



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 02:26 AM GMT

PDB ID : 2H23
Title : Structure of Rubisco LSMT bound to Trimethyllysine and AdoHcy
Authors : Couture, J.F.; Hauk, G.; Trievel, R.C.
Deposited on : 2006-05-17
Resolution : 2.45 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

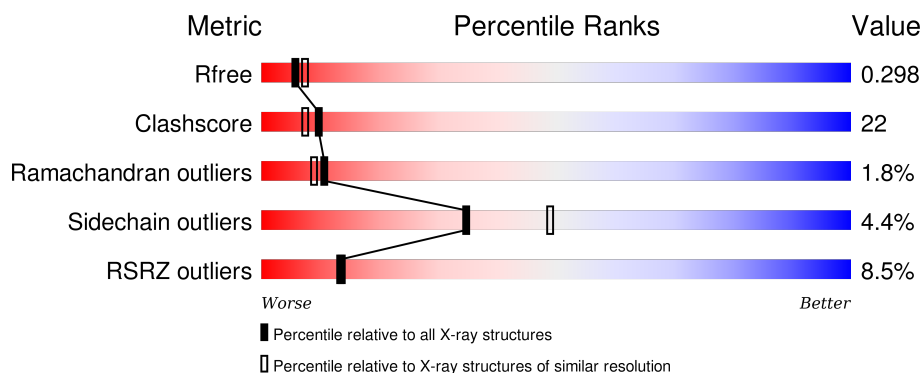
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.45 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	4776 (2.50-2.42)
Clashscore	102246	1030 (2.48-2.44)
Ramachandran outliers	100387	1024 (2.48-2.44)
Sidechain outliers	100360	1024 (2.48-2.44)
RSRZ outliers	91569	4787 (2.50-2.42)

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	440	<div> <div>14%</div> <div>57%</div> <div>36%</div> <div>.</div> <div>.</div> </div>
1	B	440	<div> <div>6%</div> <div>65%</div> <div>31%</div> <div>.</div> </div>
1	C	440	<div> <div>5%</div> <div>63%</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 criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
3	M3L	A	501	-	-	-	X
3	M3L	B	502	-	-	-	X
3	M3L	C	500	-	-	X	X

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 10988 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 Ribulose-1,5 bisphosphate carboxylase/oxygenase large subunit N-methyltransferase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	424	Total	C	N	O	S	0	0	0
			3413	2189	562	655	7			
1	B	440	Total	C	N	O	S	0	0	0
			3542	2270	585	680	7			
1	C	438	Total	C	N	O	S	0	0	0
			3526	2262	582	675	7			

There are 18 discrepancies between the modelled and reference sequences:

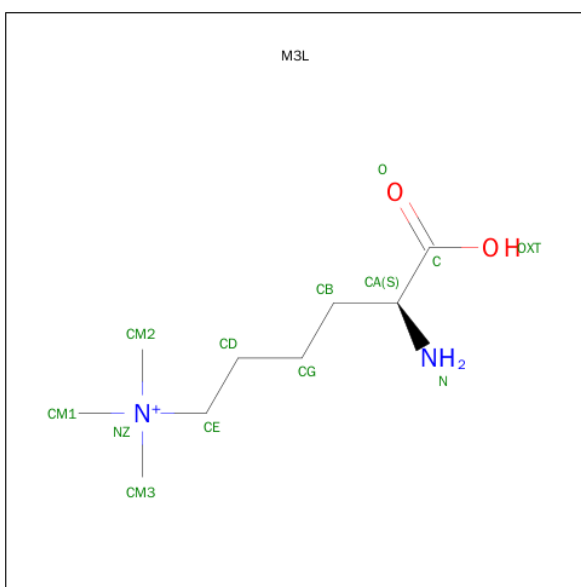
Chain	Residue	Modelled	Actual	Comment	Reference
A	483	GLU	-	CLONING ARTIFACT	UNP Q43088
A	484	ASN	-	CLONING ARTIFACT	UNP Q43088
A	485	LEU	-	CLONING ARTIFACT	UNP Q43088
A	486	TYR	-	CLONING ARTIFACT	UNP Q43088
A	487	PHE	-	CLONING ARTIFACT	UNP Q43088
A	488	GLN	-	CLONING ARTIFACT	UNP Q43088
B	483	GLU	-	CLONING ARTIFACT	UNP Q43088
B	484	ASN	-	CLONING ARTIFACT	UNP Q43088
B	485	LEU	-	CLONING ARTIFACT	UNP Q43088
B	486	TYR	-	CLONING ARTIFACT	UNP Q43088
B	487	PHE	-	CLONING ARTIFACT	UNP Q43088
B	488	GLN	-	CLONING ARTIFACT	UNP Q43088
C	483	GLU	-	CLONING ARTIFACT	UNP Q43088
C	484	ASN	-	CLONING ARTIFACT	UNP Q43088
C	485	LEU	-	CLONING ARTIFACT	UNP Q43088
C	486	TYR	-	CLONING ARTIFACT	UNP Q43088
C	487	PHE	-	CLONING ARTIFACT	UNP Q43088
C	488	GLN	-	CLONING ARTIFACT	UNP Q43088

- Molecule 2 is S-ADENOSYL-L-HOMOCYSTEINE (three-letter code: SAH) (formula: C₁₄H₂₀N₆O₅S).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total 26	C 14	N 6	O 5	S 1	0	0
2	B	1	Total 26	C 14	N 6	O 5	S 1	0	0
2	C	1	Total 26	C 14	N 6	O 5	S 1	0	0

- Molecule 3 is N-TRIMETHYLLYSINE (three-letter code: M3L) (formula: $\text{C}_9\text{H}_{21}\text{N}_2\text{O}_2$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	C	1	Total	C	N	O	0	0
			13	9	2	2		

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Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	A	1	Total	C	N	O	0	0
			13	9	2	2		
3	B	1	Total	C	N	O	0	0
			13	9	2	2		

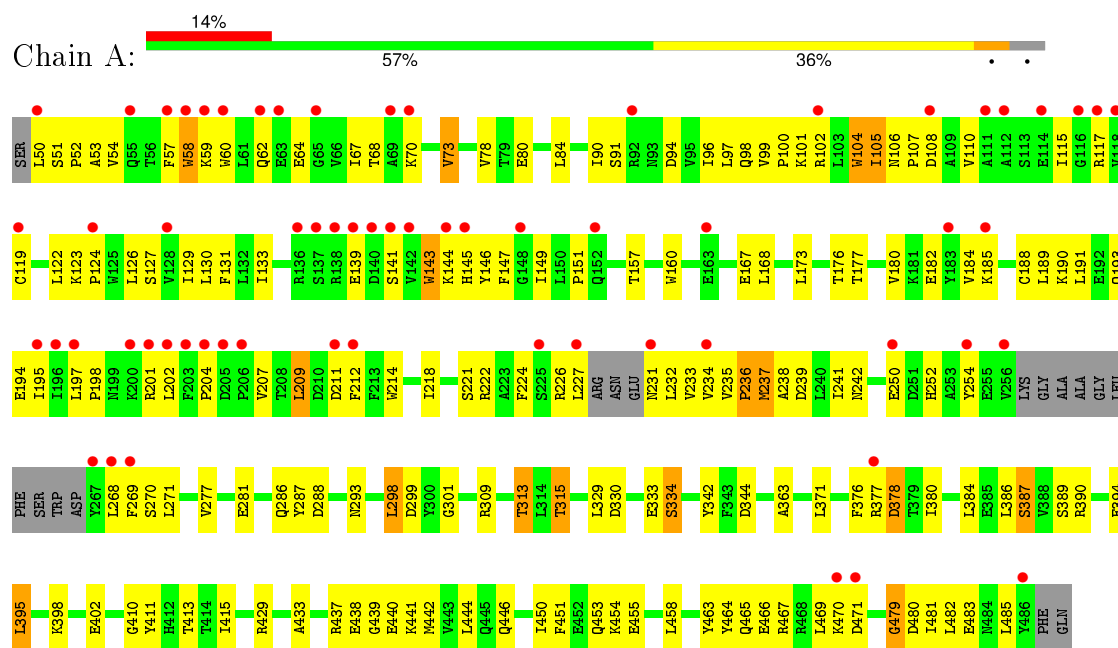
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	111	Total	O	0	0
			111	111		
4	B	136	Total	O	0	0
			136	136		
4	C	143	Total	O	0	0
			143	143		

