



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 6, 2026 – 08:43 AM UTC

PDB ID : 3D9B / pdb_00003d9b
Title : Symmetric structure of E. coli AcrB
Authors : Veesler, D.; Blangy, S.; Cambillau, C.; Sciara, G.
Deposited on : 2008-05-27
Resolution : 3.42 Å(reported)

This is a Full wwPDB X-ray Structure Validation Report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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

MolProbity	:	4-5-2 with Phenix2.0
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

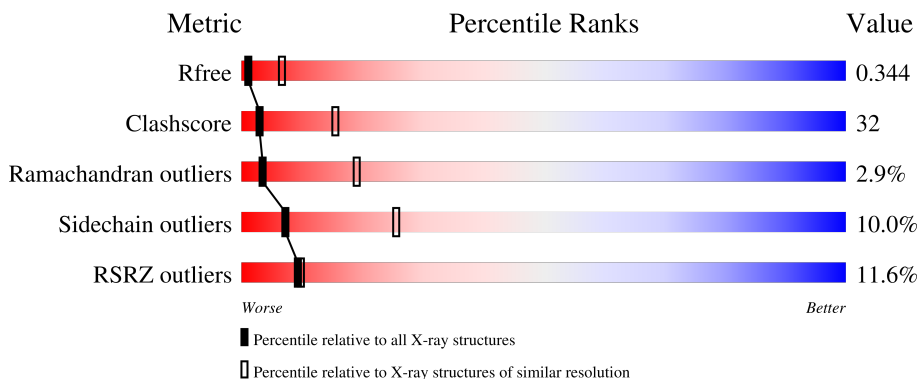
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.42 Å.

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



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	180053	1210 (3.48-3.36)
Clashscore	190562	1234 (3.48-3.36)
Ramachandran outliers	187476	1222 (3.48-3.36)
Sidechain outliers	187428	1222 (3.48-3.36)
RSRZ outliers	180081	1210 (3.48-3.36)

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

Mol	Chain	Length	Quality of chain
1	A	1049	12% 52% 41% 6%

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 7951 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 Acriflavine resistance protein B.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	1045	Total	C	N	O	S	84	0	0
			7950	5110	1316	1480	44			

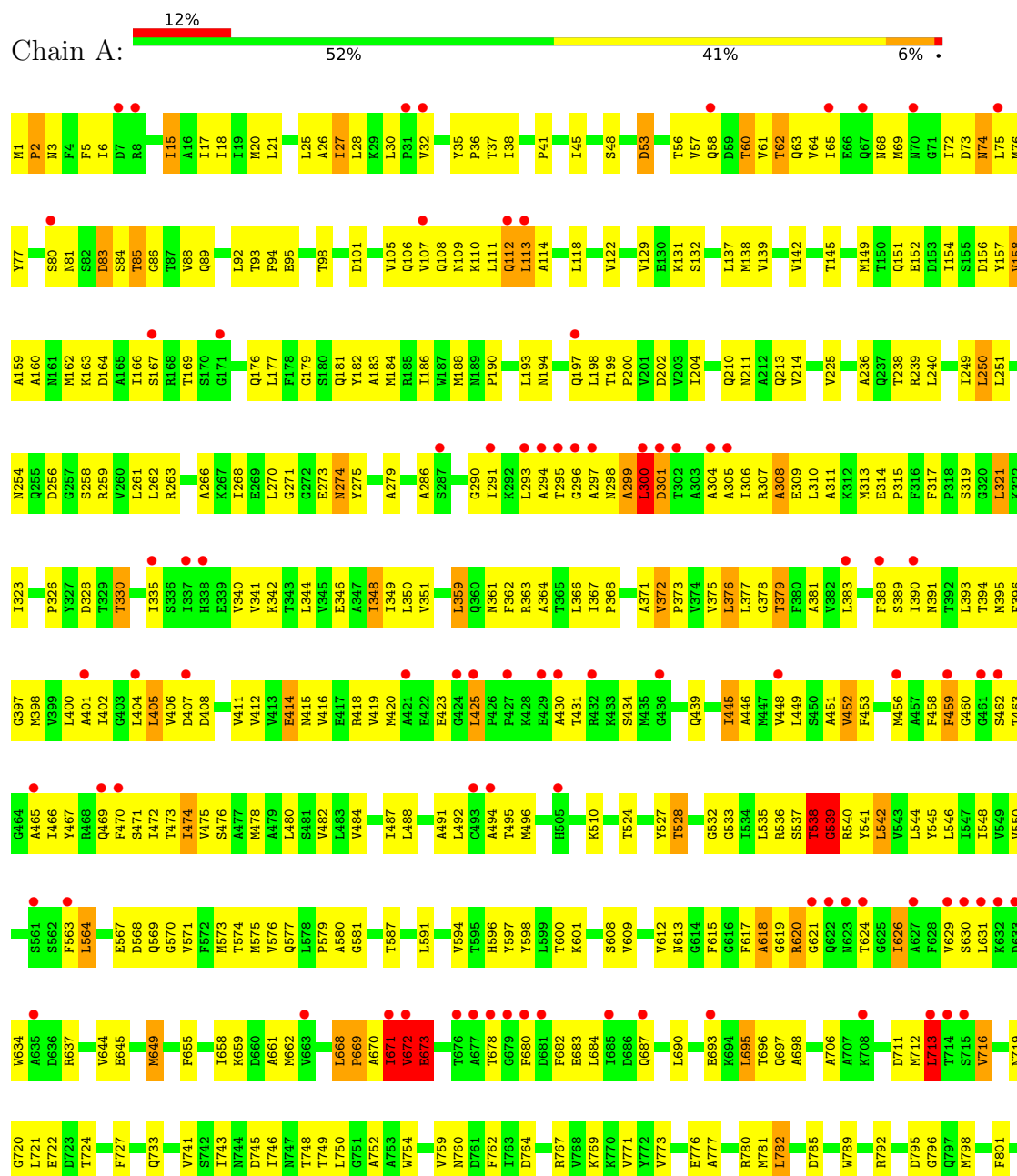
- Molecule 2 is NICKEL (II) ION (CCD ID: NI) (formula: Ni).

