C4-C3	2.15	114.61	109.45
4	C	1398	DNO	C3-C2-C1	2.18	114.90	111.68
4	C	1398	DNO	O3-C3-C2	2.19	112.80	108.93
4	C	1399	DNO	O5-C5-C6	2.19	114.32	109.22
4	C	1397	DNO	O3-C3-C2	2.22	112.85	108.93
4	C	1397	DNO	O6-C6-C5	2.24	115.97	111.10
5	A	1399	COA	O3B-C3B-C2B	2.24	120.24	111.51
4	C	1399	DNO	O5-C5-C4	2.30	114.80	109.02
4	A	1398	DNO	O4-C4-C3	2.44	115.32	109.45
4	A	1398	DNO	O5-C5-C4	2.50	115.30	109.02
4	C	1398	DNO	O5-C5-C4	2.51	115.33	109.02
4	A	1398	DNO	C3-C2-C1	2.54	115.42	111.68
5	A	1399	COA	C7P-C6P-C5P	2.56	116.54	112.31
5	B	1399	COA	C7P-C6P-C5P	2.64	116.67	112.31
5	A	1399	COA	O3B-C3B-C4B	2.66	120.42	109.99
4	C	1398	DNO	O6-C6-C5	2.71	116.99	111.10
4	C	1397	DNO	O5-C5-C4	2.75	115.94	109.02
4	C	1399	DNO	O4-C4-C3	2.87	116.33	109.45
5	B	1399	COA	CDP-CBP-CCP	3.11	112.53	108.50
5	B	1399	COA	O2B-C2B-C3B	3.14	120.22	111.16
4	C	1399	DNO	O6-C6-C5	3.21	118.07	111.10
5	A	1399	COA	O3A-P2A-O6A	3.34	111.78	102.94
5	B	1399	COA	O3B-C3B-C4B	3.34	123.09	109.99
4	A	1398	DNO	O6-C6-C5	3.43	118.55	111.10
5	B	1399	COA	O4B-C1B-N9A	3.53	115.48	108.10
5	A	1399	COA	O6A-CCP-CBP	3.83	116.70	110.55
5	A	1399	COA	O2B-C2B-C3B	3.87	122.34	111.16
5	B	1399	COA	C2B-C1B-N9A	7.38	125.56	114.29
5	A	1399	COA	C2B-C1B-N9A	9.96	129.51	114.29

All (8) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
4	C	1399	DNO	C2
4	C	1399	DNO	C3
4	A	1398	DNO	C2
4	A	1398	DNO	C3
4	C	1398	DNO	C2
4	C	1398	DNO	C3
4	C	1397	DNO	C2
4	C	1397	DNO	C3

There are no torsion outliers.

There are no ring outliers.

4 monomers are involved in 10 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	A	1399	COA	5	0
5	B	1399	COA	3	0
4	C	1397	DNO	1	0
4	C	1398	DNO	1	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

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%)	-0.47	4 (1%) 84 82	5, 13, 34, 96	0
1	B	388/392 (98%)	-0.50	3 (0%) 87 85	5, 13, 32, 88	0
2	C	389/392 (99%)	1.41	96 (24%) 1 1	18, 50, 79, 108	0
2	D	389/392 (99%)	1.73	122 (31%) 1 0	20, 57, 102, 131	0
All	All	1554/1568 (99%)	0.54	225 (14%) 3 2	5, 34, 81, 131	0

All (225) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	D	285	PRO	8.7
2	D	207	ARG	8.2
2	D	307	ILE	8.1
2	D	231	LEU	8.1
2	D	269	ILE	8.1
2	D	265	SER	7.8
2	C	303	ALA	7.7
2	D	227	SER	7.5
2	D	108	ALA	6.5
2	C	299	ALA	6.4
2	C	274	ARG	6.1
2	D	289	GLY	5.9
2	D	391	SER	5.8
2	C	308	GLY	5.7
2	C	309	ASP	5.7
2	D	238	GLU	5.7
2	C	386	ALA	5.7
2	D	385	VAL	5.6
2	D	225	LEU	5.6
2	C	391	SER	5.6
2	C	269	ILE	5.5

