



Full wwPDB X-ray Structure Validation Report

Feb 26, 2014 – 09:13 PM GMT

PDB ID : 2C8L
Title : CRYSTAL STRUCTURE OF (SR) CALCIUM-ATPASE E2(TG) FORM
Authors : Jensen, A.M.; Sorensen, T.L.; Olesen, C.; Moller, J.V.; Nissen, P.
Deposited on : 2005-12-06
Resolution : 3.10 Å(reported)

This is a full wwPDB 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/ValidationPDFNotes.html>

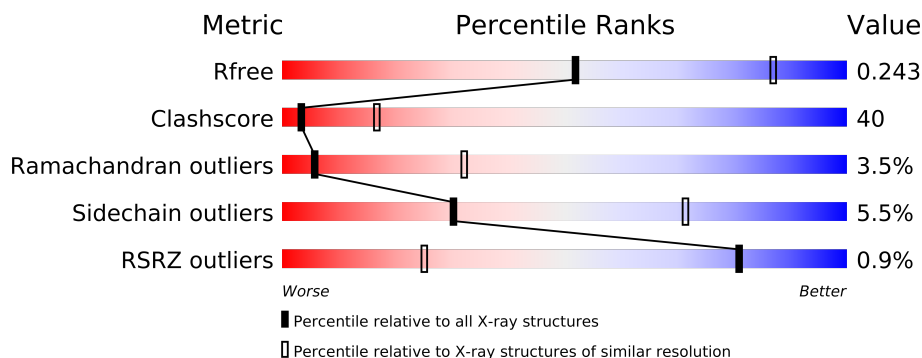
The following versions of software and data (see [references](#)) were used in the production of this report:

MolProbity : 4.02b-467
Mogul : 1.15 2013
Xtriage (Phenix) : dev-1323
EDS : stable22639
Percentile statistics : 21963
Refmac : 5.8.0049
CCP4 : 6.3.0 (Settle)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et. al. (1996)
Validation Pipeline (wwPDB-VP) : stable22683

1 Overall quality at a glance


The reported resolution of this entry is 3.10 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}	66092	1007 (3.18-3.02)
Clashscore	79885	1078 (3.16-3.04)
Ramachandran outliers	78287	1044 (3.16-3.04)
Sidechain outliers	78261	1044 (3.16-3.04)
RSRZ outliers	66119	1008 (3.18-3.02)

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. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density.

Mol	Chain	Length	Quality of chain
1	A	994	

The following table lists non-polymeric compounds that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Geometry	Electron density
3	NA	A	1996	-	X

2 Entry composition i

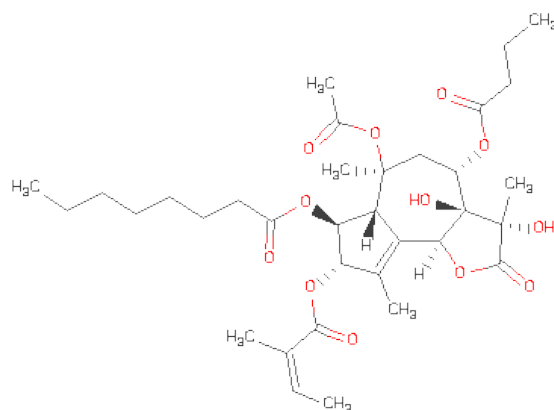
There are 3 unique types of molecules in this entry. The entry contains 7718 atoms, of which 0 are hydrogen and 0 are deuterium.

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 SARCOPLASMIC/ENDOPLASMICRETICULUM CALCIUM ATPASE 1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	994	7671	4876	1287	1451	57	0	0	0

- Molecule 2 is OCTANOIC ACID [3S-[3ALPHA, 3ABETA, 4ALPHA, 6BETA, 6ABETA, 7BETA, 8ALPHA(Z), 9BALPHA]]-6-(ACETYLOXY)-2,3,-3A,4,5,6,6A,7,8,9B-DECAHYDRO-3,3A-DIHYDROXY-3,6,9-TRIMETHYL-8-[(2-METHYL-1-OXO-2-BUTENYL)OXY]-2-OXO-4-(1-OXOBUTOXY)-AZULENO[4,5-B]FURAN-7-YLESTER (three-letter code: TG1) (formula: C₃₄H₅₀O₁₂).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
			Total	C	O		
2	A	1	46	34	12	0	0

- Molecule 3 is SODIUM ION (three-letter code: NA) (formula: Na).

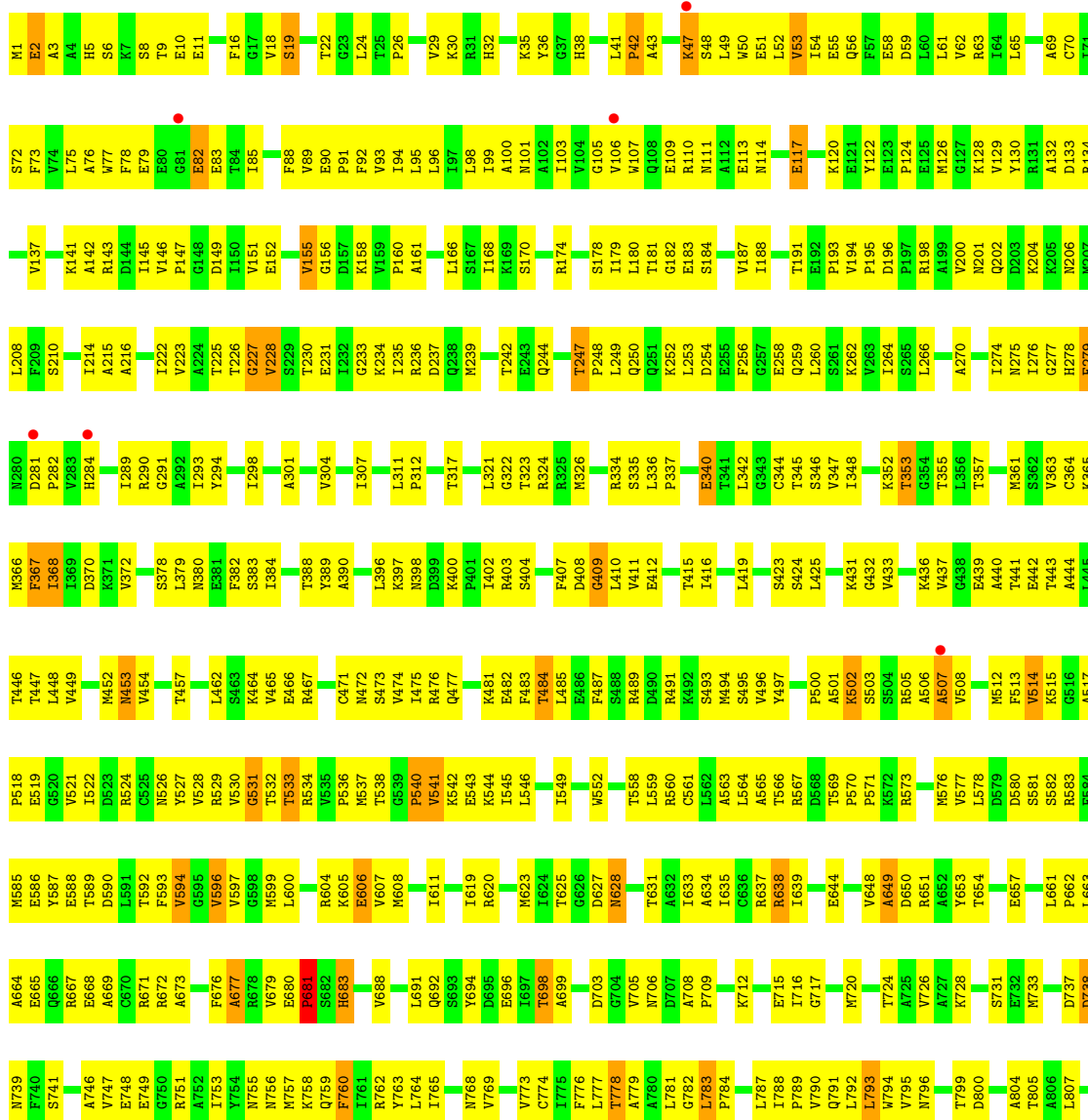
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	1	Total 1	Na 1	0	0