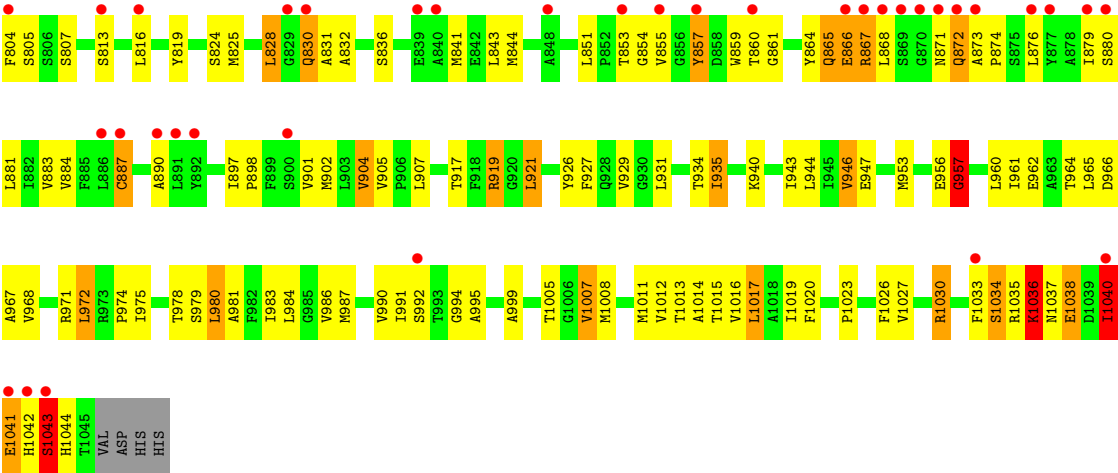
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	1	Total	Ni	0	0
			1	1		

3 Residue-property plots

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

• Molecule 1: Acriflavine resistance protein B





4 Data and refinement statistics

Property	Value	Source
Space group	H 3 2	Depositor
Cell constants a, b, c, α , β , γ	145.74Å 145.74Å 514.00Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	19.97 – 3.42 19.97 – 3.42	Depositor EDS
% Data completeness (in resolution range)	100.0 (19.97-3.42) 99.3 (19.97-3.42)	Depositor EDS
R_{merge}	0.12	Depositor
R_{sym}	0.12	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.20 (at 3.44Å)	Xtriage
Refinement program	REFMAC 5.2.0019	Depositor
R, R_{free}	0.289 , 0.355 0.282 , 0.344	Depositor DCC
R_{free} test set	1152 reflections (4.00%)	wwPDB-VP
Wilson B-factor (Å ²)	86.4	Xtriage
Anisotropy	0.343	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.25 , 73.6	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.86	EDS
Total number of atoms	7951	wwPDB-VP
Average B, all atoms (Å ²)	54.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.89% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

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

5 Model quality

5.1 Standard geometry

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

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	0.68	2/8102 (0.0%)	1.04	37/11001 (0.3%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	4	1

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	659	LYS	CA-CB	-8.39	1.40	1.53
1	A	672	VAL	C-O	5.85	1.31	1.24

All (37) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	865	GLN	N-CA-C	24.91	140.36	111.71
1	A	866	GLU	N-CA-C	14.50	141.69	110.80
1	A	672	VAL	CA-C-N	-14.40	101.22	122.24
1	A	672	VAL	C-N-CA	-14.40	101.22	122.24
1	A	1044	HIS	N-CA-C	10.15	132.41	110.80
1	A	1036	LYS	N-CA-C	-8.97	92.06	108.02
1	A	671	ILE	CB-CA-C	-8.14	97.94	111.29
1	A	672	VAL	N-CA-C	7.33	124.60	109.34
1	A	957	GLY	N-CA-C	-7.25	95.99	113.18
1	A	956	GLU	N-CA-C	7.22	126.17	110.80
1	A	510	LYS	CB-CA-C	7.10	124.55	110.42

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	619	GLY	N-CA-C	7.08	120.51	111.37
1	A	1037	ASN	N-CA-C	-6.72	98.40	107.88
1	A	510	LYS	N-CA-CB	6.28	121.11	110.49
1	A	659	LYS	N-CA-CB	6.18	119.53	109.95
1	A	538	THR	N-CA-CB	6.02	120.67	110.49
1	A	1035	ARG	N-CA-C	5.99	123.56	110.80
1	A	48	SER	N-CA-C	5.96	117.33	107.20
1	A	782	LEU	CA-C-N	5.80	127.09	119.84
1	A	782	LEU	C-N-CA	5.80	127.09	119.84
1	A	668	LEU	CA-C-N	5.73	127.01	119.84
1	A	668	LEU	C-N-CA	5.73	127.01	119.84
1	A	539	GLY	CA-C-N	-5.65	110.75	121.54
1	A	539	GLY	C-N-CA	-5.65	110.75	121.54
1	A	832	ALA	CA-C-N	5.56	126.79	119.84
1	A	832	ALA	C-N-CA	5.56	126.79	119.84
1	A	857	TYR	N-CA-C	5.49	116.61	108.60
1	A	510	LYS	CA-CB-CG	-5.40	103.31	114.10
1	A	608	SER	N-CA-C	5.39	117.97	108.75
1	A	1043	SER	N-CA-C	5.36	122.22	110.80
1	A	80	SER	N-CA-C	5.35	118.27	109.76
1	A	112	GLN	CB-CA-C	5.33	120.46	110.70
1	A	673	GLU	N-CA-C	-5.28	104.00	110.65
1	A	672	VAL	O-C-N	-5.20	116.07	122.57
1	A	792	ARG	N-CA-C	5.19	117.17	107.99
1	A	865	GLN	CB-CA-C	-5.18	101.05	110.63
1	A	132	SER	N-CA-C	5.05	116.72	108.55

All (4) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
1	A	510	LYS	CA
1	A	538	THR	CA
1	A	866	GLU	CA
1	A	956	GLU	CA

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	539	GLY	Peptide

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	7950	0	8091	503	0
2	A	1	0	0	0	0
All	All	7951	0	8091	503	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 32.

All (503) 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:957:GLY:HA2	1:A:1042:HIS:CE1	1.58	1.38
1:A:101:ASP:OD1	1:A:131:LYS:NZ	1.72	1.22
1:A:463:THR:HG21	1:A:868:LEU:HD11	1.19	1.16
1:A:463:THR:HG21	1:A:868:LEU:CD1	1.81	1.11
1:A:463:THR:CG2	1:A:868:LEU:HD11	1.81	1.10
1:A:672:VAL:HG12	1:A:673:GLU:N	1.57	1.09
1:A:990:VAL:HG23	1:A:1005:THR:HG22	1.38	1.06
1:A:672:VAL:CG1	1:A:673:GLU:N	2.15	1.05
1:A:672:VAL:CG1	1:A:673:GLU:H	1.72	1.02
1:A:45:ILE:HG23	1:A:129:VAL:HG22	1.44	0.97
1:A:612:VAL:HG23	1:A:626:ILE:HG23	1.50	0.94
1:A:990:VAL:HG23	1:A:1005:THR:CG2	1.99	0.93
1:A:375:VAL:HG22	1:A:484:VAL:HG21	1.51	0.92
1:A:612:VAL:CG2	1:A:626:ILE:HG23	1.99	0.92
1:A:188:MET:HE2	1:A:193:LEU:HD11	1.52	0.92
1:A:58:GLN:NE2	1:A:816:LEU:HD23	1.85	0.91
1:A:580:ALA:CB	1:A:724:THR:HG21	2.01	0.91
1:A:38:ILE:HD13	1:A:466:ILE:HD11	1.52	0.90
1:A:872:GLN:C	1:A:874:PRO:HD2	1.99	0.88
1:A:524:THR:O	1:A:528:THR:HG23	1.73	0.88
1:A:990:VAL:CG2	1:A:1005:THR:HG22	2.04	0.88
1:A:591:LEU:HD12	1:A:613:ASN:HD22	1.36	0.87
1:A:463:THR:HG21	1:A:868:LEU:CG	2.05	0.87
1:A:984:LEU:HD23	1:A:987:MET:HE2	1.55	0.86
1:A:306:ILE:HG23	1:A:310:LEU:HD13	1.55	0.86