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Mol	Chain	Res	Type	RSRZ
2	C	206	GLY	5.4
2	D	392	LEU	5.4
2	C	295	ALA	5.3
2	D	332	TRP	5.3
2	D	308	GLY	5.3
2	C	110	ILE	5.3
2	C	264	ALA	5.2
2	C	103	ILE	5.2
1	A	132	VAL	5.2
2	D	5	ILE	5.2
2	D	303	ALA	5.1
2	D	226	ASP	5.1
2	D	270	GLN	5.0
2	D	305	TRP	5.0
2	D	368	ARG	4.9
2	D	228	MET	4.9
1	A	207	ARG	4.9
2	D	279	ALA	4.9
2	D	224	THR	4.8
2	C	276	VAL	4.8
2	C	392	LEU	4.7
2	D	310	LEU	4.7
2	C	238	GLU	4.7
2	C	337	VAL	4.7
2	D	325	ALA	4.7
2	D	335	SER	4.6
2	C	170	LEU	4.6
2	C	324	CYS	4.6
2	C	34[A]	VAL	4.6
2	C	375	ALA	4.5
2	D	179	ALA	4.4
2	C	389	ILE	4.4
2	C	179	ALA	4.4
2	D	281	VAL	4.4
2	D	293	ILE	4.3
2	C	262	ALA	4.3
2	D	287	VAL	4.3
2	C	107	ASP	4.2
2	D	34	VAL	4.2
2	C	370	ALA	4.1
2	C	340	ASN	4.1
2	D	57	VAL	4.1

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Mol	Chain	Res	Type	RSRZ
2	C	108	ALA	4.1
2	D	178	PHE	4.1
2	C	369	GLY	4.0
2	D	209	GLY	4.0
2	D	232	ARG	4.0
2	D	328	LYS	3.9
2	C	335	SER	3.8
2	D	181	ALA	3.7
2	D	107	ASP	3.7
2	C	106	GLY	3.7
2	D	327	ASN	3.7
2	D	168	TRP	3.7
2	C	52	VAL	3.7
2	C	304	GLY	3.6
2	D	219	ILE	3.6
2	D	339	VAL	3.5
2	C	293	ILE	3.5
2	D	164	VAL	3.5
2	D	389	ILE	3.5
2	D	223	ALA	3.5
2	C	266	ARG	3.5
2	D	46	ALA	3.5
2	C	278	TRP	3.5
2	C	366	LYS	3.4
2	C	231	LEU	3.4
2	D	329	ASP	3.4
2	D	352	ALA	3.4
2	D	388	CYS	3.4
2	D	173	ASP	3.3
2	C	77	PRO	3.3
2	D	175	GLN	3.3
2	D	278	TRP	3.3
2	D	221	HIS	3.3
2	D	161	ALA	3.2
2	C	237	LYS	3.2
2	C	334	PRO	3.2
1	B	207	ARG	3.2
2	D	350	ILE	3.2
2	D	330	LEU	3.2
2	D	95	ALA	3.2
2	D	106	GLY	3.1
2	C	350	ILE	3.1

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Mol	Chain	Res	Type	RSRZ
1	B	208	LYS	3.1
2	C	177	ALA	3.1
2	D	208	LYS	3.1
2	D	301	GLU	3.1
2	C	275	ILE	3.1
2	D	176	ASP	3.1
2	C	219	ILE	3.0
2	C	368	ARG	3.0
2	D	255	ALA	3.0
2	C	341	GLY	3.0
2	D	199	ILE	3.0
2	D	312	LEU	3.0
2	D	336	ILE	3.0
2	D	272	LEU	3.0
2	D	273	GLY	3.0
2	D	262	ALA	3.0
2	D	49	VAL	2.9
2	D	96	VAL	2.9
2	D	186	ALA	2.9
2	C	321	ALA	2.9
2	D	42	ALA	2.9
2	D	359	ASN	2.9
2	D	337	VAL	2.9
2	C	104	ALA	2.9
2	D	244	GLY	2.9
2	C	105	THR	2.9
1	A	133	LYS	2.9
2	D	361	LEU	2.9
2	C	43	GLY	2.8
2	D	338	ASN	2.8
1	A	208	LYS	2.8
2	C	186	ALA	2.8
2	D	260	SER	2.8
2	C	230	LYS	2.8
2	C	5	ILE	2.7
2	C	96	VAL	2.7
2	D	319	PHE	2.7
2	C	332	TRP	2.7
2	C	75	GLY	2.7
2	C	339	VAL	2.7
2	C	226	ASP	2.7
2	D	320	ALA	2.7