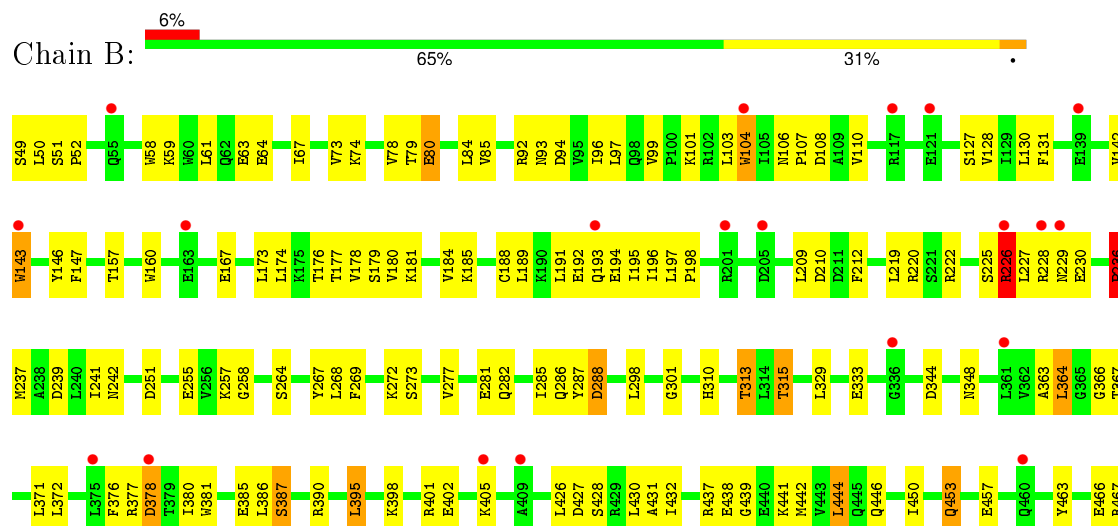
3 Residue-property plots [i](#)

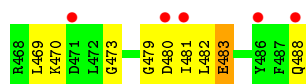
These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according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

- Molecule 1: Ribulose-1,5 biphosphate carboxylase/oxygenase large subunit N-methyltransferase

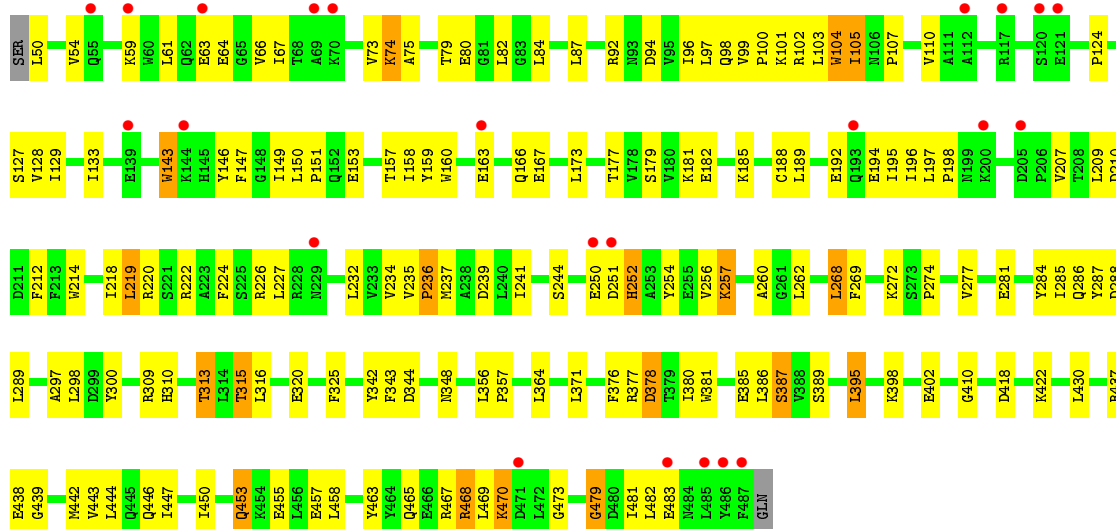


- Molecule 1: Ribulose-1,5 biphosphate carboxylase/oxygenase large subunit N-methyltransferase





- Molecule 1: Ribulose-1,5 bisphosphate carboxylase/oxygenase large subunit N-methyltransferase



4 Data and refinement statistics

Property	Value	Source
Space group	I 2 2 2	Depositor
Cell constants a, b, c, α , β , γ	131.86Å 157.55Å 267.60Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	14.98 – 2.45 14.98 – 2.44	Depositor EDS
% Data completeness (in resolution range)	96.5 (14.98-2.45) 96.6 (14.98-2.44)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.06	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.52 (at 2.45Å)	Xtriage
Refinement program	CNS 1.1	Depositor
R, R_{free}	0.253 , 0.288 0.264 , 0.298	Depositor DCC
R_{free} test set	No test flags present.	DCC
Wilson B-factor (Å ²)	55.0	Xtriage
Anisotropy	0.454	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 50.8	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.51$, $\langle L^2 \rangle = 0.34$	Xtriage
Outliers	1 of 102787 reflections (0.001%)	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	10988	wwPDB-VP
Average B, all atoms (Å ²)	67.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.03% 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 [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: SAH, M3L

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	0.41	0/3482	0.58	0/4723
1	B	0.41	0/3617	0.62	1/4906 (0.0%)
1	C	0.39	0/3601	0.60	0/4886
All	All	0.40	0/10700	0.60	1/14515 (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	236	PRO	N-CA-C	5.03	125.17	112.10

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	3413	0	3384	194	0
1	B	3542	0	3501	138	0
1	C	3526	0	3488	157	0
2	A	26	0	19	0	0
2	B	26	0	19	0	0
2	C	26	0	19	3	0
3	A	13	0	20	4	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	B	13	0	20	5	0
3	C	13	0	20	8	0
4	A	111	0	0	21	0
4	B	136	0	0	9	0
4	C	143	0	0	11	0
All	All	10988	0	10490	471	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 22.

All (471) 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:500:M3L:CG	3:C:500:M3L:CD	1.79	1.59
1:B:395:LEU:HD22	1:C:469:LEU:HD12	1.44	0.99
1:A:482:LEU:HD11	1:C:179:SER:HB3	1.43	0.98
1:A:395:LEU:HD22	1:B:469:LEU:HD12	1.45	0.98
1:C:177:THR:HB	4:C:820:HOH:O	1.64	0.96
1:B:438:GLU:HG2	1:B:442:MET:HE2	1.46	0.95
1:B:286:GLN:HE21	1:B:288:ASP:H	1.14	0.95
1:C:470:LYS:HA	1:C:470:LYS:HE2	1.50	0.94
1:C:50:LEU:HD22	1:C:54:VAL:HG11	1.51	0.91
1:A:363:ALA:HB1	1:A:395:LEU:HD13	1.55	0.86
3:C:500:M3L:CB	3:C:500:M3L:CD	2.52	0.86
1:A:254:TYR:HB3	1:A:270:SER:HB3	1.58	0.85
1:A:439:GLY:HA2	1:A:442:MET:HE3	1.57	0.85
1:A:469:LEU:HD12	1:C:395:LEU:HD22	1.59	0.83
1:A:194:GLU:C	1:A:195:ILE:HD12	1.99	0.83
1:A:438:GLU:HG2	1:A:442:MET:HE2	1.63	0.81
1:C:226:ARG:HG2	1:C:252:HIS:CE1	2.15	0.81
1:B:179:SER:HB3	1:C:482:LEU:HD11	1.62	0.80
1:B:439:GLY:HA2	1:B:442:MET:HE3	1.63	0.79
1:B:97:LEU:HD13	1:B:237:MET:HE3	1.64	0.78
1:C:73:VAL:HG21	1:C:84:LEU:HB3	1.65	0.78
1:A:130:LEU:HD11	1:A:191:LEU:HD22	1.64	0.78
1:B:286:GLN:HE21	1:B:288:ASP:N	1.82	0.77
1:B:286:GLN:NE2	1:B:288:ASP:H	1.83	0.77
1:A:106:ASN:HD21	1:A:108:ASP:HB2	1.49	0.77
1:A:102:ARG:HA	4:A:904:HOH:O	1.84	0.77
1:A:126:LEU:HD11	4:A:832:HOH:O	1.86	0.76
1:C:97:LEU:HB2	1:C:237:MET:HE1	1.66	0.76