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1016:VAL:HG23	1:A:1017:LEU:HD13	1.57	0.86
1:A:866:GLU:O	1:A:867:ARG:HB2	1.74	0.85
1:A:83:ASP:HB2	1:A:85:THR:HG22	1.58	0.85
1:A:27:ILE:CG2	1:A:28:LEU:HD23	2.07	0.85
1:A:580:ALA:HB1	1:A:724:THR:HG21	1.61	0.82
1:A:609:VAL:HG22	1:A:629:VAL:HG22	1.59	0.82
1:A:38:ILE:HD13	1:A:466:ILE:CD1	2.10	0.82
1:A:445:ILE:O	1:A:449:LEU:HD13	1.80	0.82
1:A:672:VAL:HG12	1:A:673:GLU:H	1.30	0.81
1:A:344:LEU:HD23	1:A:402:ILE:HD11	1.62	0.81
1:A:297:ALA:HB1	1:A:298:ASN:O	1.80	0.81
1:A:1011:MET:HE3	1:A:1015:THR:CG2	2.11	0.81
1:A:204:ILE:HD11	1:A:773:VAL:HG11	1.64	0.79
1:A:872:GLN:C	1:A:874:PRO:CD	2.54	0.79
1:A:214:VAL:CG2	1:A:236:ALA:HB3	2.12	0.79
1:A:680:PHE:CZ	1:A:844:MET:HE2	2.17	0.79
1:A:458:PHE:HA	1:A:459:PHE:HB3	1.65	0.78
1:A:615:PHE:CD1	1:A:620:ARG:NH1	2.51	0.78
1:A:306:ILE:CG2	1:A:310:LEU:HD13	2.13	0.78
1:A:813:SER:HB3	1:A:816:LEU:HD12	1.66	0.78
1:A:402:ILE:O	1:A:406:VAL:HG22	1.84	0.78
1:A:957:GLY:CA	1:A:1042:HIS:CE1	2.55	0.78
1:A:471:SER:O	1:A:475:VAL:HG23	1.85	0.77
1:A:987:MET:O	1:A:991:ILE:HD13	1.85	0.77
1:A:1:MET:N	1:A:2:PRO:HD3	2.01	0.76
1:A:445:ILE:HD11	1:A:943:ILE:HG21	1.66	0.76
1:A:166:ILE:HD11	1:A:310:LEU:HD12	1.67	0.75
1:A:214:VAL:HG23	1:A:236:ALA:HB3	1.66	0.75
1:A:1011:MET:HE3	1:A:1015:THR:HG21	1.68	0.75
1:A:393:LEU:CD1	1:A:466:ILE:HG23	2.16	0.75
1:A:27:ILE:HG22	1:A:28:LEU:HD23	1.68	0.75
1:A:964:THR:O	1:A:968:VAL:HG23	1.87	0.74
1:A:615:PHE:HE1	1:A:620:ARG:HH12	1.30	0.74
1:A:569:GLN:O	1:A:571:VAL:HG22	1.87	0.74
1:A:612:VAL:HG23	1:A:626:ILE:CG2	2.17	0.74
1:A:445:ILE:HD11	1:A:943:ILE:CG2	2.18	0.74
1:A:1042:HIS:CD2	1:A:1043:SER:H	2.06	0.74
1:A:393:LEU:HD13	1:A:466:ILE:HG23	1.69	0.73
1:A:873:ALA:N	1:A:874:PRO:CD	2.51	0.73
1:A:672:VAL:HG13	1:A:673:GLU:H	1.53	0.73
1:A:188:MET:HE1	1:A:200:PRO:HA	1.71	0.73