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Mol	Chain	Res	Type	RSRZ
2	C	307	ILE	2.7
2	D	321	ALA	2.7
2	D	26	PRO	2.7
2	C	6	VAL	2.7
2	D	276	VAL	2.7
2	D	282	GLY	2.7
2	C	232	ARG	2.7
2	C	258	LEU	2.7
2	C	371	ARG	2.7
2	D	196	LYS	2.6
2	D	264	ALA	2.6
2	C	208	LYS	2.6
2	D	257	LEU	2.6
2	D	314	GLU	2.6
2	D	235	PHE	2.6
2	C	45	ALA	2.6
2	C	168	TRP	2.5
2	C	372	LYS	2.5
2	D	382	GLY	2.5
2	C	95	ALA	2.5
2	C	265	SER	2.5
2	D	240	THR	2.5
2	D	326	VAL	2.5
2	D	309	ASP	2.5
2	C	379	ILE	2.5
2	C	53	ILE	2.5
2	D	30	LEU	2.5
2	C	364	GLU	2.4
2	C	195	PHE	2.4
2	D	152	PHE	2.4
2	C	310	LEU	2.4
2	C	385	VAL	2.4
2	D	203	ILE	2.4
2	C	98	LEU	2.4
2	C	181	ALA	2.4
2	D	105	THR	2.4
2	C	336	ILE	2.4
2	C	86	ASN	2.4
2	D	299	ALA	2.3
2	D	160	THR	2.3
2	D	274	ARG	2.3
2	D	294	PRO	2.3

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Mol	Chain	Res	Type	RSRZ
2	D	206	GLY	2.3
2	C	36	SER	2.3
2	C	155	TYR	2.3
2	D	239	GLY	2.3
2	C	312	LEU	2.3
2	D	180	VAL	2.3
1	B	206	GLY	2.3
2	C	131	GLY	2.3
2	D	275	ILE	2.2
2	D	191	LYS	2.2
2	C	305	TRP	2.2
2	C	244	GLY	2.2
2	D	376	THR	2.2
2	D	237	LYS	2.2
2	C	272	LEU	2.2
2	D	189	ALA	2.2
2	D	170	LEU	2.2
2	D	213	VAL	2.2
2	D	322	GLN	2.1
2	D	110	ILE	2.1
2	C	328	LYS	2.1
2	D	302	ARG	2.1
2	D	300	LEU	2.1
2	C	132	VAL	2.1
2	D	182	SER	2.1
2	D	39	LEU	2.1
2	C	207	ARG	2.1
2	C	333	ASP	2.1
2	D	36	SER	2.1
2	D	169	GLN	2.1
2	C	42	ALA	2.0
2	C	229	ALA	2.0
2	D	79	GLU	2.0
2	C	220	ARG	2.0
2	C	180	VAL	2.0
2	C	294	PRO	2.0

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

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. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains.

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	LLDF	B-factors(Å ²)	Q<0.9
1	CSO	B	89	7/8	0.98	0.07	-	2,6,26,28	0
1	CSO	A	89	7/8	0.98	0.07	-	7,9,23,28	0

6.3 Carbohydrates [i](#)

There are no carbohydrates 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. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. 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	LLDF	B-factors(Å ²)	Q<0.9
6	NA	B	1398	1/1	0.19	1.26	212.61	123,123,123,123	0
3	SO4	B	1397	5/5	0.87	0.23	16.67	71,71,73,77	0
4	DNO	C	1397	12/12	0.70	0.22	13.71	44,55,91,93	0
3	SO4	C	1394	5/5	0.53	0.31	1.44	129,131,131,131	0
3	SO4	C	1396	5/5	0.88	0.27	0.52	64,66,67,71	0
4	DNO	C	1398	12/12	0.54	0.30	0.46	57,65,78,79	0
5	COA	B	1399	48/48	0.93	0.09	0.41	12,27,61,75	0
5	COA	A	1399	48/48	0.91	0.11	0.26	15,28,76,107	0
3	SO4	A	1396	5/5	0.90	0.19	-	64,64,66,66	0
3	SO4	A	1394	5/5	0.96	0.08	-	40,44,50,56	0
4	DNO	A	1398	12/12	0.71	0.29	-	42,52,75,76	0
4	DNO	C	1399	12/12	0.70	0.23	-	42,55,72,72	0
3	SO4	C	1395	5/5	0.83	0.29	-	81,83,86,87	0
3	SO4	B	1394	5/5	0.96	0.08	-	30,39,41,43	0
3	SO4	C	1393	5/5	0.81	0.18	-	75,77,78,79	0
3	SO4	B	1396	5/5	0.77	0.29	-	77,80,81,82	0
3	SO4	A	1395	5/5	0.96	0.12	-	43,50,53,57	0
7	CL	B	1400	1/1	0.90	0.05	-	68,68,68,68	0
3	SO4	A	1397	5/5	0.93	0.13	-	72,73,76,77	0
3	SO4	D	1393	5/5	0.90	0.10	-	61,62,65,67	0
3	SO4	B	1395	5/5	0.97	0.09	-	41,44,47,48	0
3	SO4	B	1401	5/5	0.75	0.26	-	89,90,91,92	0

6.5 Other polymers [i](#)

There are no such residues in this entry.