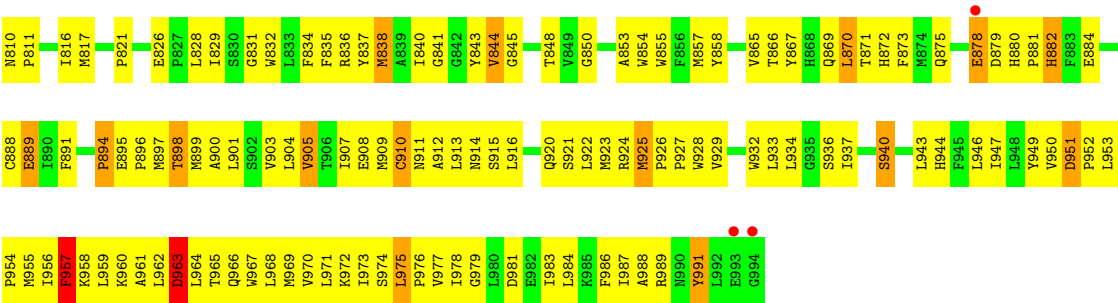
3 Residue-property plots

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 ($RSRZ > 2$). 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: SARCOPLASMIC/ENDOPLASMICRETICULUM CALCIUM ATPASE 1

Chain A: 





4 Data and refinement statistics

Property	Value	Source
Space group	P 41 21 2	Depositor
Cell constants a, b, c, α , β , γ	71.51Å 71.51Å 589.36Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	14.99 – 3.10 49.84 – 3.10	Depositor EDS
% Data completeness (in resolution range)	99.8 (14.99-3.10) 99.9 (49.84-3.10)	Depositor EDS
R_{merge}	0.10	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.95 (at 3.12Å)	Xtriage
Refinement program	CNS 1.1	Depositor
R, R_{free}	0.249 , 0.306 0.248 , 0.243	Depositor DCC
R_{free} test set	1481 reflections (5.10%)	DCC
Wilson B-factor (Å ²)	76.6	Xtriage
Anisotropy	0.247	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.28 , 34.8	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning	$\langle L \rangle = 0.46$, $\langle L^2 \rangle = 0.28$	Xtriage
Outliers	0 of 29367 reflections	Xtriage
F_o, F_c correlation	0.91	EDS
Total number of atoms	7718	wwPDB-VP
Average B, all atoms (Å ²)	71.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.06% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

5 Model quality ⓘ

5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: NA, TG1

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	0/7812	0.68	1/10592 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	2	GLU	N-CA-C	5.41	125.62	111.00

There are no chirality outliers.

There are no planarity outliers.

5.2 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 hydrogens added by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, and the number in parentheses is this value normalized per 1000 atoms of the molecule in the chain. The Symm-Clashes column gives symmetry related clashes, in the same way as for the Clashes column.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	7671	0	7764	620	0
2	A	46	0	50	5	0
3	A	1	0	0	0	0
All	All	7718	0	7814	620	0

Clashscore is defined as the number of clashes calculated for the entry per 1000 atoms (including hydrogens) of the entry. The overall clashscore for this entry is 40.

All (620) close contacts within the same asymmetric unit are listed below.

Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:898:THR:HG22	1:A:958:LYS:HB3	1.26	1.12
1:A:453:ASN:HB3	1:A:471:CYS:SG	1.94	1.07
1:A:795:VAL:HA	1:A:799:THR:OG1	1.55	1.05
1:A:484:THR:HB	1:A:496:VAL:HG12	1.39	1.04
1:A:911:ASN:HA	1:A:914:ASN:HD22	1.22	1.03
1:A:298:ILE:HD11	1:A:779:ALA:HB2	1.44	0.99
1:A:865:VAL:HG11	1:A:869:GLN:HB2	1.41	0.99
1:A:436:LYS:HG3	1:A:443:THR:HG21	1.41	0.99
1:A:411:VAL:HA	1:A:454:VAL:HG11	1.43	0.99
1:A:680:GLU:HB3	1:A:681:PRO:HD2	1.44	0.98
1:A:388:THR:HG22	1:A:390:ALA:H	1.28	0.98
1:A:879:ASP:OD1	1:A:882:HIS:HB3	1.64	0.98
1:A:680:GLU:H	1:A:683:HIS:HD2	1.08	0.97
1:A:227:GLY:O	1:A:230:THR:HG22	1.65	0.96
1:A:342:LEU:O	1:A:345:THR:HG23	1.67	0.95
1:A:411:VAL:HG12	1:A:454:VAL:HB	1.47	0.94
1:A:397:LYS:O	1:A:400:LYS:HG2	1.67	0.93
1:A:301:ALA:HA	1:A:789:PRO:HG3	1.50	0.93
1:A:759:GLN:HE22	1:A:762:ARG:HH11	1.07	0.93
1:A:527:TYR:HB2	1:A:592:THR:HG22	1.48	0.93
1:A:1:MET:HG2	1:A:225:THR:HG22	1.49	0.91
1:A:100:ALA:HA	1:A:103:ILE:HD12	1.50	0.91
1:A:654:THR:HG22	1:A:657:GLU:HG3	1.53	0.90
1:A:606:GLU:CD	1:A:606:GLU:H	1.76	0.88
1:A:439:GLU:O	1:A:443:THR:HG22	1.72	0.87
1:A:247:THR:HG23	1:A:340:GLU:OE1	1.72	0.87
1:A:759:GLN:HE22	1:A:762:ARG:NH1	1.73	0.86
1:A:99:ILE:HG22	1:A:103:ILE:HD11	1.56	0.86
1:A:969:MET:HG3	1:A:973:ILE:HD11	1.57	0.86
1:A:959:LEU:HG	1:A:960:LYS:HG2	1.58	0.86
1:A:90:GLU:HB3	1:A:91:PRO:HD3	1.56	0.86
1:A:751:ARG:HD2	1:A:817:MET:CE	2.07	0.84
1:A:355:THR:HG22	1:A:738:ASP:O	1.77	0.83
1:A:161:ALA:HA	1:A:210:SER:HB2	1.61	0.82
1:A:898:THR:CG2	1:A:958:LYS:HB3	2.08	0.81
1:A:24:LEU:HD22	1:A:149:ASP:HB3	1.62	0.81
1:A:26:PRO:O	1:A:30:LYS:HD3	1.81	0.81
1:A:951:ASP:O	1:A:954:PRO:HD2	1.81	0.81
1:A:563:ALA:O	1:A:564:LEU:HD23	1.81	0.81
1:A:278:HIS:C	1:A:282:PRO:HG3	2.02	0.80
1:A:436:LYS:CG	1:A:443:THR:HG21	2.11	0.80
1:A:180:LEU:HA	1:A:705:VAL:HG12	1.64	0.80
1:A:254:ASP:O	1:A:258:GLU:HG2	1.82	0.80

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:49:LEU:HA	1:A:52:LEU:HD12	1.64	0.79
1:A:89:VAL:O	1:A:93:VAL:HG23	1.82	0.79
1:A:95:LEU:O	1:A:99:ILE:HG12	1.83	0.79
1:A:828:LEU:HD12	2:A:1995:TG1:H302	1.64	0.79
1:A:398:ASN:HB2	1:A:400:LYS:NZ	1.99	0.78
1:A:880:HIS:HB3	1:A:881:PRO:HD3	1.65	0.78
1:A:230:THR:HG23	1:A:233:GLY:H	1.49	0.78
1:A:911:ASN:HA	1:A:914:ASN:ND2	1.97	0.77
1:A:680:GLU:H	1:A:683:HIS:CD2	1.98	0.77
1:A:352:LYS:CB	1:A:625:THR:HG22	2.15	0.77
1:A:898:THR:HG22	1:A:958:LYS:CB	2.13	0.76
1:A:933:LEU:O	1:A:937:ILE:HG13	1.85	0.76
1:A:252:LYS:HE2	1:A:826:GLU:O	1.85	0.76
1:A:200:VAL:HG21	1:A:489:ARG:HH22	1.49	0.76
1:A:361:MET:HE3	1:A:599:MET:HG3	1.68	0.76
1:A:895:GLU:HA	1:A:898:THR:HG23	1.66	0.76
1:A:774:CYS:SG	1:A:787:LEU:HD12	2.26	0.75
1:A:914:ASN:HB3	1:A:981:ASP:OD2	1.85	0.75
1:A:248:PRO:O	1:A:252:LYS:HG3	1.87	0.75
1:A:415:THR:HA	1:A:475:ILE:HG21	1.69	0.75
1:A:247:THR:HG22	1:A:250:GLN:HG3	1.67	0.75
1:A:352:LYS:HB2	1:A:625:THR:HG22	1.66	0.75
1:A:901:LEU:HD22	1:A:958:LYS:NZ	2.02	0.75
1:A:654:THR:HG22	1:A:657:GLU:CG	2.15	0.74
1:A:397:LYS:HB2	1:A:402:ILE:HD11	1.69	0.74
1:A:932:TRP:HA	1:A:932:TRP:CE3	2.22	0.74
1:A:751:ARG:HD2	1:A:817:MET:HE1	1.70	0.73
1:A:531:GLY:O	1:A:533:THR:HG23	1.87	0.73
1:A:950:VAL:O	1:A:954:PRO:HG2	1.88	0.73
1:A:865:VAL:HG11	1:A:869:GLN:CB	2.18	0.73
1:A:334:ARG:O	1:A:335:SER:HB3	1.88	0.73
1:A:909:MET:HE3	1:A:937:ILE:HG23	1.72	0.72
1:A:526:ASN:ND2	1:A:590:ASP:HA	2.03	0.72
1:A:352:LYS:HE2	1:A:627:ASP:OD2	1.89	0.72
1:A:529:ARG:HG3	1:A:533:THR:O	1.89	0.72
1:A:408:ASP:O	1:A:411:VAL:HG22	1.88	0.72
1:A:388:THR:HG22	1:A:390:ALA:N	2.04	0.72
1:A:880:HIS:O	1:A:884:GLU:HB2	1.89	0.71
1:A:651:ARG:HH11	1:A:651:ARG:HG2	1.53	0.71
1:A:397:LYS:CB	1:A:402:ILE:HD11	2.21	0.71
1:A:654:THR:CG2	1:A:657:GLU:HG3	2.20	0.71
1:A:974:SER:O	1:A:977:VAL:HG23	1.91	0.71