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:259:ARG:HD3	1:A:261:LEU:HD21	1.70	0.72
1:A:449:LEU:HB3	1:A:478:MET:HE1	1.71	0.72
1:A:110:LYS:HD3	1:A:113:LEU:HD22	1.70	0.72
1:A:45:ILE:HG23	1:A:129:VAL:CG2	2.17	0.72
1:A:587:THR:HB	1:A:613:ASN:HD21	1.52	0.72
1:A:407:ASP:OD2	1:A:978:THR:HG21	1.89	0.71
1:A:297:ALA:HA	1:A:298:ASN:HB2	1.69	0.71
1:A:254:ASN:HD22	1:A:258:SER:HB2	1.55	0.71
1:A:445:ILE:HG21	1:A:940:LYS:NZ	2.06	0.71
1:A:35:TYR:HD2	1:A:671:ILE:HD12	1.56	0.70
1:A:307:ARG:O	1:A:311:ALA:N	2.21	0.70
1:A:445:ILE:CD1	1:A:943:ILE:HG21	2.20	0.70
1:A:777:ALA:O	1:A:781:MET:HE3	1.92	0.70
1:A:159:ALA:HB1	1:A:181:GLN:HB2	1.74	0.69
1:A:53:ASP:O	1:A:57:VAL:HG23	1.92	0.69
1:A:344:LEU:CD2	1:A:402:ILE:HD11	2.22	0.69
1:A:394:THR:HG23	1:A:473:THR:HG21	1.74	0.69
1:A:943:ILE:O	1:A:946:VAL:HG13	1.93	0.69
1:A:957:GLY:HA2	1:A:1042:HIS:NE2	2.04	0.69
1:A:690:LEU:HD11	1:A:854:GLY:HA3	1.75	0.68
1:A:866:GLU:O	1:A:867:ARG:CB	2.42	0.68
1:A:451:ALA:HB1	1:A:883:VAL:HG12	1.75	0.68
1:A:111:LEU:HD12	1:A:129:VAL:HG21	1.74	0.68
1:A:137:LEU:HD12	1:A:293:LEU:HD12	1.74	0.68
1:A:669:PRO:O	1:A:670:ALA:HB3	1.93	0.67
1:A:1038:GLU:HB2	1:A:1040:ILE:HG22	1.77	0.67
1:A:350:LEU:HD23	1:A:984:LEU:HB3	1.75	0.67
1:A:972:LEU:HD23	1:A:1019:ILE:HD11	1.77	0.67
1:A:3:ASN:HA	1:A:6:ILE:HD12	1.77	0.67
1:A:204:ILE:HD11	1:A:773:VAL:CG1	2.25	0.67
1:A:169:THR:OG1	1:A:309:GLU:HG3	1.94	0.67
1:A:541:TYR:O	1:A:544:LEU:N	2.27	0.67
1:A:573:MET:HE2	1:A:668:LEU:CD2	2.25	0.67
1:A:83:ASP:C	1:A:85:THR:H	2.03	0.66
1:A:449:LEU:HD23	1:A:478:MET:CE	2.25	0.66
1:A:615:PHE:HD1	1:A:620:ARG:NH1	1.93	0.66
1:A:671:ILE:HG12	1:A:672:VAL:N	2.10	0.66
1:A:293:LEU:HD21	1:A:297:ALA:CB	2.26	0.66
1:A:524:THR:HG22	1:A:972:LEU:HD12	1.76	0.66
1:A:448:VAL:HG23	1:A:449:LEU:CD1	2.26	0.66
1:A:448:VAL:HG13	1:A:887:CYS:HB2	1.77	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1016:VAL:O	1:A:1019:ILE:HG22	1.96	0.65
1:A:75:LEU:HD12	1:A:92:LEU:HD23	1.78	0.65
1:A:177:LEU:HD23	1:A:179:GLY:O	1.97	0.65
1:A:446:ALA:HB2	1:A:482:VAL:HG21	1.79	0.65
1:A:372:VAL:HG22	1:A:405:LEU:HD13	1.77	0.65
1:A:383:LEU:HD21	1:A:473:THR:HG22	1.78	0.64
1:A:944:LEU:HB3	1:A:971:ARG:HD3	1.80	0.64
1:A:204:ILE:CD1	1:A:773:VAL:HG11	2.27	0.64
1:A:37:THR:HG21	1:A:296:GLY:HA2	1.80	0.63
1:A:5:PHE:CD2	1:A:487:ILE:HG23	2.34	0.63
1:A:577:GLN:HB2	1:A:662:MET:HE2	1.78	0.63
1:A:580:ALA:CB	1:A:724:THR:CG2	2.77	0.63
1:A:72:ILE:HG23	1:A:106:GLN:HB3	1.79	0.63
1:A:254:ASN:ND2	1:A:258:SER:HB2	2.13	0.63
1:A:431:THR:HG21	1:A:494:ALA:HB2	1.80	0.63
1:A:268:ILE:HD12	1:A:268:ILE:N	2.14	0.62
1:A:720:GLY:O	1:A:721:LEU:HD23	1.99	0.62
1:A:965:LEU:HA	1:A:968:VAL:HG23	1.80	0.62
1:A:27:ILE:HG23	1:A:28:LEU:HD23	1.81	0.62
1:A:372:VAL:HG13	1:A:376:LEU:HD22	1.81	0.62
1:A:335:ILE:HG22	1:A:335:ILE:O	1.99	0.62
1:A:907:LEU:HD13	1:A:1017:LEU:HB3	1.81	0.62
1:A:211:ASN:HA	1:A:240:LEU:HD13	1.82	0.62
1:A:404:LEU:HD13	1:A:478:MET:HE3	1.82	0.62
1:A:190:PRO:HB3	1:A:789:TRP:CZ3	2.35	0.61
1:A:449:LEU:HD23	1:A:478:MET:HE1	1.82	0.61
1:A:448:VAL:HG23	1:A:449:LEU:HD13	1.81	0.61
1:A:371:ALA:O	1:A:375:VAL:HG23	2.01	0.61
1:A:1:MET:H2	1:A:2:PRO:HD3	1.64	0.61
1:A:931:LEU:O	1:A:935:ILE:HG23	2.01	0.61
1:A:3:ASN:HA	1:A:6:ILE:HB	1.83	0.61
1:A:57:VAL:HG12	1:A:88:VAL:HG22	1.81	0.61
1:A:393:LEU:HD22	1:A:470:PHE:CE2	2.36	0.61
1:A:38:ILE:HG12	1:A:465:ALA:HB3	1.83	0.60
1:A:527:TYR:OH	1:A:968:VAL:CG1	2.49	0.60
1:A:533:GLY:HA2	1:A:536:ARG:NE	2.16	0.60
1:A:684:LEU:HD23	1:A:695:LEU:CD2	2.31	0.60
1:A:537:SER:O	1:A:538:THR:C	2.42	0.60
1:A:76:MET:HE3	1:A:864:TYR:CE2	2.37	0.60
1:A:138:MET:HE2	1:A:328:ASP:OD1	2.01	0.60
1:A:379:THR:HG21	1:A:398:MET:HE1	1.82	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:706:ALA:HB1	1:A:716:VAL:HG21	1.83	0.60