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:96:ILE:HD11	1:B:273:SER:HB2	1.69	0.75
1:B:173:LEU:O	1:B:177:THR:HG23	1.88	0.74
1:B:78:VAL:HG11	1:B:282:GLN:HE22	1.53	0.73
1:C:348:ASN:H	1:C:446:GLN:HE22	1.37	0.73
1:A:100:PRO:HA	1:A:268:LEU:HD12	1.71	0.73
1:C:185:LYS:HD3	4:C:852:HOH:O	1.86	0.73
1:C:371:LEU:HB3	1:C:380:ILE:HD13	1.68	0.73
1:B:315:THR:HG22	4:C:808:HOH:O	1.87	0.73
1:C:104:TRP:HH2	1:C:269:PHE:H	1.37	0.73
1:A:395:LEU:CD2	1:B:469:LEU:HD12	2.18	0.72
1:A:214:TRP:O	1:A:218:ILE:HG12	1.89	0.72
1:A:139:GLU:HG3	4:A:836:HOH:O	1.89	0.72
1:B:371:LEU:HB3	1:B:380:ILE:HD13	1.70	0.72
1:A:115:ILE:HG22	1:A:202:LEU:HD13	1.71	0.72
1:C:177:THR:HG22	1:C:298:LEU:HD13	1.71	0.71
1:A:479:GLY:HA3	1:C:342:TYR:CE2	2.25	0.71
1:A:119:CYS:HA	1:A:122:LEU:HD12	1.73	0.71
1:B:99:VAL:O	1:B:104:TRP:CH2	2.45	0.70
1:A:207:VAL:HB	4:A:806:HOH:O	1.92	0.70
1:A:286:GLN:HE21	1:A:288:ASP:C	1.95	0.69
1:A:147:PHE:HA	4:A:845:HOH:O	1.91	0.69
1:A:99:VAL:O	1:A:104:TRP:HH2	1.74	0.69
1:C:73:VAL:CG2	1:C:84:LEU:HB3	2.23	0.68
1:B:99:VAL:O	1:B:104:TRP:HH2	1.76	0.68
1:A:226:ARG:HH12	1:A:250:GLU:HG2	1.59	0.68
1:C:194:GLU:C	1:C:195:ILE:HD12	2.13	0.68
1:C:74:LYS:HG2	1:C:87:LEU:HD21	1.75	0.68
1:A:173:LEU:O	1:A:177:THR:HG23	1.93	0.68
1:B:107:PRO:O	1:B:110:VAL:HG22	1.93	0.68
1:A:129:ILE:O	1:A:133:ILE:HG13	1.93	0.67
1:A:101:LYS:HA	1:A:104:TRP:CD2	2.29	0.67
1:A:226:ARG:C	1:A:227:LEU:HD22	2.15	0.67
1:B:395:LEU:CD2	1:C:469:LEU:HD12	2.24	0.67
1:A:465:GLN:HB3	1:C:395:LEU:HD11	1.77	0.67
1:B:287:TYR:CZ	3:B:502:M3L:HM13	2.30	0.66
1:B:142:VAL:HG23	4:B:819:HOH:O	1.94	0.66
1:B:467:ARG:HA	1:B:470:LYS:HG2	1.77	0.66
1:A:188:CYS:HB3	1:A:212:PHE:CD1	2.31	0.65
1:B:67:ILE:HD11	1:B:237:MET:SD	2.37	0.65
1:B:197:LEU:HB2	1:B:198:PRO:HD3	1.78	0.65
1:B:73:VAL:HG21	1:B:84:LEU:HB3	1.77	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:143:TRP:HB2	1:A:147:PHE:CE1	2.32	0.65
1:A:198:PRO:HG3	4:A:805:HOH:O	1.97	0.65
1:A:98:GLN:HG2	1:A:270:SER:HA	1.78	0.64
1:C:438:GLU:CD	1:C:442:MET:HE2	2.18	0.64
1:A:330:ASP:O	1:A:334:SER:HB2	1.96	0.64
1:C:222:ARG:NH2	2:C:802:SAH:O	2.29	0.64
1:A:53:ALA:C	1:A:149:ILE:HD11	2.18	0.64
1:B:401:ARG:O	1:B:405:LYS:HG3	1.97	0.64
1:A:101:LYS:HA	1:A:104:TRP:CE3	2.33	0.64
1:A:167:GLU:HG3	1:A:437:ARG:NH1	2.12	0.64
1:C:468:ARG:HH11	1:C:468:ARG:HB3	1.63	0.63
1:A:313:THR:HB	1:A:344:ASP:OD1	1.98	0.63
1:B:128:VAL:HG11	1:B:219:LEU:HD11	1.81	0.63
1:C:300:TYR:OH	3:C:500:M3L:HB3	1.99	0.63
1:C:250:GLU:OE2	1:C:288:ASP:HA	1.99	0.63
1:A:98:GLN:HE21	1:A:270:SER:HB2	1.64	0.62
1:B:222:ARG:HA	3:B:502:M3L:HM23	1.80	0.62
1:C:214:TRP:O	1:C:218:ILE:HG12	1.99	0.62
1:A:160:TRP:CD1	1:A:429:ARG:HD3	2.35	0.62
1:A:105:ILE:O	1:A:105:ILE:HG22	1.99	0.62
1:C:67:ILE:HD11	1:C:237:MET:SD	2.39	0.62
1:B:101:LYS:HA	1:B:104:TRP:CD2	2.33	0.62
1:A:222:ARG:HD3	1:A:239:ASP:OD2	2.00	0.62
1:A:481:ILE:HG23	1:C:220:ARG:HH22	1.65	0.62
1:A:99:VAL:O	1:A:104:TRP:CH2	2.52	0.62
1:A:238:ALA:HB1	1:A:271:LEU:HD22	1.81	0.62
1:A:222:ARG:HA	3:A:501:M3L:HM23	1.81	0.61
1:C:107:PRO:O	1:C:110:VAL:HG22	2.00	0.61
1:A:78:VAL:HG23	1:A:80:GLU:HG2	1.81	0.61
1:B:438:GLU:HG2	1:B:442:MET:CE	2.25	0.61
1:B:78:VAL:HG12	1:B:80:GLU:H	1.65	0.61
1:C:222:ARG:O	3:C:500:M3L:HM13	2.01	0.61
1:C:227:LEU:HD11	1:C:256:VAL:HG23	1.82	0.61
1:B:427:ASP:HA	4:B:893:HOH:O	1.99	0.61
1:C:286:GLN:HE21	1:C:288:ASP:C	2.03	0.61
1:C:479:GLY:O	1:C:483:GLU:HG2	2.00	0.61
1:B:176:THR:HG21	1:C:481:ILE:HD12	1.82	0.60
1:A:99:VAL:HG21	1:A:237:MET:HB3	1.82	0.60
1:C:157:THR:HA	1:C:160:TRP:CD1	2.36	0.60
1:C:97:LEU:HD22	1:C:237:MET:HE3	1.84	0.60
1:A:130:LEU:HD21	1:A:191:LEU:HD13	1.84	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:463:TYR:O	1:A:467:ARG:HG3	2.02	0.60
1:A:437:ARG:O	1:A:441:LYS:HG3	2.02	0.60
1:A:58:TRP:CE3	1:A:58:TRP:HA	2.36	0.59
1:A:293:ASN:ND2	1:A:309:ARG:HB2	2.18	0.59
1:C:188:CYS:SG	1:C:212:PHE:CD1	2.95	0.59
1:B:381:TRP:O	1:B:385:GLU:HG3	2.02	0.59
1:A:218:ILE:HG23	1:A:222:ARG:HD2	1.83	0.59
1:C:453:GLN:O	1:C:457:GLU:HG3	2.02	0.59
1:A:105:ILE:HD11	1:A:143:TRP:CD2	2.37	0.59
1:A:413:THR:O	1:A:441:LYS:HE2	2.03	0.58
1:A:106:ASN:ND2	1:A:108:ASP:HB2	2.17	0.58
1:A:78:VAL:CG2	1:A:80:GLU:HG2	2.33	0.58
1:A:313:THR:HG22	4:A:909:HOH:O	2.04	0.58
1:A:107:PRO:O	1:A:110:VAL:HG22	2.03	0.58
1:A:466:GLU:O	1:A:470:LYS:HG2	2.04	0.58
1:A:189:LEU:O	1:A:193:GLN:HG2	2.03	0.58
1:B:61:LEU:HB3	1:B:67:ILE:HG12	1.84	0.58
1:B:59:LYS:O	1:B:63:GLU:HG3	2.04	0.58
1:B:49:SER:O	1:B:52:PRO:HG2	2.03	0.58
1:C:97:LEU:HD22	1:C:237:MET:CE	2.34	0.58
1:A:99:VAL:CG2	1:A:237:MET:HB3	2.33	0.58
1:C:226:ARG:HD2	1:C:252:HIS:NE2	2.19	0.58
1:C:92:ARG:HG3	1:C:274:PRO:O	2.03	0.57
1:C:103:LEU:O	1:C:143:TRP:CZ3	2.57	0.57
1:A:64:GLU:HA	1:A:102:ARG:HH12	1.69	0.57
1:A:54:VAL:N	1:A:149:ILE:HD11	2.19	0.57
1:B:188:CYS:HB3	1:B:212:PHE:CD1	2.39	0.57
1:A:110:VAL:HG12	1:A:131:PHE:CG	2.39	0.57