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:751:ARG:HD2	1:A:817:MET:HE2	1.72	0.70
1:A:680:GLU:N	1:A:683:HIS:HD2	1.85	0.70
1:A:577:VAL:HB	1:A:580:ASP:OD1	1.90	0.70
1:A:925:MET:HE1	1:A:929:VAL:HG11	1.71	0.70
1:A:608:MET:SD	1:A:639:ILE:HA	2.31	0.70
1:A:720:MET:HB3	1:A:738:ASP:OD1	1.92	0.70
1:A:921:SER:OG	1:A:923:MET:HG2	1.91	0.70
1:A:962:LEU:HB3	1:A:966:GLN:HG3	1.74	0.70
1:A:926:PRO:HG2	1:A:929:VAL:HG23	1.74	0.70
1:A:415:THR:HG22	1:A:475:ILE:HG23	1.74	0.69
1:A:19:SER:OG	1:A:22:THR:HB	1.92	0.69
1:A:526:ASN:HD22	1:A:590:ASP:HA	1.57	0.69
1:A:317:THR:O	1:A:321:LEU:HG	1.92	0.69
1:A:201:ASN:HA	1:A:204:LYS:HD2	1.75	0.69
1:A:989:ARG:C	1:A:991:TYR:H	1.94	0.69
1:A:680:GLU:HB3	1:A:681:PRO:CD	2.20	0.69
1:A:368:ILE:HD13	1:A:410:LEU:CD2	2.21	0.69
1:A:298:ILE:CD1	1:A:779:ALA:HB2	2.21	0.69
1:A:247:THR:HG22	1:A:250:GLN:H	1.58	0.69
1:A:59:ASP:O	1:A:62:VAL:HG12	1.92	0.69
1:A:244:GLN:CD	1:A:244:GLN:H	1.95	0.69
1:A:756:ASN:OD1	1:A:810:ASN:HB2	1.92	0.69
1:A:901:LEU:HD13	1:A:958:LYS:HZ1	1.58	0.68
1:A:527:TYR:O	1:A:592:THR:HA	1.94	0.68
1:A:431:LYS:O	1:A:433:VAL:HG23	1.93	0.68
1:A:82:GLU:OE2	1:A:83:GLU:HG3	1.94	0.67
1:A:950:VAL:HG12	1:A:951:ASP:N	2.10	0.67
1:A:342:LEU:HD21	1:A:746:ALA:HB1	1.76	0.67
1:A:522:ILE:HG22	1:A:542:LYS:HE3	1.74	0.67
1:A:950:VAL:CG1	1:A:951:ASP:N	2.59	0.66
1:A:143:ARG:HH11	1:A:143:ARG:HG2	1.61	0.66
1:A:166:LEU:HD11	1:A:222:ILE:HB	1.77	0.66
1:A:411:VAL:HA	1:A:454:VAL:CG1	2.24	0.65
1:A:757:MET:HA	1:A:760:PHE:CE2	2.31	0.65
1:A:59:ASP:HB3	1:A:62:VAL:HG12	1.77	0.65
1:A:281:ASP:N	1:A:282:PRO:HD2	2.12	0.65
1:A:471:CYS:O	1:A:474:VAL:HG22	1.97	0.65
1:A:69:ALA:HB2	1:A:94:ILE:HG21	1.78	0.65
1:A:528:VAL:HG12	1:A:593:PHE:HB3	1.77	0.65
1:A:901:LEU:CD1	1:A:958:LYS:HZ1	2.10	0.65
1:A:835:PHE:O	1:A:838:MET:HB3	1.97	0.65
1:A:855:TRP:CE3	1:A:896:PRO:HB3	2.32	0.64

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:969:MET:O	1:A:973:ILE:HG13	1.97	0.64
1:A:75:LEU:HD22	1:A:293:ILE:HG13	1.79	0.64
1:A:304:VAL:HG21	1:A:789:PRO:HA	1.79	0.64
1:A:932:TRP:HA	1:A:932:TRP:HE3	1.59	0.63
1:A:161:ALA:CA	1:A:210:SER:HB2	2.27	0.63
1:A:900:ALA:O	1:A:903:VAL:HG12	1.98	0.63
1:A:473:SER:O	1:A:477:GLN:HG3	1.98	0.63
1:A:398:ASN:HB2	1:A:400:LYS:HZ3	1.64	0.63
1:A:24:LEU:HD13	1:A:149:ASP:HA	1.80	0.63
1:A:347:VAL:HG22	1:A:620:ARG:HB3	1.79	0.63
1:A:32:HIS:CB	1:A:146:VAL:HG11	2.28	0.63
1:A:77:TRP:C	1:A:79:GLU:H	2.01	0.63
1:A:737:ASP:OD2	1:A:739:ASN:HB2	1.99	0.62
1:A:661:LEU:HD13	1:A:665:GLU:HG3	1.81	0.62
1:A:72:SER:OG	1:A:91:PRO:HG3	1.98	0.62
1:A:501:ALA:O	1:A:502:LYS:HB2	1.99	0.62
1:A:512:MET:HE3	1:A:571:PRO:HD2	1.82	0.62
1:A:519:GLU:H	1:A:519:GLU:CD	2.03	0.62
1:A:100:ALA:HA	1:A:103:ILE:CD1	2.28	0.62
1:A:530:VAL:O	1:A:530:VAL:HG23	1.98	0.62
1:A:870:LEU:O	1:A:870:LEU:HD12	1.98	0.62
1:A:436:LYS:HG3	1:A:443:THR:CG2	2.22	0.62
1:A:99:ILE:O	1:A:103:ILE:HG13	1.99	0.62
1:A:85:ILE:HG13	1:A:85:ILE:O	1.99	0.62
1:A:397:LYS:HG3	1:A:398:ASN:HD22	1.65	0.61
1:A:397:LYS:HB2	1:A:402:ILE:CD1	2.31	0.61
1:A:527:TYR:HB2	1:A:592:THR:CG2	2.28	0.61
1:A:404:SER:OG	1:A:452:MET:HB2	2.01	0.61
1:A:122:TYR:HE2	1:A:726:VAL:HG21	1.65	0.61
1:A:951:ASP:HB3	1:A:952:PRO:HD3	1.83	0.61
1:A:795:VAL:HA	1:A:799:THR:HG1	1.60	0.61
1:A:607:VAL:O	1:A:611:ILE:HG12	2.00	0.61
1:A:370:ASP:HB2	1:A:379:LEU:O	2.00	0.60
1:A:788:ILE:HG22	1:A:790:VAL:H	1.66	0.60
1:A:679:VAL:HG13	1:A:683:HIS:CB	2.31	0.60
1:A:247:THR:CG2	1:A:250:GLN:HG3	2.30	0.60
1:A:953:LEU:HB2	1:A:954:PRO:HD3	1.83	0.60
1:A:47:LYS:HD3	1:A:51:GLU:HB3	1.84	0.60
1:A:402:ILE:HG22	1:A:403:ARG:N	2.17	0.60
1:A:909:MET:HE3	1:A:937:ILE:CG2	2.30	0.60
1:A:963:ASP:O	1:A:967:TRP:HB2	2.00	0.60
1:A:679:VAL:HG13	1:A:683:HIS:HB2	1.84	0.60