1:A:463:THR:HG23	1:A:563:PHE:CE2	2.37	0.60
1:A:575:MET:HE3	1:A:576:VAL:H	1.65	0.60
1:A:706:ALA:CB	1:A:716:VAL:HG21	2.31	0.60
1:A:181:GLN:NE2	1:A:769:LYS:HG2	2.17	0.59
1:A:539:GLY:C	1:A:541:TYR:N	2.59	0.59
1:A:1038:GLU:H	1:A:1038:GLU:CD	2.10	0.59
1:A:897:ILE:N	1:A:898:PRO:HD2	2.17	0.59
1:A:35:TYR:CD2	1:A:671:ILE:HD12	2.37	0.59
1:A:75:LEU:CD1	1:A:92:LEU:HD23	2.32	0.59
1:A:176:GLN:CD	1:A:620:ARG:HH22	2.12	0.58
1:A:972:LEU:HD23	1:A:1019:ILE:CD1	2.33	0.58
1:A:274:ASN:C	1:A:274:ASN:OD1	2.47	0.58
1:A:299:ALA:C	1:A:301:ASP:N	2.61	0.58
1:A:480:LEU:O	1:A:484:VAL:HG23	2.03	0.58
1:A:720:GLY:C	1:A:721:LEU:HD23	2.27	0.58
1:A:210:GLN:NE2	1:A:249:ILE:HG23	2.18	0.58
1:A:830:GLN:HA	1:A:830:GLN:HE21	1.66	0.58
1:A:990:VAL:HG22	1:A:990:VAL:O	2.02	0.58
1:A:711:ASP:OD1	1:A:712:MET:HE3	2.04	0.58
1:A:458:PHE:CA	1:A:459:PHE:HB3	2.33	0.58
1:A:32:VAL:O	1:A:299:ALA:HB1	2.04	0.58
1:A:449:LEU:O	1:A:452:VAL:HG22	2.03	0.58
1:A:873:ALA:N	1:A:874:PRO:HD3	2.19	0.58
1:A:684:LEU:O	1:A:824:SER:HB2	2.04	0.57
1:A:3:ASN:CA	1:A:6:ILE:HD12	2.34	0.57
1:A:570:GLY:O	1:A:571:VAL:HG13	2.03	0.57
1:A:669:PRO:O	1:A:670:ALA:CB	2.53	0.57
1:A:111:LEU:HD23	1:A:111:LEU:O	2.04	0.57
1:A:259:ARG:CD	1:A:261:LEU:HD21	2.33	0.57
1:A:372:VAL:HG22	1:A:405:LEU:CD1	2.33	0.57
1:A:719:ASN:HB2	1:A:828:LEU:HD13	1.85	0.57
1:A:307:ARG:HG3	1:A:311:ALA:HB2	1.85	0.57
1:A:416:VAL:HG12	1:A:420:MET:HE2	1.87	0.57
1:A:76:MET:HE3	1:A:864:TYR:CD2	2.40	0.56
1:A:580:ALA:HB3	1:A:724:THR:CG2	2.34	0.56
1:A:960:LEU:HD13	1:A:1027:VAL:HG12	1.87	0.56
1:A:61:VAL:CG1	1:A:88:VAL:HG21	2.35	0.56
1:A:111:LEU:HD12	1:A:129:VAL:CG2	2.35	0.56
1:A:105:VAL:O	1:A:108:GLN:N	2.36	0.56
1:A:162:MET:O	1:A:166:ILE:HG12	2.06	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:186:ILE:HB	1:A:773:VAL:HG23	1.86	0.56
1:A:463:THR:HG23	1:A:563:PHE:HE2	1.69	0.56
1:A:300:LEU:HD23	1:A:304:ALA:HB2	1.87	0.55
1:A:149:MET:SD	1:A:321:LEU:HD23	2.46	0.55
1:A:1042:HIS:CG	1:A:1043:SER:H	2.24	0.55
1:A:188:MET:CE	1:A:193:LEU:HD11	2.32	0.55
1:A:750:LEU:HD12	1:A:754:TRP:CD1	2.42	0.55
1:A:957:GLY:HA2	1:A:1042:HIS:ND1	2.12	0.55
1:A:131:LYS:HG3	1:A:131:LYS:O	2.06	0.55
1:A:400:LEU:HD21	1:A:1007:VAL:HG21	1.87	0.55
1:A:596:HIS:NE2	1:A:600:THR:HG21	2.21	0.55
1:A:160:ALA:HB1	1:A:767:ARG:HD2	1.88	0.55
1:A:383:LEU:HD21	1:A:473:THR:CG2	2.37	0.55
1:A:383:LEU:HD22	1:A:388:PHE:HB2	1.89	0.55
1:A:631:LEU:HD11	1:A:644:VAL:HG12	1.89	0.55
1:A:1011:MET:HE3	1:A:1015:THR:HG23	1.85	0.55
1:A:293:LEU:HD21	1:A:297:ALA:HB3	1.88	0.55
1:A:713:LEU:HD13	1:A:843:LEU:HD23	1.88	0.54
1:A:156:ASP:O	1:A:157:TYR:C	2.50	0.54
1:A:405:LEU:C	1:A:405:LEU:HD23	2.33	0.54
1:A:972:LEU:HA	1:A:975:ILE:HD12	1.90	0.54
1:A:451:ALA:CB	1:A:883:VAL:HG12	2.37	0.54
1:A:533:GLY:HA2	1:A:536:ARG:HE	1.72	0.54
1:A:142:VAL:HG12	1:A:154:ILE:CG2	2.38	0.54
1:A:305:ALA:O	1:A:308:ALA:HB3	2.08	0.54
1:A:405:LEU:C	1:A:405:LEU:CD2	2.80	0.54
1:A:880:SER:O	1:A:884:VAL:HG23	2.08	0.54
1:A:631:LEU:HD13	1:A:637:ARG:NH2	2.23	0.54
1:A:617:PHE:O	1:A:618:ALA:CB	2.56	0.53
1:A:658:ILE:HG22	1:A:661:ALA:HB3	1.90	0.53
1:A:990:VAL:HG11	1:A:1008:MET:CE	2.38	0.53
1:A:394:THR:HG23	1:A:473:THR:CG2	2.38	0.53
1:A:960:LEU:O	1:A:964:THR:HG23	2.08	0.53
1:A:598:TYR:CE2	1:A:629:VAL:HG21	2.44	0.53
1:A:615:PHE:CE1	1:A:620:ARG:NH1	2.61	0.53
1:A:1:MET:N	1:A:2:PRO:CD	2.69	0.53
1:A:463:THR:HG21	1:A:868:LEU:HG	1.89	0.52
1:A:68:ASN:HB2	1:A:114:ALA:HB2	1.90	0.52
1:A:456:MET:HG3	1:A:467:TYR:HB3	1.90	0.52
1:A:294:ALA:O	1:A:295:THR:C	2.53	0.52
1:A:58:GLN:O	1:A:63:GLN:HG3	2.09	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:297:ALA:CA	1:A:298:ASN:HB2	2.38	0.52
1:A:533:GLY:CA	1:A:536:ARG:HE	2.23	0.52
1:A:546:LEU:O	1:A:550:VAL:HG23	2.10	0.52