1:C:398:LYS:O	1:C:402:GLU:HG2	2.05	0.57
1:A:479:GLY:HA3	1:C:342:TYR:CZ	2.40	0.57
1:C:157:THR:OG1	1:C:177:THR:HG21	2.04	0.56
1:C:104:TRP:CH2	1:C:269:PHE:HB2	2.40	0.56
1:B:227:LEU:HD22	1:B:255:GLU:CD	2.26	0.56
1:C:286:GLN:HE22	1:C:309:ARG:HH22	1.53	0.56
1:A:101:LYS:HG3	1:A:104:TRP:CD1	2.41	0.56
1:A:221:SER:O	3:A:501:M3L:HM12	2.06	0.56
1:C:222:ARG:HD3	1:C:239:ASP:OD2	2.06	0.56
1:C:104:TRP:HH2	1:C:269:PHE:N	2.02	0.56
1:A:455:GLU:O	1:A:458:LEU:HB2	2.05	0.56
1:C:470:LYS:HA	1:C:470:LYS:CE	2.31	0.56
1:A:105:ILE:HD11	1:A:143:TRP:CE2	2.40	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:78:VAL:HG12	1:B:80:GLU:HG2	1.88	0.56
1:A:167:GLU:HG3	1:A:437:ARG:HH12	1.71	0.56
1:A:376:PHE:O	1:A:378:ASP:N	2.39	0.56
1:C:463:TYR:O	1:C:467:ARG:HG3	2.06	0.56
1:C:73:VAL:HG11	1:C:96:ILE:HG22	1.88	0.55
1:C:222:ARG:HH11	1:C:239:ASP:CG	2.10	0.55
1:A:286:GLN:HE22	1:A:309:ARG:HH22	1.54	0.55
1:C:74:LYS:HD3	1:C:75:ALA:O	2.06	0.55
1:A:226:ARG:O	1:A:227:LEU:HD13	2.07	0.55
1:B:78:VAL:CG1	1:B:79:THR:N	2.69	0.55
1:B:110:VAL:HG21	1:B:127:SER:HB3	1.87	0.55
1:A:51:SER:HB3	1:A:54:VAL:HB	1.88	0.54
1:B:194:GLU:C	1:B:195:ILE:HD12	2.28	0.54
1:C:105:ILE:HB	1:C:234:VAL:HB	1.90	0.54
1:A:315:THR:HG23	1:B:473:GLY:O	2.06	0.54
1:B:103:LEU:O	1:B:143:TRP:HZ3	1.91	0.54
1:B:73:VAL:CG2	1:B:84:LEU:HB3	2.37	0.54
1:B:73:VAL:HG23	1:B:85:VAL:O	2.08	0.54
1:A:376:PHE:C	1:A:378:ASP:H	2.10	0.54
1:A:277:VAL:HG13	1:A:281:GLU:HB2	1.90	0.54
1:A:97:LEU:HD12	1:A:97:LEU:O	2.09	0.53
1:C:173:LEU:O	1:C:177:THR:HG23	2.08	0.53
1:B:80:GLU:HG3	1:B:242:ASN:ND2	2.24	0.53
1:B:241:ILE:CD1	1:B:285:ILE:HG23	2.39	0.53
1:C:250:GLU:HB3	1:C:286:GLN:CG	2.38	0.53
1:B:51:SER:N	1:B:52:PRO:HD2	2.23	0.53
1:C:455:GLU:O	1:C:458:LEU:HB2	2.09	0.53
1:C:316:LEU:HA	4:C:942:HOH:O	2.07	0.53
1:C:54:VAL:HA	1:C:149:ILE:HD11	1.91	0.53
1:A:58:TRP:NE1	4:A:852:HOH:O	2.32	0.52
1:A:398:LYS:O	1:A:402:GLU:HG2	2.09	0.52
1:C:386:LEU:O	1:C:387:SER:CB	2.57	0.52
1:A:315:THR:HG22	4:B:807:HOH:O	2.09	0.52
1:A:104:TRP:CZ2	1:A:269:PHE:HB2	2.45	0.52
1:A:91:SER:O	1:A:94:ASP:HB2	2.10	0.52
1:B:78:VAL:HG12	1:B:79:THR:N	2.24	0.52
1:A:182:GLU:O	1:A:185:LYS:HB3	2.09	0.52
1:A:141:SER:HB3	4:A:808:HOH:O	2.09	0.52
1:B:177:THR:HG22	1:B:298:LEU:HD13	1.92	0.52
1:A:123:LYS:CB	1:A:124:PRO:HD2	2.40	0.52
1:B:222:ARG:HH11	1:B:239:ASP:CG	2.13	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:227:LEU:HB2	1:B:230:GLU:HB2	1.91	0.52
1:B:103:LEU:O	1:B:143:TRP:CZ3	2.63	0.52
1:A:180:VAL:O	1:A:184:VAL:HG23	2.10	0.51
1:A:197:LEU:HB2	1:A:198:PRO:HD3	1.91	0.51
1:A:123:LYS:HB3	1:A:124:PRO:HD2	1.91	0.51
1:A:54:VAL:HG22	1:A:149:ILE:HD12	1.92	0.51
1:A:157:THR:OG1	1:A:177:THR:HG21	2.11	0.51
1:B:174:LEU:O	1:B:178:VAL:HG23	2.10	0.51
1:B:428:SER:O	1:B:432:ILE:HG13	2.09	0.51
1:A:50:LEU:HD22	1:A:54:VAL:HG11	1.93	0.51
1:C:438:GLU:HG2	1:C:442:MET:HE3	1.92	0.51
1:B:479:GLY:O	1:B:483:GLU:HB2	2.10	0.51
1:A:119:CYS:CA	1:A:122:LEU:HD12	2.41	0.51
1:A:157:THR:OG1	1:A:177:THR:CG2	2.59	0.51
1:A:211:ASP:O	1:A:214:TRP:HB3	2.11	0.51
4:A:809:HOH:O	1:C:315:THR:HG22	2.11	0.51
1:B:78:VAL:CG1	1:B:80:GLU:HG2	2.42	0.50
1:C:103:LEU:O	1:C:143:TRP:HZ3	1.94	0.50
1:C:80:GLU:N	1:C:80:GLU:OE2	2.39	0.50
1:C:224:PHE:HD2	1:C:254:TYR:CE2	2.28	0.50
1:A:410:GLY:HA3	4:A:824:HOH:O	2.11	0.50
1:B:106:ASN:HD21	1:B:108:ASP:HB2	1.76	0.50
1:B:101:LYS:HA	1:B:104:TRP:CE2	2.47	0.50
1:A:277:VAL:CG1	1:A:281:GLU:HB2	2.41	0.50
1:B:386:LEU:O	1:B:387:SER:CB	2.59	0.50
1:B:92:ARG:O	1:B:93:ASN:HB2	2.10	0.50
1:A:371:LEU:HB3	1:A:380:ILE:HD13	1.92	0.50
1:A:68:THR:C	1:A:70:LYS:H	2.14	0.50
1:A:104:TRP:CH2	1:A:269:PHE:HB2	2.46	0.50
3:C:500:M3L:CE	3:C:500:M3L:CG	2.80	0.50
1:C:226:ARG:HG2	1:C:252:HIS:NE2	2.25	0.50
1:C:438:GLU:HG2	1:C:442:MET:CE	2.42	0.50
1:B:222:ARG:CA	3:B:502:M3L:HM23	2.42	0.50
1:A:301:GLY:HA3	4:A:804:HOH:O	2.11	0.50
1:C:250:GLU:C	1:C:252:HIS:H	2.16	0.49
1:A:151:PRO:HD2	1:A:222:ARG:HH21	1.77	0.49
1:A:286:GLN:NE2	1:A:288:ASP:H	2.10	0.49
1:A:60:TRP:HB2	1:A:145:HIS:CD2	2.47	0.49
1:C:66:VAL:HA	4:C:849:HOH:O	2.13	0.49
1:A:100:PRO:HA	1:A:268:LEU:CD1	2.41	0.49
1:B:128:VAL:CG1	1:B:219:LEU:HD11	2.42	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:316:LEU:HD12	1:C:343:PHE:CE1	2.47	0.49
1:A:380:ILE:O	1:A:384:LEU:HG	2.13	0.49
1:B:226:ARG:HE	1:B:226:ARG:HA	1.77	0.49
1:A:390:ARG:HA	1:A:463:TYR:CZ	2.48	0.49
1:A:59:LYS:HA	1:A:62:GLN:OE1	2.13	0.49
1:B:446:GLN:O	1:B:450:ILE:HG13	2.13	0.49
1:C:446:GLN:O	1:C:450:ILE:HG13	2.13	0.49
1:A:57:PHE:CE1	1:A:146:TYR:HA	2.48	0.49
1:A:224:PHE:CZ	3:A:501:M3L:HM22	2.48	0.49
1:B:453:GLN:O	1:B:457:GLU:HG3	2.13	0.49
1:A:96:ILE:HG13	1:A:97:LEU:HG	1.94	0.49
1:C:61:LEU:HB3	1:C:67:ILE:HG12	1.94	0.49
1:C:74:LYS:HG2	1:C:87:LEU:CD2	2.42	0.49
1:A:231:ASN:O	1:A:232:LEU:HG	2.13	0.48
1:A:329:LEU:O	1:A:333:GLU:HG3	2.13	0.48