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:99:ILE:HG22	1:A:103:ILE:CD1	2.32	0.60
1:A:733:MET:HE1	1:A:746:ALA:CB	2.31	0.60
1:A:903:VAL:O	1:A:907:ILE:HG13	2.02	0.60
1:A:495:SER:HB3	1:A:514:VAL:HB	1.83	0.60
1:A:628:ASN:HD22	1:A:628:ASN:N	1.99	0.60
1:A:637:ARG:HD3	1:A:644:GLU:HA	1.83	0.60
1:A:536:PRO:O	1:A:538:THR:HG23	2.02	0.59
1:A:781:LEU:C	1:A:783:LEU:H	2.06	0.59
1:A:389:TYR:CE2	1:A:436:LYS:HB2	2.37	0.59
1:A:365:LYS:HB3	1:A:552:TRP:CH2	2.37	0.59
1:A:47:LYS:HB3	1:A:51:GLU:HB2	1.85	0.59
1:A:749:GLU:O	1:A:753:ILE:HG12	2.02	0.59
1:A:505:ARG:HG3	1:A:505:ARG:O	2.03	0.59
1:A:518:PRO:HA	1:A:563:ALA:HB2	1.85	0.59
1:A:18:VAL:CG2	1:A:24:LEU:HD12	2.33	0.59
1:A:248:PRO:HG2	1:A:340:GLU:OE2	2.04	0.58
1:A:281:ASP:N	1:A:282:PRO:CD	2.66	0.58
1:A:545:ILE:O	1:A:549:ILE:HG12	2.03	0.58
1:A:512:MET:CE	1:A:571:PRO:HD2	2.33	0.58
1:A:483:PHE:HE1	1:A:485:LEU:HD21	1.67	0.58
1:A:565:ALA:HA	1:A:594:VAL:HG13	1.84	0.58
1:A:765:ILE:O	1:A:769:VAL:HG23	2.04	0.58
1:A:946:LEU:HD12	1:A:950:VAL:HG23	1.85	0.58
1:A:909:MET:HB3	1:A:937:ILE:CG2	2.34	0.58
1:A:716:ILE:HD12	1:A:716:ILE:N	2.18	0.58
1:A:126:MET:SD	1:A:141:LYS:HG2	2.43	0.58
1:A:909:MET:HB3	1:A:937:ILE:HG23	1.85	0.58
1:A:840:ILE:O	1:A:844:VAL:HG12	2.03	0.58
1:A:482:GLU:HG3	1:A:497:TYR:HD2	1.69	0.58
1:A:895:GLU:N	1:A:896:PRO:HD2	2.19	0.58
1:A:361:MET:HB3	1:A:599:MET:HE2	1.85	0.58
1:A:32:HIS:HB3	1:A:146:VAL:CG1	2.34	0.57
1:A:654:THR:HA	1:A:677:ALA:HB3	1.86	0.57
1:A:92:PHE:CE2	1:A:96:LEU:HD11	2.39	0.57
1:A:5:HIS:HE1	1:A:196:ASP:O	1.86	0.57
1:A:788:ILE:HB	1:A:791:GLN:HG3	1.86	0.57
1:A:836:ARG:O	1:A:840:ILE:HG12	2.04	0.57
1:A:748:GLU:HA	1:A:817:MET:CE	2.35	0.57
1:A:278:HIS:O	1:A:282:PRO:HG3	2.04	0.57
1:A:530:VAL:O	1:A:531:GLY:O	2.22	0.57
1:A:133:ASP:O	1:A:134:ARG:HG3	2.05	0.57
1:A:368:ILE:HD13	1:A:410:LEU:HD21	1.84	0.57

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:563:ALA:C	1:A:564:LEU:HD23	2.24	0.57
1:A:969:MET:HE3	1:A:972:LYS:HG3	1.87	0.57
1:A:580:ASP:N	1:A:580:ASP:OD1	2.38	0.57
1:A:423:SER:OG	1:A:442:GLU:HB2	2.05	0.57
1:A:47:LYS:HB3	1:A:51:GLU:CB	2.35	0.56
1:A:628:ASN:HD21	1:A:631:THR:HB	1.70	0.56
1:A:76:ALA:HB1	1:A:88:PHE:HD1	1.70	0.56
1:A:129:VAL:HG12	1:A:151:VAL:HG22	1.86	0.56
1:A:957:PHE:O	1:A:957:PHE:HD1	1.88	0.56
1:A:366:MET:HG3	1:A:384:ILE:HD11	1.87	0.56
1:A:436:LYS:CD	1:A:443:THR:HG21	2.35	0.56
1:A:513:PHE:HD1	1:A:566:THR:HG22	1.71	0.56
1:A:462:LEU:HD22	1:A:466:GLU:OE1	2.06	0.56
1:A:943:LEU:O	1:A:946:LEU:HB3	2.06	0.56
1:A:2:GLU:OE1	1:A:16:PHE:HE2	1.89	0.56
1:A:628:ASN:HD21	1:A:631:THR:CB	2.18	0.56
1:A:18:VAL:HG22	1:A:19:SER:N	2.21	0.55
1:A:841:GLY:O	1:A:844:VAL:HG13	2.05	0.55
1:A:907:ILE:HG23	1:A:977:VAL:HG21	1.87	0.55
1:A:65:LEU:CD2	1:A:94:ILE:HG23	2.36	0.55
1:A:688:VAL:O	1:A:692:GLN:HG3	2.05	0.55
1:A:848:THR:HG22	1:A:903:VAL:HG13	1.89	0.55
1:A:6:SER:HA	1:A:194:VAL:O	2.07	0.55
1:A:950:VAL:CG1	1:A:951:ASP:H	2.20	0.55
1:A:38:HIS:CE1	1:A:143:ARG:HH12	2.25	0.55
1:A:951:ASP:C	1:A:954:PRO:HD2	2.27	0.55
1:A:122:TYR:O	1:A:158:LYS:HD3	2.06	0.55
1:A:342:LEU:HD21	1:A:733:MET:HE3	1.89	0.54
1:A:322:GLY:O	1:A:326:MET:HG3	2.06	0.54
1:A:235:ILE:HG23	1:A:709:PRO:HD3	1.89	0.54
1:A:974:SER:C	1:A:976:PRO:HD2	2.28	0.54
1:A:452:MET:O	1:A:453:ASN:C	2.46	0.54
1:A:508:VAL:HG12	1:A:508:VAL:O	2.07	0.54
1:A:901:LEU:HD22	1:A:958:LYS:HZ3	1.72	0.54
1:A:843:TYR:CE2	1:A:977:VAL:HG22	2.43	0.54
1:A:964:LEU:C	1:A:966:GLN:H	2.12	0.54
1:A:559:LEU:HD23	1:A:600:LEU:HB2	1.88	0.54
1:A:901:LEU:CD2	1:A:958:LYS:HZ1	2.21	0.54
1:A:783:LEU:HD21	1:A:853:ALA:HB2	1.90	0.54
1:A:909:MET:HE2	1:A:940:SER:CB	2.38	0.54
1:A:628:ASN:ND2	1:A:631:THR:H	2.06	0.54
1:A:909:MET:HE1	1:A:937:ILE:HA	1.88	0.54

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:32:HIS:HB2	1:A:146:VAL:HG11	1.90	0.53
1:A:98:LEU:O	1:A:101:ASN:HB2	2.08	0.53
1:A:181:THR:OG1	1:A:183:GLU:HG2	2.07	0.53
1:A:605:LYS:HB2	1:A:606:GLU:OE2	2.08	0.53
1:A:278:HIS:HA	1:A:282:PRO:HD3	1.89	0.53
1:A:151:VAL:HG12	1:A:152:GLU:N	2.24	0.53
1:A:147:PRO:HA	1:A:223:VAL:HG12	1.91	0.53
1:A:59:ASP:OD2	1:A:61:LEU:HB2	2.09	0.53
1:A:50:TRP:CE2	1:A:54:ILE:HD11	2.42	0.53
1:A:397:LYS:HG3	1:A:398:ASN:ND2	2.23	0.53
1:A:114:ASN:OD1	1:A:117:GLU:HB3	2.08	0.53
1:A:901:LEU:HD22	1:A:958:LYS:HZ1	1.74	0.53
1:A:954:PRO:O	1:A:957:PHE:O	2.27	0.53
1:A:840:ILE:O	1:A:843:TYR:HB3	2.08	0.53
1:A:363:VAL:HG13	1:A:597:VAL:HG13	1.90	0.53
1:A:534:ARG:HD2	1:A:592:THR:HG21	1.89	0.53
1:A:442:GLU:O	1:A:446:THR:HG23	2.08	0.53
1:A:367:PHE:C	1:A:367:PHE:CD1	2.82	0.53
1:A:955:MET:C	1:A:957:PHE:H	2.12	0.53
1:A:979:GLY:O	1:A:983:ILE:HG13	2.09	0.53
1:A:962:LEU:HB3	1:A:966:GLN:CG	2.40	0.52
1:A:389:TYR:HB3	1:A:425:LEU:HD21	1.91	0.52
1:A:965:THR:H	1:A:968:LEU:HD12	1.74	0.52
1:A:352:LYS:HB3	1:A:625:THR:HG22	1.90	0.52
1:A:196:ASP:OD1	1:A:198:ARG:N	2.41	0.52
1:A:633:ILE:HG22	1:A:637:ARG:NH1	2.23	0.52
1:A:8:SER:OG	1:A:11:GLU:HG3	2.09	0.52
1:A:128:LYS:HB3	1:A:137:VAL:HG21	1.90	0.52
1:A:239:MET:O	1:A:242:THR:HG22	2.09	0.52
1:A:909:MET:HE2	1:A:940:SER:HB3	1.92	0.52
1:A:546:LEU:O	1:A:549:ILE:HB	2.10	0.52
1:A:558:THR:HG22	1:A:634:ALA:HB1	1.90	0.52
1:A:146:VAL:HG13	1:A:147:PRO:HD2	1.92	0.52
1:A:848:THR:HA	1:A:903:VAL:HG11	1.91	0.52
1:A:183:GLU:HG3	1:A:183:GLU:O	2.07	0.52
1:A:415:THR:HG22	1:A:475:ILE:CG2	2.39	0.52
1:A:733:MET:HE1	1:A:746:ALA:HB2	1.90	0.52
1:A:244:GLN:CD	1:A:244:GLN:N	2.63	0.52
1:A:441:THR:HG21	1:A:560:ARG:NH1	2.25	0.52
1:A:944:HIS:C	1:A:946:LEU:H	2.12	0.52
1:A:760:PHE:C	1:A:760:PHE:CD1	2.83	0.52
1:A:623:MET:HE3	1:A:635:ILE:HG22	1.92	0.52