1:A:306:ILE:O	1:A:309:GLU:N	2.44	0.51
1:A:26:ALA:O	1:A:30:LEU:HB2	2.09	0.51
1:A:190:PRO:HB3	1:A:789:TRP:CE3	2.45	0.51
1:A:539:GLY:O	1:A:542:LEU:HB2	2.10	0.51
1:A:983:ILE:HD13	1:A:1012:VAL:HG22	1.93	0.51
1:A:112:GLN:O	1:A:113:LEU:C	2.53	0.51
1:A:142:VAL:HG12	1:A:154:ILE:HG23	1.91	0.51
1:A:539:GLY:HA3	1:A:542:LEU:HD13	1.92	0.51
1:A:72:ILE:HG23	1:A:106:GLN:CB	2.41	0.51
1:A:564:LEU:HD22	1:A:926:TYR:CE1	2.46	0.51
1:A:960:LEU:HD12	1:A:961:ILE:N	2.26	0.51
1:A:527:TYR:CE2	1:A:1019:ILE:HG13	2.45	0.51
1:A:831:ALA:HB1	1:A:836:SER:O	2.10	0.51
1:A:45:ILE:HD11	1:A:92:LEU:HD11	1.92	0.51
1:A:214:VAL:CG2	1:A:236:ALA:CB	2.88	0.51
1:A:300:LEU:CD2	1:A:304:ALA:HB2	2.41	0.51
1:A:38:ILE:HG22	1:A:38:ILE:O	2.10	0.50
1:A:157:TYR:C	1:A:157:TYR:CD2	2.89	0.50
1:A:407:ASP:CG	1:A:978:THR:HG21	2.36	0.50
1:A:367:ILE:HB	1:A:368:PRO:CD	2.41	0.50
1:A:463:THR:HA	1:A:466:ILE:HD13	1.94	0.50
1:A:946:VAL:O	1:A:947:GLU:C	2.54	0.50
1:A:393:LEU:HD22	1:A:470:PHE:HE2	1.72	0.50
1:A:872:GLN:O	1:A:874:PRO:N	2.44	0.50
1:A:972:LEU:HD22	1:A:972:LEU:O	2.12	0.50
1:A:1016:VAL:C	1:A:1019:ILE:HG22	2.37	0.50
1:A:62:THR:HG23	1:A:88:VAL:CG1	2.42	0.50
1:A:162:MET:HA	1:A:313:MET:SD	2.52	0.50
1:A:453:PHE:CE2	1:A:474:ILE:HG21	2.46	0.50
1:A:781:MET:CA	1:A:781:MET:HE2	2.41	0.50
1:A:533:GLY:O	1:A:536:ARG:HB2	2.12	0.49
1:A:733:GLN:HE22	1:A:743:ILE:HG21	1.76	0.49
1:A:872:GLN:O	1:A:873:ALA:C	2.54	0.49
1:A:139:VAL:O	1:A:326:PRO:HD2	2.12	0.49
1:A:580:ALA:HA	1:A:581:GLY:C	2.37	0.49
1:A:391:ASN:HD21	1:A:469:GLN:CD	2.21	0.49
1:A:407:ASP:CB	1:A:978:THR:HG21	2.42	0.49
1:A:211:ASN:CG	1:A:211:ASN:O	2.54	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:88:VAL:HG12	1:A:89:GLN:N	2.28	0.49
1:A:1038:GLU:HG2	1:A:1040:ILE:H	1.76	0.49
1:A:1042:HIS:O	1:A:1043:SER:CB	2.60	0.49
1:A:57:VAL:HG21	1:A:86:GLY:HA2	1.95	0.49
1:A:876:LEU:O	1:A:880:SER:HB2	2.12	0.49
1:A:65:ILE:HG13	1:A:118:LEU:HD21	1.94	0.49
1:A:378:GLY:O	1:A:381:ALA:HB3	2.13	0.49
1:A:412:VAL:O	1:A:416:VAL:HG23	2.11	0.49
1:A:1036:LYS:HD2	1:A:1036:LYS:O	2.13	0.49
1:A:448:VAL:CG1	1:A:887:CYS:HB2	2.42	0.49
1:A:990:VAL:C	1:A:991:ILE:HD12	2.38	0.49
1:A:83:ASP:OD2	1:A:83:ASP:N	2.45	0.48
1:A:682:PHE:HD1	1:A:859:TRP:CH2	2.31	0.48
1:A:60:THR:HG23	1:A:61:VAL:HG23	1.95	0.48
1:A:340:VAL:HG11	1:A:395:MET:HB3	1.95	0.48
1:A:449:LEU:HD23	1:A:478:MET:HE2	1.96	0.48
1:A:879:ILE:O	1:A:883:VAL:HG23	2.14	0.48
1:A:463:THR:CG2	1:A:868:LEU:HD21	2.43	0.48
1:A:631:LEU:HD11	1:A:644:VAL:CG1	2.43	0.48
1:A:919:ARG:C	1:A:921:LEU:H	2.22	0.48
1:A:964:THR:O	1:A:967:ALA:HB3	2.13	0.48
1:A:984:LEU:HD23	1:A:987:MET:CE	2.37	0.48
1:A:1:MET:H3	1:A:2:PRO:HD3	1.75	0.48
1:A:193:LEU:HB3	1:A:198:LEU:O	2.13	0.48
1:A:423:GLU:HB3	1:A:425:LEU:HD13	1.94	0.48
1:A:137:LEU:C	1:A:137:LEU:HD23	2.38	0.48
1:A:213:GLN:HB2	1:A:239:ARG:HG2	1.96	0.47
1:A:541:TYR:O	1:A:542:LEU:C	2.57	0.47
1:A:746:ILE:HD13	1:A:804:PHE:CE2	2.49	0.47
1:A:58:GLN:HA	1:A:62:THR:OG1	2.14	0.47
1:A:453:PHE:CD2	1:A:474:ILE:HG21	2.49	0.47
1:A:693:GLU:O	1:A:696:THR:HB	2.15	0.47
1:A:860:THR:OG1	1:A:861:GLY:N	2.46	0.47
1:A:965:LEU:HD12	1:A:966:ASP:N	2.29	0.47
1:A:990:VAL:HG11	1:A:1008:MET:HE2	1.96	0.47
1:A:414:GLU:HG2	1:A:974:PRO:HB3	1.96	0.47
1:A:617:PHE:O	1:A:618:ALA:HB2	2.15	0.47
1:A:56:THR:O	1:A:60:THR:HG22	2.15	0.47
1:A:488:LEU:O	1:A:492:LEU:HD13	2.15	0.47
1:A:108:GLN:O	1:A:109:ASN:C	2.57	0.47
1:A:372:VAL:HG12	1:A:373:PRO:N	2.29	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:379:THR:CG2	1:A:398:MET:HE1	2.45	0.47
1:A:743:ILE:HD12	1:A:743:ILE:H	1.80	0.47
1:A:35:TYR:HB3	1:A:36:PRO:HD2	1.97	0.46
1:A:445:ILE:HD11	1:A:943:ILE:HG22	1.95	0.46
1:A:445:ILE:HG21	1:A:940:LYS:HZ1	1.75	0.46
1:A:795:ASP:OD1	1:A:796:GLY:N	2.48	0.46
1:A:960:LEU:HD22	1:A:1030:ARG:HB3	1.96	0.46