1:A:51:SER:HB3	1:A:54:VAL:CG2	2.44	0.48
1:B:92:ARG:CZ	1:B:92:ARG:HB2	2.42	0.48
1:C:260:ALA:O	1:C:262:LEU:HD22	2.13	0.48
1:A:58:TRP:HE3	1:A:58:TRP:HA	1.78	0.48
1:B:376:PHE:O	1:B:378:ASP:N	2.43	0.48
1:C:124:PRO:O	1:C:128:VAL:HG23	2.14	0.48
1:C:235:VAL:HG21	1:C:269:PHE:CD1	2.48	0.48
1:B:110:VAL:HG12	1:B:131:PHE:CG	2.48	0.48
1:B:167:GLU:HG2	1:B:430:LEU:HD12	1.95	0.48
1:C:192:GLU:HA	1:C:196:ILE:HB	1.94	0.48
1:B:167:GLU:HG3	1:B:437:ARG:NH1	2.28	0.48
1:C:241:ILE:CD1	1:C:285:ILE:HG23	2.44	0.48
1:B:480:ASP:HA	4:B:860:HOH:O	2.12	0.48
1:A:233:VAL:HG12	1:A:234:VAL:N	2.28	0.48
1:C:167:GLU:HG2	1:C:430:LEU:CD1	2.43	0.48
1:A:64:GLU:CA	1:A:102:ARG:HH12	2.27	0.48
1:B:177:THR:O	1:B:181:LYS:HG3	2.14	0.48
1:A:58:TRP:O	1:A:62:GLN:HG3	2.13	0.48
1:A:144:LYS:HA	4:A:808:HOH:O	2.13	0.48
1:A:209:LEU:O	1:A:212:PHE:HB2	2.13	0.48
1:B:225:SER:C	1:B:227:LEU:H	2.17	0.48
1:A:143:TRP:O	1:A:147:PHE:HD1	1.96	0.48
1:C:226:ARG:NH1	4:C:809:HOH:O	2.47	0.47
1:A:107:PRO:HA	1:A:110:VAL:HG22	1.96	0.47
1:C:182:GLU:O	1:C:185:LYS:HB3	2.14	0.47
1:A:415:ILE:HG13	1:A:441:LYS:HD2	1.96	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:241:ILE:HD13	1:B:285:ILE:HG23	1.94	0.47
1:B:264:SER:HA	1:B:267:TYR:CZ	2.49	0.47
1:C:251:ASP:HB2	4:C:912:HOH:O	2.13	0.47
1:C:348:ASN:H	1:C:446:GLN:NE2	2.09	0.47
1:C:128:VAL:HG11	1:C:219:LEU:HD11	1.95	0.47
1:B:228:ARG:O	1:B:229:ASN:HB2	2.15	0.47
1:C:250:GLU:O	1:C:250:GLU:HG3	2.13	0.47
1:B:227:LEU:CB	1:B:230:GLU:HB2	2.44	0.47
1:A:386:LEU:O	1:A:387:SER:CB	2.63	0.47
1:C:224:PHE:CZ	3:C:500:M3L:HM12	2.49	0.47
1:A:464:TYR:HB3	4:A:838:HOH:O	2.15	0.47
1:C:104:TRP:CH2	1:C:269:PHE:N	2.81	0.47
1:A:57:PHE:CD1	1:A:146:TYR:HA	2.50	0.47
1:C:226:ARG:CD	1:C:252:HIS:NE2	2.79	0.47
1:B:277:VAL:HG13	1:B:281:GLU:HB2	1.97	0.47
1:A:193:GLN:HA	1:A:197:LEU:HD12	1.97	0.46
1:B:264:SER:HA	1:B:267:TYR:CE2	2.50	0.46
1:B:251:ASP:OD2	1:B:272:LYS:NZ	2.47	0.46
1:A:194:GLU:O	1:A:195:ILE:HD12	2.14	0.46
1:C:226:ARG:HH12	1:C:250:GLU:HB2	1.80	0.46
1:C:250:GLU:HG2	1:C:289:LEU:HD12	1.97	0.46
1:B:398:LYS:O	1:B:402:GLU:HG2	2.15	0.46
1:C:226:ARG:NE	1:C:252:HIS:CD2	2.83	0.46
1:C:250:GLU:HB3	1:C:286:GLN:HG3	1.97	0.46
1:A:101:LYS:HA	1:A:104:TRP:CE2	2.49	0.46
1:B:97:LEU:HB2	1:B:237:MET:CE	2.45	0.46
1:B:220:ARG:HH22	1:C:481:ILE:HG23	1.79	0.46
1:B:143:TRP:HB2	1:B:147:PHE:CE1	2.51	0.46
1:B:363:ALA:O	1:B:364:LEU:C	2.54	0.46
1:C:277:VAL:HG13	1:C:281:GLU:HB2	1.97	0.46
1:A:96:ILE:HD11	1:A:271:LEU:HD23	1.98	0.46
1:A:286:GLN:NE2	1:A:288:ASP:C	2.67	0.46
1:C:376:PHE:HA	4:C:859:HOH:O	2.16	0.46
1:C:99:VAL:O	1:C:104:TRP:HH2	1.99	0.46
1:B:301:GLY:HA3	4:B:804:HOH:O	2.15	0.46
1:A:395:LEU:HD22	1:B:469:LEU:CD1	2.31	0.45
1:C:157:THR:OG1	1:C:177:THR:CG2	2.63	0.45
1:A:106:ASN:HB2	1:A:107:PRO:CD	2.46	0.45
1:C:59:LYS:O	1:C:63:GLU:HG3	2.16	0.45
1:A:73:VAL:HG21	1:A:84:LEU:HB3	1.99	0.45
1:B:146:TYR:CE1	1:B:236:PRO:HA	2.51	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:482:LEU:HD11	1:C:179:SER:CB	2.31	0.45
1:A:227:LEU:HD22	1:A:227:LEU:N	2.31	0.45
1:B:257:LYS:HA	1:B:267:TYR:CD1	2.52	0.45
1:C:310:HIS:CD2	1:C:439:GLY:HA3	2.51	0.45
1:A:54:VAL:HA	1:A:149:ILE:HD11	1.99	0.45
1:C:64:GLU:OE1	1:C:102:ARG:NH1	2.50	0.45
1:A:168:LEU:HD21	1:A:433:ALA:HA	1.99	0.45
1:C:320:GLU:HA	1:C:325:PHE:CD1	2.51	0.45
1:C:92:ARG:NH1	1:C:92:ARG:HB2	2.31	0.45
1:C:158:ILE:HA	1:C:181:LYS:HD2	1.99	0.45
1:B:313:THR:HB	1:B:344:ASP:OD1	2.17	0.45
1:A:157:THR:HA	1:A:160:TRP:CD1	2.52	0.45
1:A:177:THR:HG22	1:A:298:LEU:HG	1.98	0.45
1:B:50:LEU:C	1:B:52:PRO:HD2	2.36	0.45
1:B:192:GLU:HA	1:B:196:ILE:HB	1.98	0.45
1:B:310:HIS:CD2	1:B:439:GLY:HA3	2.51	0.45
1:B:97:LEU:HB2	1:B:237:MET:HE1	1.98	0.45
1:A:212:PHE:HB3	4:A:843:HOH:O	2.17	0.45
1:C:92:ARG:HB2	1:C:92:ARG:HH11	1.82	0.45
1:B:376:PHE:C	1:B:378:ASP:H	2.20	0.45
1:C:94:ASP:O	1:C:272:LYS:HB2	2.17	0.45
1:A:146:TYR:CD2	4:A:845:HOH:O	2.57	0.44
1:C:97:LEU:C	1:C:97:LEU:HD12	2.37	0.44
1:A:67:ILE:HD11	4:A:852:HOH:O	2.17	0.44
1:C:241:ILE:HD13	1:C:285:ILE:HG23	1.99	0.44
1:A:73:VAL:CG2	1:A:84:LEU:HB3	2.47	0.44
1:C:381:TRP:O	1:C:385:GLU:HG3	2.18	0.44
3:B:502:M3L:HB2	3:B:502:M3L:HE2	1.75	0.44
1:B:49:SER:C	1:B:52:PRO:HD2	2.37	0.44
1:B:329:LEU:O	1:B:333:GLU:HG3	2.17	0.44
1:A:147:PHE:CA	4:A:845:HOH:O	2.59	0.44
1:B:167:GLU:HG2	1:B:430:LEU:CD1	2.47	0.44
1:C:97:LEU:HD13	1:C:237:MET:HE3	1.99	0.44
1:C:110:VAL:HG21	1:C:127:SER:HB3	1.98	0.44
1:B:255:GLU:HA	1:B:268:LEU:O	2.17	0.44
1:B:439:GLY:HA2	1:B:442:MET:CE	2.41	0.44
1:A:389:SER:HA	1:A:463:TYR:CG	2.52	0.44
1:A:363:ALA:HB2	1:B:469:LEU:HD11	2.00	0.44
1:C:143:TRP:HB2	1:C:147:PHE:CE1	2.53	0.44
1:B:64:GLU:OE2	1:B:64:GLU:HA	2.18	0.44
1:C:153:GLU:HG2	1:C:159:TYR:CD1	2.52	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:202:LEU:C	1:A:204:PRO:HD3	2.38	0.43
1:C:244:SER:HB2	1:C:284:TYR:CG	2.54	0.43
1:B:185:LYS:O	1:B:189:LEU:HG	2.18	0.43