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:239:MET:HE2	1:A:712:LYS:HD2	1.92	0.52
1:A:388:THR:HG22	1:A:389:TYR:N	2.23	0.52
1:A:256:PHE:HB2	2:A:1995:TG1:H291	1.91	0.51
1:A:831:GLY:O	1:A:834:PHE:HB3	2.09	0.51
1:A:29:VAL:HG12	1:A:30:LYS:HD2	1.91	0.51
1:A:70:CYS:O	1:A:73:PHE:N	2.43	0.51
1:A:353:THR:HA	1:A:357:THR:OG1	2.10	0.51
1:A:532:THR:O	1:A:533:THR:HG22	2.11	0.51
1:A:964:LEU:O	1:A:966:GLN:N	2.38	0.51
1:A:606:GLU:HB2	1:A:741:SER:OG	2.11	0.51
1:A:961:ALA:HB3	1:A:967:TRP:NE1	2.25	0.51
1:A:793:LEU:O	1:A:794:TRP:C	2.49	0.51
1:A:654:THR:CG2	1:A:657:GLU:H	2.24	0.51
1:A:361:MET:CE	1:A:441:THR:HG22	2.41	0.51
1:A:628:ASN:ND2	1:A:628:ASN:O	2.44	0.51
1:A:342:LEU:CD2	1:A:733:MET:HE3	2.41	0.51
1:A:604:ARG:O	1:A:607:VAL:HB	2.10	0.51
1:A:648:VAL:O	1:A:649:ALA:C	2.49	0.51
1:A:291:GLY:O	1:A:294:TYR:HB3	2.11	0.51
1:A:781:LEU:O	1:A:871:THR:HG23	2.11	0.51
1:A:755:ASN:O	1:A:758:LYS:HB3	2.11	0.51
1:A:606:GLU:CD	1:A:606:GLU:N	2.53	0.51
1:A:487:PHE:HA	1:A:493:SER:O	2.11	0.51
1:A:512:MET:HE3	1:A:570:PRO:CB	2.41	0.50
1:A:370:ASP:HB3	1:A:378:SER:OG	2.11	0.50
1:A:77:TRP:O	1:A:79:GLU:N	2.37	0.50
1:A:567:ARG:HD3	1:A:570:PRO:HA	1.92	0.50
1:A:2:GLU:OE1	1:A:16:PHE:CE2	2.64	0.50
1:A:130:TYR:CE2	1:A:137:VAL:HB	2.47	0.50
1:A:202:GLN:HB3	1:A:489:ARG:NH2	2.27	0.50
1:A:580:ASP:O	1:A:582:SER:N	2.44	0.50
1:A:724:THR:O	1:A:728:LYS:HG3	2.11	0.50
1:A:855:TRP:CE2	1:A:895:GLU:HG3	2.46	0.50
1:A:397:LYS:HB3	1:A:402:ILE:HD11	1.93	0.50
1:A:857:MET:O	1:A:858:TYR:HB2	2.12	0.50
1:A:174:ARG:NE	1:A:188:ILE:HG12	2.27	0.50
1:A:467:ARG:NH1	1:A:467:ARG:O	2.44	0.50
1:A:284:HIS:ND1	1:A:284:HIS:O	2.45	0.50
1:A:748:GLU:HA	1:A:817:MET:HE1	1.93	0.50
1:A:913:LEU:HD21	1:A:937:ILE:CD1	2.42	0.50
1:A:412:GLU:OE1	1:A:529:ARG:NE	2.45	0.50
1:A:367:PHE:CD1	1:A:367:PHE:O	2.64	0.50

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:384:ILE:HD12	1:A:384:ILE:N	2.27	0.50
1:A:696:GLU:O	1:A:698:THR:HG22	2.12	0.50
1:A:777:LEU:O	1:A:778:THR:C	2.50	0.49
1:A:628:ASN:ND2	1:A:631:THR:HB	2.26	0.49
1:A:482:GLU:HG3	1:A:497:TYR:CD2	2.47	0.49
1:A:253:LEU:HD23	2:A:1995:TG1:H301	1.94	0.49
1:A:909:MET:CE	1:A:937:ILE:HA	2.42	0.49
1:A:336:LEU:N	1:A:337:PRO:HD2	2.27	0.49
1:A:901:LEU:CD2	1:A:958:LYS:NZ	2.75	0.49
1:A:910:CYS:SG	1:A:978:ILE:HD11	2.52	0.49
1:A:795:VAL:O	1:A:800:ASP:HB2	2.13	0.49
1:A:873:PHE:HB2	1:A:891:PHE:CD2	2.48	0.49
1:A:577:VAL:O	1:A:580:ASP:OD1	2.30	0.49
1:A:522:ILE:CG2	1:A:542:LYS:HE3	2.41	0.49
1:A:142:ALA:HA	1:A:145:ILE:CD1	2.42	0.49
1:A:984:LEU:HA	1:A:987:ILE:HG12	1.94	0.49
1:A:748:GLU:HG3	1:A:817:MET:HE3	1.94	0.49
1:A:228:VAL:HG13	1:A:237:ASP:OD2	2.13	0.49
1:A:76:ALA:HB1	1:A:88:PHE:CD1	2.47	0.49
1:A:901:LEU:HD13	1:A:958:LYS:NZ	2.28	0.49
1:A:113:GLU:HB2	1:A:117:GLU:OE1	2.13	0.49
1:A:231:GLU:OE2	1:A:234:LYS:NZ	2.46	0.49
1:A:155:VAL:O	1:A:214:ILE:O	2.31	0.49
1:A:408:ASP:O	1:A:409:GLY:C	2.51	0.49
1:A:383:SER:C	1:A:384:ILE:HD12	2.33	0.49
1:A:465:VAL:O	1:A:465:VAL:HG12	2.12	0.49
1:A:894:PRO:O	1:A:898:THR:HG23	2.12	0.48
1:A:398:ASN:HB2	1:A:400:LYS:HZ2	1.73	0.48
1:A:346:SER:OG	1:A:696:GLU:HG2	2.13	0.48
1:A:900:ALA:O	1:A:903:VAL:CG1	2.60	0.48
1:A:989:ARG:C	1:A:991:TYR:N	2.65	0.48
1:A:411:VAL:HG12	1:A:454:VAL:CB	2.33	0.48
1:A:180:LEU:HD23	1:A:705:VAL:CG1	2.42	0.48
1:A:483:PHE:CE1	1:A:485:LEU:HD21	2.48	0.48
1:A:32:HIS:HB3	1:A:146:VAL:HG13	1.96	0.48
1:A:59:ASP:HB3	1:A:62:VAL:CG1	2.43	0.48
1:A:361:MET:HE2	1:A:441:THR:HG22	1.95	0.48
1:A:909:MET:CE	1:A:940:SER:HB2	2.44	0.48
1:A:49:LEU:O	1:A:53:VAL:HG23	2.13	0.48
1:A:793:LEU:O	1:A:796:ASN:N	2.47	0.48
1:A:751:ARG:NH2	1:A:821:PRO:HA	2.29	0.48
1:A:202:GLN:HB3	1:A:489:ARG:HH21	1.79	0.48