1:A:1040:ILE:HG23	1:A:1041:GLU:N	2.30	0.46
1:A:348:ILE:HG22	1:A:349:ILE:N	2.30	0.46
1:A:670:ALA:O	1:A:671:ILE:HB	2.15	0.46
1:A:293:LEU:HD21	1:A:297:ALA:HB2	1.98	0.46
1:A:727:PHE:CE2	1:A:807:SER:HB2	2.49	0.46
1:A:1033:PHE:O	1:A:1034:SER:CB	2.63	0.46
1:A:1:MET:H2	1:A:2:PRO:CD	2.28	0.46
1:A:35:TYR:HD2	1:A:671:ILE:CD1	2.27	0.46
1:A:574:THR:OG1	1:A:598:TYR:OH	2.27	0.46
1:A:671:ILE:HG12	1:A:672:VAL:H	1.80	0.46
1:A:407:ASP:HB2	1:A:978:THR:HG21	1.97	0.46
1:A:383:LEU:HD11	1:A:473:THR:HG22	1.98	0.46
1:A:38:ILE:CD1	1:A:466:ILE:CD1	2.89	0.46
1:A:56:THR:O	1:A:56:THR:HG22	2.16	0.46
1:A:256:ASP:OD1	1:A:258:SER:OG	2.30	0.46
1:A:326:PRO:O	1:A:630:SER:HB2	2.15	0.46
1:A:363:ARG:NE	1:A:496:MET:O	2.48	0.46
1:A:904:VAL:O	1:A:905:VAL:C	2.58	0.46
1:A:158:VAL:HG23	1:A:177:LEU:HD11	1.98	0.46
1:A:451:ALA:HB1	1:A:883:VAL:CG1	2.43	0.46
1:A:411:VAL:HG22	1:A:971:ARG:HH22	1.81	0.45
1:A:567:GLU:OE2	1:A:999:ALA:N	2.45	0.45
1:A:62:THR:HG23	1:A:88:VAL:HG13	1.98	0.45
1:A:274:ASN:OD1	1:A:275:TYR:N	2.50	0.45
1:A:112:GLN:C	1:A:114:ALA:N	2.74	0.45
1:A:314:GLU:N	1:A:315:PRO:HD3	2.32	0.45
1:A:760:ASN:O	1:A:760:ASN:OD1	2.34	0.45
1:A:979:SER:OG	1:A:1015:THR:HG21	2.17	0.45
1:A:314:GLU:N	1:A:315:PRO:CD	2.79	0.45
1:A:527:TYR:OH	1:A:968:VAL:HG11	2.16	0.45
1:A:672:VAL:HG13	1:A:673:GLU:N	2.15	0.45
1:A:760:ASN:O	1:A:771:VAL:HG23	2.16	0.45
1:A:72:ILE:HD11	1:A:110:LYS:HG3	1.98	0.45
1:A:204:ILE:HD12	1:A:759:VAL:HG22	1.97	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:139:VAL:HG22	1:A:290:GLY:HA2	1.97	0.45
1:A:393:LEU:HD11	1:A:466:ILE:HG23	1.95	0.45
1:A:527:TYR:CE1	1:A:968:VAL:HG12	2.51	0.45
1:A:782:LEU:O	1:A:785:ASP:HB2	2.17	0.45
1:A:68:ASN:O	1:A:110:LYS:HB3	2.17	0.45
1:A:68:ASN:CB	1:A:114:ALA:HB2	2.46	0.45
1:A:314:GLU:HA	1:A:317:PHE:CE2	2.52	0.45
1:A:532:GLY:HA2	1:A:535:LEU:HD12	1.98	0.45
1:A:539:GLY:O	1:A:540:ARG:C	2.56	0.45
1:A:568:ASP:OD2	1:A:637:ARG:NH2	2.49	0.45
1:A:684:LEU:HD23	1:A:695:LEU:HD22	1.97	0.45
1:A:658:ILE:CG2	1:A:661:ALA:HB3	2.47	0.45
1:A:881:LEU:HD12	1:A:902:MET:HE1	1.98	0.45
1:A:266:ALA:O	1:A:268:ILE:HD12	2.17	0.45
1:A:404:LEU:HD22	1:A:478:MET:CE	2.46	0.45
1:A:527:TYR:CZ	1:A:1019:ILE:HG13	2.52	0.45
1:A:535:LEU:HD22	1:A:1027:VAL:HG11	1.98	0.45
1:A:748:THR:O	1:A:752:ALA:CB	2.65	0.45
1:A:980:LEU:HD23	1:A:984:LEU:HD12	1.98	0.45
1:A:390:ILE:HG22	1:A:390:ILE:O	2.17	0.45
1:A:575:MET:HE3	1:A:576:VAL:N	2.29	0.45
1:A:745:ASP:O	1:A:749:THR:HG23	2.17	0.45
1:A:1020:PHE:O	1:A:1023:PRO:HD2	2.17	0.45
1:A:594:VAL:HG13	1:A:655:PHE:CZ	2.51	0.44
1:A:45:ILE:HD11	1:A:92:LEU:CD1	2.48	0.44
1:A:307:ARG:O	1:A:311:ALA:HB3	2.17	0.44
1:A:307:ARG:O	1:A:311:ALA:CB	2.65	0.44
1:A:372:VAL:HA	1:A:405:LEU:HD11	1.99	0.44
1:A:415:ASN:O	1:A:419:VAL:HG23	2.17	0.44
1:A:431:THR:HA	1:A:434:SER:HB3	2.00	0.44
1:A:383:LEU:HD22	1:A:388:PHE:CB	2.48	0.44
1:A:449:LEU:CB	1:A:478:MET:HE1	2.46	0.44
1:A:597:TYR:HD1	1:A:601:LYS:HD2	1.83	0.44
1:A:621:GLY:O	1:A:624:THR:HG22	2.16	0.44
1:A:668:LEU:O	1:A:670:ALA:N	2.51	0.44
1:A:151:GLN:HA	1:A:154:ILE:HD12	1.99	0.44
1:A:293:LEU:HD23	1:A:293:LEU:C	2.42	0.44
1:A:762:PHE:CZ	1:A:764:ASP:HB2	2.52	0.44
1:A:819:TYR:CE1	1:A:860:THR:HB	2.52	0.44
1:A:57:VAL:HG12	1:A:88:VAL:CG2	2.48	0.44
1:A:183:ALA:O	1:A:184:MET:C	2.60	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:213:GLN:NE2	1:A:238:THR:HA	2.32	0.44
1:A:964:THR:HG22	1:A:1026:PHE:CD2	2.53	0.44
1:A:198:LEU:HD23	1:A:202:ASP:OD2	2.17	0.44
1:A:307:ARG:HA	1:A:310:LEU:HB2	1.99	0.44
1:A:335:ILE:O	1:A:335:ILE:CG2	2.65	0.44
1:A:596:HIS:CE1	1:A:600:THR:HG21	2.52	0.44
1:A:748:THR:O	1:A:752:ALA:HB2	2.16	0.44
1:A:342:LYS:HG2	1:A:346:GLU:OE2	2.18	0.43
1:A:527:TYR:OH	1:A:968:VAL:HG12	2.18	0.43
1:A:38:ILE:O	1:A:38:ILE:CG2	2.66	0.43