1:A:446:GLN:O	1:A:450:ILE:HG13	2.18	0.43
1:C:252:HIS:N	1:C:252:HIS:CD2	2.85	0.43
1:C:348:ASN:ND2	4:C:816:HOH:O	2.34	0.43
1:C:99:VAL:O	1:C:104:TRP:CH2	2.71	0.43
1:A:242:ASN:HA	1:A:287:TYR:OH	2.19	0.43
1:C:98:GLN:HA	1:C:269:PHE:O	2.17	0.43
1:C:167:GLU:HG2	1:C:430:LEU:HD12	2.00	0.43
1:C:313:THR:HB	1:C:344:ASP:OD1	2.18	0.43
1:C:146:TYR:CE1	1:C:236:PRO:HA	2.52	0.43
1:A:54:VAL:CA	1:A:149:ILE:HD11	2.47	0.43
1:C:348:ASN:N	1:C:446:GLN:HE22	2.11	0.43
1:B:189:LEU:O	1:B:193:GLN:HG2	2.19	0.43
1:A:104:TRP:O	1:A:105:ILE:HG13	2.18	0.43
1:A:98:GLN:HA	1:A:269:PHE:O	2.18	0.43
1:A:190:LYS:O	1:A:194:GLU:HB2	2.18	0.43
1:A:222:ARG:NH1	1:A:239:ASP:OD2	2.46	0.43
1:A:176:THR:HG21	1:B:481:ILE:HD12	2.00	0.43
1:A:224:PHE:CE1	3:A:501:M3L:HM22	2.53	0.43
1:C:410:GLY:HA3	4:C:834:HOH:O	2.18	0.43
1:C:54:VAL:HA	1:C:149:ILE:CD1	2.48	0.43
1:A:97:LEU:HD13	1:A:237:MET:HG3	2.01	0.43
1:A:479:GLY:O	1:A:483:GLU:HG3	2.18	0.43
1:A:451:PHE:O	1:A:455:GLU:HG3	2.19	0.43
1:A:106:ASN:HB2	1:A:107:PRO:HD2	1.99	0.43
1:A:119:CYS:CB	1:A:122:LEU:HD12	2.48	0.43
1:C:418:ASP:O	1:C:422:LYS:HG3	2.19	0.43
1:B:426:LEU:HD23	1:B:431:ALA:HA	2.01	0.43
1:C:371:LEU:HB3	1:C:380:ILE:CD1	2.43	0.43
1:A:411:TYR:OH	1:A:440:GLU:OE1	2.25	0.43
1:C:101:LYS:HA	1:C:104:TRP:CD2	2.53	0.43
1:B:104:TRP:CH2	1:B:269:PHE:HB2	2.54	0.43
1:C:438:GLU:OE2	1:C:442:MET:HE2	2.19	0.43
1:B:167:GLU:HG3	1:B:437:ARG:HH12	1.84	0.43
1:B:488:GLN:HB3	4:B:864:HOH:O	2.19	0.43
1:C:100:PRO:HA	1:C:268:LEU:HB3	2.01	0.43
1:B:348:ASN:N	1:B:446:GLN:HE22	2.18	0.42
1:C:443:VAL:O	1:C:447:ILE:HG13	2.19	0.42
1:C:185:LYS:O	1:C:189:LEU:HG	2.18	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:286:GLN:NE2	1:C:288:ASP:C	2.70	0.42
1:A:342:TYR:CZ	1:B:479:GLY:HA3	2.54	0.42
1:B:78:VAL:HG11	1:B:282:GLN:NE2	2.28	0.42
1:A:176:THR:O	1:A:180:VAL:HG23	2.19	0.42
1:C:257:LYS:CB	1:C:257:LYS:NZ	2.83	0.42
1:B:157:THR:HA	1:B:160:TRP:CD1	2.55	0.42
1:A:68:THR:C	1:A:70:LYS:N	2.73	0.42
1:C:129:ILE:O	1:C:133:ILE:HG13	2.19	0.42
1:A:100:PRO:C	1:A:102:ARG:H	2.23	0.42
1:B:348:ASN:H	1:B:446:GLN:HE22	1.68	0.42
1:C:287:TYR:CZ	3:C:500:M3L:HM33	2.55	0.42
1:B:395:LEU:HD13	1:C:469:LEU:HD11	2.01	0.42
1:A:146:TYR:CE1	1:A:236:PRO:HA	2.54	0.42
1:B:427:ASP:CB	4:B:893:HOH:O	2.68	0.42
1:B:444:LEU:HA	1:B:444:LEU:HD12	1.77	0.42
1:B:257:LYS:HB3	1:B:258:GLY:H	1.61	0.42
1:A:483:GLU:C	1:A:485:LEU:H	2.23	0.41
1:C:386:LEU:O	1:C:387:SER:HB3	2.19	0.41
1:B:441:LYS:NZ	4:B:806:HOH:O	2.51	0.41
1:B:130:LEU:HD11	1:B:191:LEU:HD22	2.01	0.41
1:A:390:ARG:HB2	1:A:463:TYR:CE1	2.55	0.41
1:C:167:GLU:HG3	1:C:437:ARG:NH1	2.35	0.41
1:C:195:ILE:N	1:C:195:ILE:HD12	2.34	0.41
1:C:197:LEU:N	1:C:198:PRO:HD2	2.35	0.41
1:A:117:ARG:HB2	4:A:869:HOH:O	2.20	0.41
1:B:142:VAL:HG12	1:B:142:VAL:O	2.19	0.41
1:A:241:ILE:HG23	1:A:241:ILE:O	2.20	0.41
1:B:463:TYR:O	1:B:467:ARG:HG3	2.21	0.41
1:A:398:LYS:NZ	1:B:466:GLU:OE1	2.44	0.41
1:B:180:VAL:O	1:B:184:VAL:HG23	2.20	0.41
1:A:454:LYS:HE2	4:A:853:HOH:O	2.19	0.41
1:A:102:ARG:HG2	1:A:102:ARG:O	2.20	0.41
1:B:315:THR:HG23	1:C:473:GLY:O	2.20	0.41
1:B:287:TYR:CE2	3:B:502:M3L:HD3	2.56	0.41
1:A:376:PHE:C	1:A:378:ASP:N	2.74	0.41
1:B:395:LEU:HD11	1:C:465:GLN:HB3	2.03	0.41
1:C:251:ASP:O	1:C:252:HIS:O	2.39	0.41
1:B:61:LEU:CB	1:B:67:ILE:HG12	2.48	0.41
1:A:151:PRO:HD2	1:A:222:ARG:NH2	2.35	0.41
1:A:394:GLU:HB2	1:A:458:LEU:HD21	2.03	0.41
1:C:376:PHE:C	1:C:378:ASP:H	2.24	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:356:LEU:N	1:C:357:PRO:HD2	2.36	0.41
1:B:58:TRP:CZ2	1:B:74:LYS:HA	2.56	0.41
2:C:802:SAH:SD	3:C:500:M3L:HM31	2.60	0.41
1:A:96:ILE:HD11	1:A:271:LEU:CD2	2.50	0.41
1:C:82:LEU:O	2:C:802:SAH:N	2.54	0.41
1:A:62:GLN:HG2	1:A:67:ILE:HG23	2.03	0.41
1:A:470:LYS:HE2	1:A:470:LYS:HA	2.02	0.41
1:B:51:SER:N	1:B:52:PRO:CD	2.83	0.41
1:C:150:LEU:HA	1:C:151:PRO:HD3	1.93	0.41
1:C:250:GLU:HB3	1:C:286:GLN:HG2	2.02	0.41
1:A:102:ARG:HB2	4:A:829:HOH:O	2.21	0.41
1:C:97:LEU:HD22	1:C:237:MET:SD	2.61	0.41
1:B:427:ASP:OD2	1:B:428:SER:N	2.53	0.41
1:C:163:GLU:O	1:C:166:GLN:HB2	2.21	0.41
1:C:286:GLN:HG2	1:C:289:LEU:HG	2.03	0.40
1:A:53:ALA:O	1:A:57:PHE:HB2	2.21	0.40
1:A:90:ILE:HD13	1:A:96:ILE:HG22	2.03	0.40
1:A:218:ILE:O	1:A:222:ARG:HB2	2.22	0.40
1:B:390:ARG:HB2	1:B:463:TYR:CE1	2.57	0.40
1:B:188:CYS:HB3	1:B:212:PHE:CE1	2.56	0.40
1:C:389:SER:HB2	4:C:858:HOH:O	2.21	0.40
1:C:297:ALA:O	1:C:300:TYR:O	2.38	0.40
1:A:438:GLU:CG	1:A:442:MET:HE2	2.43	0.40
1:A:99:VAL:HG21	1:A:235:VAL:HG12	2.04	0.40
1:A:91:SER:HB2	1:A:94:ASP:OD1	2.22	0.40
1:A:201:ARG:HH11	1:A:201:ARG:HG2	1.85	0.40
1:A:101:LYS:HA	1:A:104:TRP:CZ3	2.56	0.40
1:C:226:ARG:CD	1:C:252:HIS:CD2	3.05	0.40
1:A:100:PRO:C	1:A:102:ARG:N	2.75	0.40
1:A:60:TRP:O	1:A:64:GLU:HG2	2.21	0.40
1:C:196:ILE:HD13	1:C:207:VAL:HG21	2.03	0.40
1:B:364:LEU:HD23	1:B:372:LEU:HD11	2.03	0.40
1:B:367:THR:OG1	4:B:816:HOH:O	2.22	0.40