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:151:VAL:CG1	1:A:152:GLU:N	2.77	0.48
1:A:668:GLU:O	1:A:671:ARG:HG2	2.13	0.48
1:A:276:ILE:HG13	1:A:276:ILE:O	2.14	0.48
1:A:737:ASP:O	1:A:739:ASN:N	2.47	0.48
1:A:222:ILE:O	1:A:222:ILE:HG23	2.14	0.47
1:A:124:PRO:HB3	1:A:158:LYS:HB3	1.95	0.47
1:A:916:LEU:CD1	1:A:927:PRO:HA	2.44	0.47
1:A:604:ARG:HB2	1:A:607:VAL:HG23	1.96	0.47
1:A:452:MET:O	1:A:454:VAL:N	2.48	0.47
1:A:596:VAL:CG2	1:A:597:VAL:N	2.78	0.47
1:A:878:GLU:C	1:A:880:HIS:H	2.18	0.47
1:A:472:ASN:O	1:A:476:ARG:HG3	2.13	0.47
1:A:680:GLU:CB	1:A:681:PRO:CD	2.88	0.47
1:A:946:LEU:CD1	1:A:950:VAL:HG23	2.45	0.47
1:A:93:VAL:O	1:A:96:LEU:HB2	2.15	0.47
1:A:837:TYR:HB2	2:A:1995:TG1:C33	2.45	0.47
1:A:541:VAL:O	1:A:545:ILE:HG13	2.15	0.47
1:A:379:LEU:HD11	1:A:544:LYS:HG3	1.96	0.47
1:A:662:PRO:O	1:A:664:ALA:N	2.47	0.47
1:A:653:TYR:CE2	1:A:669:ALA:HB1	2.50	0.47
1:A:872:HIS:HB3	1:A:875:GLN:NE2	2.30	0.47
1:A:758:LYS:O	1:A:762:ARG:HG3	2.14	0.47
1:A:388:THR:CG2	1:A:389:TYR:N	2.77	0.47
1:A:143:ARG:NH1	1:A:143:ARG:HG2	2.28	0.47
1:A:69:ALA:HB2	1:A:94:ILE:CG2	2.43	0.47
1:A:77:TRP:C	1:A:79:GLU:N	2.67	0.47
1:A:500:PRO:HG3	1:A:506:ALA:HA	1.96	0.47
1:A:352:LYS:HD3	1:A:625:THR:HG21	1.96	0.47
1:A:141:LYS:O	1:A:142:ALA:C	2.53	0.47
1:A:879:ASP:OD1	1:A:882:HIS:CB	2.52	0.46
1:A:832:TRP:HZ2	1:A:987:ILE:HG13	1.80	0.46
1:A:41:LEU:O	1:A:42:PRO:C	2.53	0.46
1:A:402:ILE:CG2	1:A:403:ARG:N	2.78	0.46
1:A:416:ILE:HD11	1:A:566:THR:CG2	2.46	0.46
1:A:236:ARG:HG2	1:A:236:ARG:O	2.14	0.46
1:A:474:VAL:CG2	1:A:475:ILE:N	2.79	0.46
1:A:950:VAL:O	1:A:954:PRO:CG	2.60	0.46
1:A:671:ARG:HD2	1:A:694:TYR:CZ	2.50	0.46
1:A:323:THR:HG22	1:A:324:ARG:N	2.31	0.46
1:A:174:ARG:CB	1:A:215:ALA:HB3	2.46	0.46
1:A:363:VAL:O	1:A:384:ILE:HB	2.16	0.46
1:A:505:ARG:NH1	1:A:507:ALA:HB3	2.30	0.46

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:155:VAL:HG12	1:A:156:GLY:N	2.31	0.46
1:A:586:GLU:O	1:A:589:THR:HG23	2.15	0.46
1:A:927:PRO:HB2	1:A:934:LEU:HD21	1.97	0.46
1:A:436:LYS:HD2	1:A:440:ALA:HA	1.96	0.46
1:A:913:LEU:C	1:A:915:SER:H	2.18	0.46
1:A:412:GLU:CD	1:A:529:ARG:HE	2.20	0.46
1:A:577:VAL:HG23	1:A:583:ARG:NH1	2.31	0.46
1:A:567:ARG:CD	1:A:570:PRO:HA	2.46	0.46
1:A:363:VAL:CG1	1:A:597:VAL:HG13	2.46	0.46
1:A:50:TRP:O	1:A:54:ILE:HG13	2.16	0.46
1:A:676:PHE:HB3	1:A:679:VAL:CG2	2.46	0.46
1:A:364:CYS:O	1:A:383:SER:HA	2.15	0.45
1:A:174:ARG:CG	1:A:216:ALA:HB3	2.46	0.45
1:A:448:LEU:HD12	1:A:448:LEU:O	2.16	0.45
1:A:909:MET:O	1:A:913:LEU:HG	2.16	0.45
1:A:174:ARG:HG2	1:A:216:ALA:HB3	1.97	0.45
1:A:193:PRO:HA	1:A:206:ASN:ND2	2.32	0.45
1:A:52:LEU:HD13	1:A:106:VAL:HG13	1.98	0.45
1:A:540:PRO:HG2	1:A:541:VAL:H	1.82	0.45
1:A:411:VAL:O	1:A:415:THR:HG23	2.16	0.45
1:A:922:LEU:HD23	1:A:925:MET:O	2.16	0.45
1:A:857:MET:HG2	1:A:866:THR:HA	1.98	0.45
1:A:850:GLY:O	1:A:854:TRP:N	2.49	0.45
1:A:955:MET:C	1:A:957:PHE:N	2.69	0.45
1:A:56:GLN:OE1	1:A:105:GLY:HA3	2.17	0.45
1:A:174:ARG:HA	1:A:187:VAL:O	2.16	0.45
1:A:352:LYS:HD2	1:A:635:ILE:HG21	1.98	0.45
1:A:788:ILE:HG23	1:A:789:PRO:HD2	1.98	0.45
1:A:361:MET:CE	1:A:599:MET:HG3	2.43	0.45
1:A:577:VAL:HB	1:A:580:ASP:CG	2.37	0.45
1:A:567:ARG:HE	1:A:570:PRO:HA	1.82	0.45
1:A:174:ARG:HB2	1:A:216:ALA:H	1.82	0.45
1:A:259:GLN:O	1:A:260:LEU:C	2.54	0.45
1:A:227:GLY:O	1:A:230:THR:CG2	2.50	0.45
1:A:372:VAL:HG13	1:A:541:VAL:HG22	1.98	0.45
1:A:442:GLU:HG2	1:A:515:LYS:NZ	2.31	0.45
1:A:130:TYR:CZ	1:A:137:VAL:HB	2.52	0.45
1:A:259:GLN:NE2	1:A:262:LYS:HD2	2.32	0.45
1:A:179:ILE:C	1:A:179:ILE:HD12	2.38	0.45
1:A:950:VAL:HB	1:A:953:LEU:HD12	1.99	0.45
1:A:230:THR:O	1:A:233:GLY:N	2.50	0.44
1:A:109:GLU:O	1:A:111:ASN:N	2.50	0.44

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:576:MET:HE2	1:A:587:TYR:CD2	2.52	0.44
1:A:348:ILE:HA	1:A:699:ALA:HB3	1.98	0.44
1:A:518:PRO:HD3	1:A:561:CYS:O	2.18	0.44
1:A:638:ARG:HH11	1:A:638:ARG:HG3	1.82	0.44
1:A:178:SER:O	1:A:182:GLY:N	2.50	0.44
1:A:855:TRP:CZ2	1:A:895:GLU:HG3	2.52	0.44
1:A:947:ILE:HB	1:A:957:PHE:CE1	2.52	0.44
1:A:925:MET:CE	1:A:929:VAL:HG11	2.43	0.44
1:A:888:CYS:O	1:A:889:GLU:HB2	2.17	0.44
1:A:174:ARG:HB2	1:A:216:ALA:N	2.32	0.44
1:A:619:ILE:CD1	1:A:747:VAL:HG11	2.47	0.44
1:A:717:GLY:O	1:A:731:SER:HB2	2.17	0.44
1:A:904:LEU:O	1:A:905:VAL:C	2.56	0.44
1:A:783:LEU:HG	1:A:784:PRO:HD2	1.98	0.44
1:A:651:ARG:HH11	1:A:651:ARG:CG	2.24	0.44
1:A:65:LEU:HB3	1:A:98:LEU:HD21	2.00	0.44
1:A:648:VAL:O	1:A:648:VAL:HG12	2.17	0.44
1:A:895:GLU:HA	1:A:898:THR:CG2	2.41	0.44
1:A:448:LEU:O	1:A:452:MET:HG2	2.18	0.44
1:A:967:TRP:O	1:A:970:VAL:HB	2.18	0.44
1:A:897:MET:C	1:A:899:MET:N	2.70	0.44
1:A:262:LYS:O	1:A:266:LEU:HG	2.18	0.43
1:A:788:ILE:H	1:A:791:GLN:CD	2.20	0.43
1:A:30:LYS:N	1:A:30:LYS:CD	2.80	0.43
1:A:619:ILE:HD11	1:A:747:VAL:HG11	1.99	0.43
1:A:491:ARG:HE	1:A:588:GLU:CD	2.22	0.43
1:A:524:ARG:HD2	1:A:588:GLU:O	2.18	0.43
1:A:955:MET:O	1:A:957:PHE:N	2.51	0.43
1:A:517:ALA:O	1:A:521:VAL:HG13	2.18	0.43
1:A:633:ILE:CG2	1:A:637:ARG:NH1	2.81	0.43
1:A:894:PRO:C	1:A:896:PRO:HD2	2.39	0.43
1:A:474:VAL:HG23	1:A:475:ILE:N	2.33	0.43
1:A:959:LEU:HD21	1:A:960:LYS:HZ3	1.83	0.43
1:A:22:THR:HG22	1:A:132:ALA:HB2	2.01	0.43
1:A:444:ALA:O	1:A:447:THR:N	2.51	0.43
1:A:368:ILE:HG21	1:A:410:LEU:HD23	2.00	0.43
1:A:949:TYR:C	1:A:950:VAL:O	2.55	0.43
1:A:505:ARG:O	1:A:505:ARG:CG	2.67	0.43
1:A:307:ILE:O	1:A:768:ASN:ND2	2.51	0.43
1:A:226:THR:HG23	1:A:227:GLY:N	2.31	0.43
1:A:759:GLN:NE2	1:A:762:ARG:HH11	1.91	0.43
1:A:462:LEU:HD13	1:A:466:GLU:HG2	2.01	0.43