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

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	418/440 (95%)	366 (88%)	44 (10%)	8 (2%)	10	8
1	B	438/440 (100%)	412 (94%)	19 (4%)	7 (2%)	12	11
1	C	436/440 (99%)	402 (92%)	26 (6%)	8 (2%)	11	9
All	All	1292/1320 (98%)	1180 (91%)	89 (7%)	23 (2%)	11	9

All (23) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	C	364	LEU
1	C	387	SER
1	A	73	VAL
1	A	105	ILE
1	A	377	ARG
1	A	387	SER
1	A	479	GLY
1	B	364	LEU
1	B	387	SER
1	C	252	HIS
1	C	470	LYS
1	A	52	PRO
1	A	236	PRO
1	A	471	ASP
1	B	377	ARG
1	C	232	LEU
1	B	226	ARG
1	B	288	ASP
1	B	366	GLY
1	C	377	ARG
1	C	105	ILE
1	C	479	GLY
1	B	236	PRO

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	374/386 (97%)	357 (96%)	17 (4%)	34	47
1	B	386/386 (100%)	370 (96%)	16 (4%)	37	52
1	C	384/386 (100%)	367 (96%)	17 (4%)	35	49
All	All	1144/1158 (99%)	1094 (96%)	50 (4%)	35	49

All (50) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	58	TRP
1	A	104	TRP
1	A	127	SER
1	A	143	TRP
1	A	209	LEU
1	A	237	MET
1	A	252	HIS
1	A	298	LEU
1	A	299	ASP
1	A	313	THR
1	A	315	THR
1	A	334	SER
1	A	378	ASP
1	A	395	LEU
1	A	444	LEU
1	A	453	GLN
1	A	480	ASP
1	B	80	GLU
1	B	94	ASP
1	B	104	TRP
1	B	143	TRP
1	B	209	LEU
1	B	210	ASP
1	B	226	ARG
1	B	236	PRO
1	B	313	THR