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:178:SER:HB3	1:A:184:SER:HA	2.01	0.43
1:A:260:LEU:O	1:A:264:ILE:HG13	2.19	0.43
1:A:792:LEU:O	1:A:795:VAL:HB	2.18	0.43
1:A:147:PRO:HG3	1:A:226:THR:HB	2.00	0.43
1:A:926:PRO:HB2	1:A:928:TRP:CE2	2.54	0.43
1:A:540:PRO:O	1:A:543:GLU:N	2.52	0.43
1:A:446:THR:O	1:A:449:VAL:HG22	2.18	0.43
1:A:909:MET:CE	1:A:937:ILE:HG23	2.44	0.43
1:A:442:GLU:C	1:A:444:ALA:N	2.71	0.43
1:A:43:ALA:HA	1:A:120:LYS:NZ	2.34	0.43
1:A:424:SER:O	1:A:437:VAL:HB	2.19	0.43
1:A:788:ILE:HG22	1:A:790:VAL:N	2.32	0.43
1:A:502:LYS:HB3	1:A:503:SER:H	1.60	0.43
1:A:506:ALA:O	1:A:507:ALA:C	2.57	0.43
1:A:905:VAL:O	1:A:908:GLU:N	2.52	0.43
1:A:804:ALA:O	1:A:807:LEU:HB2	2.19	0.43
1:A:230:THR:HG23	1:A:233:GLY:N	2.26	0.42
1:A:275:ASN:HB3	1:A:278:HIS:HD2	1.84	0.42
1:A:178:SER:HB3	1:A:183:GLU:O	2.19	0.42
1:A:380:ASN:O	1:A:382:PHE:CD2	2.72	0.42
1:A:895:GLU:N	1:A:896:PRO:CD	2.82	0.42
1:A:146:VAL:HG13	1:A:147:PRO:CD	2.49	0.42
1:A:18:VAL:HG21	1:A:24:LEU:CD1	2.49	0.42
1:A:18:VAL:HG21	1:A:24:LEU:HD12	2.01	0.42
1:A:234:LYS:O	1:A:237:ASP:HB2	2.19	0.42
1:A:576:MET:HE3	1:A:587:TYR:HB3	2.00	0.42
1:A:773:VAL:HB	1:A:845:GLY:HA3	2.01	0.42
1:A:30:LYS:N	1:A:30:LYS:HD2	2.34	0.42
1:A:651:ARG:HG2	1:A:651:ARG:NH1	2.27	0.42
1:A:82:GLU:H	1:A:82:GLU:CD	2.22	0.42
1:A:372:VAL:HG11	1:A:541:VAL:HG21	2.01	0.42
1:A:567:ARG:NE	1:A:570:PRO:HA	2.33	0.42
1:A:698:THR:HG23	1:A:715:GLU:OE1	2.20	0.42
1:A:782:GLY:O	1:A:873:PHE:HE2	2.03	0.42
1:A:680:GLU:CB	1:A:681:PRO:HD2	2.30	0.42
1:A:950:VAL:HG13	1:A:951:ASP:H	1.83	0.42
1:A:757:MET:HA	1:A:760:PHE:CD2	2.54	0.42
1:A:464:LYS:C	1:A:466:GLU:H	2.22	0.42
1:A:168:ILE:HG22	1:A:170:SER:O	2.19	0.42
1:A:751:ARG:HH21	1:A:821:PRO:HA	1.85	0.42
1:A:370:ASP:HB3	1:A:378:SER:O	2.19	0.42
1:A:365:LYS:CB	1:A:552:TRP:CH2	3.02	0.42

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:367:PHE:CE2	1:A:596:VAL:CG1	3.03	0.42
1:A:442:GLU:HG2	1:A:515:LYS:HZ2	1.83	0.42
1:A:691:LEU:O	1:A:696:GLU:HB2	2.20	0.42
1:A:352:LYS:HD3	1:A:625:THR:CG2	2.48	0.42
1:A:708:ALA:N	1:A:709:PRO:HD2	2.35	0.42
1:A:986:PHE:C	1:A:988:ALA:H	2.22	0.42
1:A:397:LYS:O	1:A:398:ASN:C	2.55	0.42
1:A:534:ARG:HD2	1:A:592:THR:CG2	2.50	0.42
1:A:763:TYR:CZ	1:A:912:ALA:HB2	2.55	0.42
1:A:270:ALA:O	1:A:274:ILE:HG12	2.20	0.42
1:A:781:LEU:O	1:A:783:LEU:N	2.53	0.42
1:A:277:GLY:O	1:A:282:PRO:HD3	2.20	0.42
1:A:829:ILE:HG21	2:A:1995:TG1:H333	2.00	0.42
1:A:628:ASN:ND2	1:A:628:ASN:N	2.67	0.42
1:A:975:LEU:HB2	1:A:976:PRO:HD3	2.02	0.41
1:A:276:ILE:HD12	1:A:279:PHE:HD2	1.85	0.41
1:A:491:ARG:HD2	1:A:585:MET:HA	2.01	0.41
1:A:35:LYS:HD3	1:A:36:TYR:CZ	2.55	0.41
1:A:355:THR:CG2	1:A:720:MET:SD	3.08	0.41
1:A:737:ASP:C	1:A:739:ASN:H	2.24	0.41
1:A:784:PRO:HG3	1:A:873:PHE:CD2	2.55	0.41
1:A:971:LEU:C	1:A:973:ILE:H	2.23	0.41
1:A:53:VAL:O	1:A:56:GLN:HB2	2.20	0.41
1:A:494:MET:O	1:A:514:VAL:HG23	2.20	0.41
1:A:544:LYS:HD2	1:A:544:LYS:HA	1.82	0.41
1:A:242:THR:HG23	1:A:712:LYS:NZ	2.35	0.41
1:A:573:ARG:HH21	1:A:578:LEU:HD11	1.85	0.41
1:A:107:TRP:O	1:A:111:ASN:ND2	2.52	0.41
1:A:402:ILE:HG21	1:A:407:PHE:HE2	1.86	0.41
1:A:2:GLU:HB3	1:A:3:ALA:H	1.52	0.41
1:A:436:LYS:HG2	1:A:437:VAL:N	2.36	0.41
1:A:247:THR:HG23	1:A:249:LEU:H	1.85	0.41
1:A:589:THR:O	1:A:590:ASP:C	2.58	0.41
1:A:521:VAL:CG2	1:A:522:ILE:N	2.82	0.41
1:A:419:LEU:HD12	1:A:513:PHE:CE2	2.55	0.41
1:A:419:LEU:O	1:A:481:LYS:HE3	2.21	0.41
1:A:778:THR:HG22	1:A:779:ALA:N	2.35	0.41
1:A:965:THR:O	1:A:969:MET:HB2	2.21	0.41
1:A:947:ILE:HB	1:A:957:PHE:HE1	1.85	0.41
1:A:737:ASP:C	1:A:739:ASN:N	2.74	0.41
1:A:181:THR:HG22	1:A:706:ASN:ND2	2.36	0.41
1:A:48:SER:O	1:A:52:LEU:HG	2.21	0.41