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Mol	Chain	Res	Type
1	B	315	THR
1	B	378	ASP
1	B	395	LEU
1	B	444	LEU
1	B	453	GLN
1	B	482	LEU
1	B	483	GLU
1	C	74	LYS
1	C	79	THR
1	C	104	TRP
1	C	143	TRP
1	C	209	LEU
1	C	210	ASP
1	C	219	LEU
1	C	236	PRO
1	C	257	LYS
1	C	268	LEU
1	C	313	THR
1	C	315	THR
1	C	378	ASP
1	C	395	LEU
1	C	444	LEU
1	C	453	GLN
1	C	468	ARG

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (26) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	55	GLN
1	A	93	ASN
1	A	98	GLN
1	A	106	ASN
1	A	145	HIS
1	A	152	GLN
1	A	169	GLN
1	A	286	GLN
1	B	55	GLN
1	B	106	ASN
1	B	152	GLN
1	B	169	GLN
1	B	286	GLN
1	B	310	HIS

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Mol	Chain	Res	Type
1	B	453	GLN
1	B	488	GLN
1	C	55	GLN
1	C	98	GLN
1	C	145	HIS
1	C	152	GLN
1	C	166	GLN
1	C	169	GLN
1	C	286	GLN
1	C	310	HIS
1	C	392	ASN
1	C	446	GLN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no carbohydrates in this entry.

5.6 Ligand geometry [i](#)

6 ligands are modelled in this entry.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
3	M3L	A	501	-	9,12,12	0.68	0	10,16,16	0.42	0
2	SAH	A	800	-	20,28,28	0.94	1 (5%)	19,40,40	1.02	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
3	M3L	B	502	-	9,12,12	0.69	0	10,16,16	0.38	0
2	SAH	B	801	-	20,28,28	1.15	2 (10%)	19,40,40	0.85	0
3	M3L	C	500	-	9,12,12	2.17	2 (22%)	10,16,16	0.78	0
2	SAH	C	802	-	20,28,28	0.94	1 (5%)	19,40,40	0.81	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	M3L	A	501	-	-	0/8/12/12	0/0/0/0
2	SAH	A	800	-	-	0/7/31/31	0/3/3/3
3	M3L	B	502	-	-	0/8/12/12	0/0/0/0
2	SAH	B	801	-	-	0/7/31/31	0/3/3/3
3	M3L	C	500	-	-	0/8/12/12	0/0/0/0
2	SAH	C	802	-	-	0/7/31/31	0/3/3/3

All (6) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	C	500	M3L	CG-CB	-3.93	1.34	1.52
2	C	802	SAH	C2-N3	2.26	1.36	1.32
2	A	800	SAH	C2-N3	2.40	1.36	1.32
2	B	801	SAH	C2-N3	2.77	1.37	1.32
2	B	801	SAH	C4-N3	2.89	1.39	1.35
3	C	500	M3L	CD-CG	4.78	1.79	1.51

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

4 monomers are involved in 19 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	501	M3L	4	0
3	B	502	M3L	5	0
3	C	500	M3L	8	0
2	C	802	SAH	3	0

5.7 Other polymers

There are no such residues in this entry.

5.8 Polymer linkage issues

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	424/440 (96%)	0.66	63 (14%) 3 3	45, 66, 123, 137	0
1	B	440/440 (100%)	0.14	25 (5%) 27 30	37, 60, 97, 127	0
1	C	438/440 (99%)	0.14	23 (5%) 30 33	40, 62, 95, 124	0
All	All	1302/1320 (98%)	0.31	111 (8%) 13 13	37, 62, 105, 137	0

All (111) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	487	PHE	8.6
1	A	267	TYR	7.3
1	A	140	ASP	7.2
1	A	145	HIS	6.6
1	C	250	GLU	6.5
1	A	112	ALA	6.4
1	C	471	ASP	5.4
1	A	139	GLU	5.3
1	A	117	ARG	5.2
1	B	486	TYR	5.1
1	A	59	LYS	4.9
1	B	480	ASP	4.6
1	A	206	PRO	4.5
1	B	471	ASP	4.3
1	A	231	ASN	4.3
1	A	63	GLU	4.2
1	A	471	ASP	4.2
1	A	144	LYS	4.2
1	C	486	TYR	4.2
1	A	486	TYR	4.1
1	A	60	TRP	4.0
1	C	112	ALA	4.0
1	A	148	GLY	4.0

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Mol	Chain	Res	Type	RSRZ
1	A	57	PHE	3.9
1	A	254	TYR	3.9
1	A	201	ARG	3.8
1	B	226	ARG	3.7
1	A	197	LEU	3.7
1	A	124	PRO	3.6
1	A	114	GLU	3.6
1	A	118	VAL	3.6
1	C	70	LYS	3.5
1	A	50	LEU	3.5
1	C	251	ASP	3.5
1	A	137	SER	3.5
1	A	55	GLN	3.4
1	C	139	GLU	3.4
1	A	108	ASP	3.3
1	A	116	GLY	3.3
1	C	117	ARG	3.3
1	A	205	ASP	3.2
1	C	193	GLN	3.2
1	A	211	ASP	3.2
1	A	92	ARG	3.0
1	A	256	VAL	3.0
1	A	141	SER	3.0
1	C	121	GLU	3.0
1	A	268	LEU	2.9
1	A	128	VAL	2.9
1	B	488	GLN	2.9
1	C	69	ALA	2.9
1	B	55	GLN	2.9
1	B	143	TRP	2.9
1	A	183	TYR	2.8
1	B	375	LEU	2.8
1	B	193	GLN	2.8
1	A	70	LYS	2.8
1	A	62	GLN	2.7
1	A	152	GLN	2.7
1	B	229	ASN	2.7
1	A	269	PHE	2.7
1	A	196	ILE	2.7
1	A	203	PHE	2.7
1	B	228	ARG	2.6
1	A	138	ARG	2.6

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Mol	Chain	Res	Type	RSRZ
1	C	200	LYS	2.6
1	A	136	ARG	2.6
1	A	200	LYS	2.5
1	B	117	ARG	2.5
1	B	378	ASP	2.5
1	A	204	PRO	2.5
1	B	121	GLU	2.5
1	B	409	ALA	2.5
1	A	225	SER	2.4
1	A	234	VAL	2.4
1	A	119	CYS	2.4
1	A	65	GLY	2.4
1	A	377	ARG	2.4
1	A	470	LYS	2.4
1	B	481	ILE	2.4
1	B	104	TRP	2.4
1	C	229	ASN	2.3
1	B	201	ARG	2.3
1	B	163	GLU	2.3
1	A	69	ALA	2.3
1	A	227	LEU	2.3
1	A	212	PHE	2.3
1	C	483	GLU	2.3
1	C	205	ASP	2.3
1	A	58	TRP	2.3
1	A	102	ARG	2.3
1	C	59	LYS	2.2
1	B	405	LYS	2.2
1	B	336	GLY	2.2
1	B	139	GLU	2.2
1	C	144	LYS	2.2
1	A	202	LEU	2.2
1	A	142	VAL	2.2
1	C	55	GLN	2.2
1	A	250	GLU	2.1
1	A	111	ALA	2.1
1	A	195	ILE	2.1
1	C	163	GLU	2.1
1	A	185	LYS	2.1
1	B	460	GLN	2.1
1	C	120	SER	2.1
1	B	361	LEU	2.0

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Mol	Chain	Res	Type	RSRZ
1	A	163	GLU	2.0
1	C	485	LEU	2.0
1	C	63	GLU	2.0
1	B	205	ASP	2.0

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

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

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
3	M3L	C	500	13/13	0.83	0.63	10.28	86,110,156,158	0
3	M3L	A	501	13/13	0.72	0.77	8.95	148,161,189,191	0
3	M3L	B	502	13/13	0.83	0.67	5.36	111,128,164,165	0
2	SAH	C	802	26/26	0.96	0.12	-0.07	43,48,49,50	0
2	SAH	A	800	26/26	0.94	0.14	-0.10	57,59,70,72	0
2	SAH	B	801	26/26	0.97	0.11	-0.69	36,40,43,46	0

6.5 Other polymers [i](#)

There are no such residues in this entry.