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:52:LEU:O	1:A:53:VAL:C	2.58	0.41
1:A:200:VAL:HG21	1:A:489:ARG:NH2	2.27	0.41
1:A:408:ASP:O	1:A:410:LEU:N	2.54	0.41
1:A:751:ARG:NH2	1:A:821:PRO:CA	2.84	0.41
1:A:180:LEU:HD23	1:A:705:VAL:HG11	2.02	0.41
1:A:495:SER:HA	1:A:513:PHE:O	2.20	0.41
1:A:512:MET:O	1:A:566:THR:HA	2.20	0.41
1:A:669:ALA:O	1:A:673:ALA:HB2	2.21	0.41
1:A:289:ILE:O	1:A:289:ILE:HG22	2.21	0.41
1:A:920:GLN:OE1	1:A:924:ARG:HD3	2.21	0.41
1:A:505:ARG:C	1:A:507:ALA:H	2.24	0.41
1:A:558:THR:OG1	1:A:638:ARG:NH1	2.53	0.41
1:A:10:GLU:OE1	1:A:10:GLU:N	2.51	0.41
1:A:776:PHE:O	1:A:777:LEU:C	2.60	0.40
1:A:781:LEU:C	1:A:783:LEU:N	2.73	0.40
1:A:52:LEU:O	1:A:55:GLU:N	2.54	0.40
1:A:964:LEU:C	1:A:966:GLN:N	2.72	0.40
1:A:764:LEU:HD21	1:A:804:ALA:HB2	2.04	0.40
1:A:90:GLU:HB3	1:A:91:PRO:CD	2.39	0.40
1:A:244:GLN:H	1:A:244:GLN:NE2	2.19	0.40
1:A:869:GLN:C	1:A:871:THR:N	2.75	0.40
1:A:936:SER:O	1:A:937:ILE:C	2.59	0.40
1:A:473:SER:HA	1:A:476:ARG:HD2	2.03	0.40
1:A:290:ARG:O	1:A:290:ARG:HG2	2.21	0.40
1:A:311:LEU:HB3	1:A:312:PRO:HD3	2.03	0.40
1:A:667:ARG:NH1	1:A:694:TYR:CZ	2.89	0.40
1:A:58:GLU:O	1:A:63:ARG:NH1	2.55	0.40
1:A:18:VAL:HG23	1:A:24:LEU:HD12	2.02	0.40
1:A:962:LEU:O	1:A:966:GLN:HB2	2.21	0.40
1:A:540:PRO:O	1:A:542:LYS:N	2.54	0.40
1:A:650:ASP:O	1:A:672:ARG:HD2	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	992/994 (100%)	811 (82%)	146 (15%)	35 (4%)	6	32

All (35) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	155	VAL
1	A	531	GLY
1	A	581	SER
1	A	681	PRO
1	A	683	HIS
1	A	889	GLU
1	A	78	PHE
1	A	110	ARG
1	A	227	GLY
1	A	432	GLY
1	A	507	ALA
1	A	663	LEU
1	A	677	ALA
1	A	738	ASP
1	A	905	VAL
1	A	957	PHE
1	A	963	ASP
1	A	991	TYR
1	A	47	LYS
1	A	453	ASN
1	A	502	LYS
1	A	649	ALA
1	A	793	LEU
1	A	882	HIS
1	A	42	PRO
1	A	975	LEU
1	A	540	PRO
1	A	956	ILE
1	A	541	VAL
1	A	951	ASP
1	A	409	GLY
1	A	53	VAL
1	A	195	PRO
1	A	783	LEU
1	A	894	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	840/840 (100%)	794 (94%)	46 (6%)	30 71

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

Mol	Chain	Res	Type
1	A	9	THR
1	A	19	SER
1	A	82	GLU
1	A	117	GLU
1	A	160	PRO
1	A	191	THR
1	A	208	LEU
1	A	228	VAL
1	A	247	THR
1	A	279	PHE
1	A	340	GLU
1	A	344	CYS
1	A	353	THR
1	A	367	PHE
1	A	368	ILE
1	A	396	LEU
1	A	457	THR
1	A	484	THR
1	A	514	VAL
1	A	533	THR
1	A	537	MET
1	A	569	THR
1	A	594	VAL
1	A	596	VAL
1	A	606	GLU
1	A	628	ASN
1	A	638	ARG
1	A	681	PRO
1	A	698	THR
1	A	703	ASP
1	A	760	PHE

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Mol	Chain	Res	Type
1	A	778	THR
1	A	805	THR
1	A	811	PRO
1	A	816	ILE
1	A	838	MET
1	A	844	VAL
1	A	867	TYR
1	A	870	LEU
1	A	878	GLU
1	A	898	THR
1	A	910	CYS
1	A	925	MET
1	A	940	SER
1	A	957	PHE
1	A	963	ASP

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (17) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	5	HIS
1	A	177	GLN
1	A	259	GLN
1	A	278	HIS
1	A	398	ASN
1	A	453	ASN
1	A	472	ASN
1	A	526	ASN
1	A	628	ASN
1	A	666	GLN
1	A	683	HIS
1	A	706	ASN
1	A	759	GLN
1	A	875	GLN
1	A	914	ASN
1	A	944	HIS
1	A	990	ASN

5.3.3 RNA ⓘ

There are no RNA chains in this entry.

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

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

5.5 Carbohydrates ⓘ

There are no carbohydrates in this entry.

5.6 Ligand geometry ⓘ

Of 2 ligands modelled in this entry, 1 is monoatomic - leaving 1 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	$\# Z > 2$
2	TG1	A	1995	-	48,48,48	2.08	15 (31%)	72,72,72	2.01	21 (29%)

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
2	TG1	A	1995	-	-	0/33/99/99	0/0/3/3

All (15) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	1995	TG1	C6-C5	6.65	1.58	1.50
2	A	1995	TG1	O4-C21	5.42	1.33	1.21
2	A	1995	TG1	O3-C3	3.95	1.52	1.44
2	A	1995	TG1	O6-C7	3.71	1.50	1.43
2	A	1995	TG1	O1-C13	3.45	1.44	1.34
2	A	1995	TG1	C10-C1	3.39	1.63	1.54
2	A	1995	TG1	C7-C8	3.27	1.59	1.53
2	A	1995	TG1	C34-C11	3.01	1.57	1.53

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	1995	TG1	O7-C27	2.50	1.41	1.34
2	A	1995	TG1	O11-C11	2.46	1.47	1.42
2	A	1995	TG1	C1-C2	2.43	1.58	1.54
2	A	1995	TG1	C21-C22	2.25	1.58	1.50
2	A	1995	TG1	C9-C8	2.23	1.55	1.52
2	A	1995	TG1	C4-C5	2.06	1.37	1.33
2	A	1995	TG1	C31-C10	2.04	1.57	1.52

All (21) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	1995	TG1	C10-O9-C32	6.05	137.68	122.10
2	A	1995	TG1	O12-C12-C11	-5.16	124.92	128.26
2	A	1995	TG1	O3-C3-C2	-4.63	100.71	112.92
2	A	1995	TG1	C7-C6-C5	3.90	124.44	115.55
2	A	1995	TG1	O5-C6-C7	-3.78	99.69	104.28
2	A	1995	TG1	C11-C7-C6	-3.45	96.50	102.71
2	A	1995	TG1	O11-C11-C7	3.13	119.59	107.52
2	A	1995	TG1	C9-C10-C1	3.09	120.67	114.04
2	A	1995	TG1	C24-C22-C21	3.01	133.92	120.66
2	A	1995	TG1	C6-O5-C12	-2.97	106.37	110.79
2	A	1995	TG1	C2-O1-C13	-2.89	113.29	117.92
2	A	1995	TG1	C6-C5-C4	2.87	128.25	123.41
2	A	1995	TG1	C23-C22-C21	-2.76	108.81	116.05
2	A	1995	TG1	O9-C10-C31	-2.75	96.57	107.74
2	A	1995	TG1	O5-C12-O12	2.72	125.74	121.67
2	A	1995	TG1	O9-C10-C1	2.68	113.61	103.50
2	A	1995	TG1	C1-C2-C3	2.46	109.10	104.83
2	A	1995	TG1	C3-O3-C21	2.38	119.77	116.40
2	A	1995	TG1	C34-C11-C12	2.22	116.86	112.78
2	A	1995	TG1	C31-C10-C9	-2.13	106.17	110.42
2	A	1995	TG1	O11-C11-C12	-2.09	100.38	105.80

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

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	994/994 (100%)	-0.18	9 (0%) 81 25	19, 62, 136, 184	0

All (9) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	878	GLU	3.5
1	A	281	ASP	2.9
1	A	507	ALA	2.9
1	A	994	GLY	2.6
1	A	993	GLU	2.3
1	A	47	LYS	2.3
1	A	284	HIS	2.2
1	A	81	GLY	2.1
1	A	106	VAL	2.1

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

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

6.3 Carbohydrates ⓘ

There are no carbohydrates in this entry.

6.4 Ligands ⓘ

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	RSR	LLDF	B-factors(\AA^2)	Q<0.9
3	NA	A	1996	1/1	0.34	3.09	52,52,52,52	0
2	TG1	A	1995	46/46	0.26	1.82	55,59,60,61	0

6.5 Other polymers ⓘ

There are no such residues in this entry.