1:A:58:GLN:CD	1:A:816:LEU:HD23	2.42	0.43
1:A:263:ARG:HA	1:A:268:ILE:HD11	2.00	0.43
1:A:408:ASP:O	1:A:412:VAL:HG23	2.17	0.43
1:A:425:LEU:O	1:A:430:ALA:HB2	2.17	0.43
1:A:884:VAL:CG1	1:A:902:MET:HE3	2.48	0.43
1:A:445:ILE:HG23	1:A:449:LEU:HD22	2.00	0.43
1:A:297:ALA:CB	1:A:298:ASN:O	2.58	0.43
1:A:415:ASN:O	1:A:418:ARG:HB3	2.18	0.43
1:A:404:LEU:HD22	1:A:478:MET:HE2	2.00	0.43
1:A:307:ARG:CG	1:A:311:ALA:HB2	2.49	0.43
1:A:363:ARG:O	1:A:366:LEU:N	2.47	0.43
1:A:866:GLU:O	1:A:866:GLU:HG2	2.18	0.43
1:A:17:ILE:HG12	1:A:20:MET:HE3	2.01	0.43
1:A:197:GLN:HA	1:A:798:MET:HE2	2.00	0.43
1:A:402:ILE:O	1:A:406:VAL:N	2.36	0.43
1:A:545:TYR:HA	1:A:548:ILE:HD12	2.00	0.43
1:A:61:VAL:HG11	1:A:88:VAL:HG21	2.00	0.42
1:A:472:ILE:O	1:A:476:SER:OG	2.28	0.42
1:A:645:GLU:O	1:A:649:MET:HB2	2.19	0.42
1:A:780:ARG:C	1:A:781:MET:HE2	2.44	0.42
1:A:401:ALA:O	1:A:402:ILE:C	2.62	0.42
1:A:953:MET:HE1	1:A:1030:ARG:HH11	1.84	0.42
1:A:65:ILE:CG1	1:A:118:LEU:HD21	2.50	0.42
1:A:396:PHE:O	1:A:397:GLY:C	2.62	0.42
1:A:466:ILE:HD12	1:A:466:ILE:H	1.84	0.42
1:A:612:VAL:CG2	1:A:626:ILE:CG2	2.82	0.42
1:A:781:MET:HE2	1:A:781:MET:HA	2.01	0.42
1:A:851:LEU:HD13	1:A:855:VAL:HG11	2.02	0.42
1:A:986:VAL:HG11	1:A:1007:VAL:HG11	2.01	0.42
1:A:394:THR:CG2	1:A:473:THR:HG21	2.46	0.42
1:A:712:MET:HG3	1:A:843:LEU:HD22	2.01	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:183:ALA:N	1:A:271:GLY:O	2.52	0.42
1:A:263:ARG:HA	1:A:268:ILE:CD1	2.50	0.42
1:A:364:ALA:O	1:A:368:PRO:HD2	2.19	0.42
1:A:591:LEU:HD12	1:A:613:ASN:ND2	2.19	0.42
1:A:609:VAL:O	1:A:609:VAL:HG12	2.19	0.42
1:A:279:ALA:HB3	1:A:286:ALA:O	2.20	0.42
1:A:359:LEU:N	1:A:359:LEU:HD23	2.35	0.42
1:A:463:THR:HG21	1:A:868:LEU:CD2	2.48	0.42
1:A:108:GLN:HA	1:A:111:LEU:HB2	2.02	0.42
1:A:198:LEU:CD2	1:A:202:ASP:OD2	2.68	0.42
1:A:351:VAL:HG22	1:A:981:ALA:HB1	2.02	0.42
1:A:74:ASN:HB3	1:A:95:GLU:HG2	2.02	0.42
1:A:541:TYR:O	1:A:545:TYR:N	2.45	0.42
1:A:73:ASP:O	1:A:75:LEU:N	2.53	0.42
1:A:367:ILE:HG22	1:A:368:PRO:N	2.35	0.42
1:A:841:MET:HG2	1:A:859:TRP:CH2	2.55	0.42
1:A:901:VAL:HG11	1:A:943:ILE:HG13	2.02	0.42
1:A:162:MET:HE1	1:A:323:ILE:HD11	2.01	0.41
1:A:250:LEU:HD12	1:A:251:LEU:N	2.35	0.41
1:A:841:MET:O	1:A:844:MET:N	2.53	0.41
1:A:1038:GLU:CD	1:A:1038:GLU:N	2.78	0.41
1:A:64:VAL:O	1:A:64:VAL:HG22	2.20	0.41
1:A:76:MET:HE2	1:A:77:TYR:CE2	2.55	0.41
1:A:367:ILE:CB	1:A:368:PRO:CD	2.97	0.41
1:A:695:LEU:HD13	1:A:825:MET:HG3	2.01	0.41
1:A:713:LEU:HD21	1:A:844:MET:HG2	2.01	0.41
1:A:1011:MET:CE	1:A:1015:THR:HG21	2.46	0.41
1:A:361:ASN:HB3	1:A:364:ALA:HB3	2.02	0.41
1:A:166:ILE:HD11	1:A:310:LEU:CD1	2.45	0.41
1:A:535:LEU:CD2	1:A:1027:VAL:HG11	2.50	0.41
1:A:105:VAL:O	1:A:106:GLN:C	2.62	0.41
1:A:162:MET:O	1:A:313:MET:HE1	2.21	0.41
1:A:991:ILE:HD12	1:A:991:ILE:N	2.35	0.41
1:A:183:ALA:HB2	1:A:273:GLU:HG2	2.03	0.41
1:A:887:CYS:O	1:A:890:ALA:HB3	2.20	0.41
1:A:926:TYR:O	1:A:927:PHE:C	2.63	0.41
1:A:83:ASP:C	1:A:85:THR:N	2.73	0.41
1:A:158:VAL:CG2	1:A:177:LEU:HD11	2.51	0.41
1:A:177:LEU:HD23	1:A:179:GLY:C	2.46	0.41
1:A:414:GLU:CD	1:A:414:GLU:C	2.88	0.41
1:A:154:ILE:O	1:A:158:VAL:HG13	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:741:VAL:CG2	1:A:746:ILE:HD11	2.51	0.41
1:A:142:VAL:HG13	1:A:321:LEU:HD13	2.03	0.41
1:A:176:GLN:NE2	1:A:620:ARG:NH2	2.69	0.41
1:A:452:VAL:HA	1:A:880:SER:OG	2.20	0.41
1:A:452:VAL:HG12	1:A:884:VAL:HG21	2.02	0.41
1:A:580:ALA:HB3	1:A:724:THR:HG22	2.01	0.41
1:A:15:ILE:HD12	1:A:487:ILE:HD13	2.03	0.41
1:A:56:THR:O	1:A:60:THR:CG2	2.69	0.41
1:A:871:ASN:O	1:A:872:GLN:NE2	2.54	0.41
1:A:1013:THR:OG1	1:A:1014:ALA:N	2.54	0.41
1:A:163:LYS:HD3	1:A:177:LEU:HD13	2.03	0.40
1:A:176:GLN:NE2	1:A:620:ARG:HH22	2.19	0.40
1:A:983:ILE:HG23	1:A:1008:MET:HG3	2.02	0.40
1:A:21:LEU:O	1:A:25:LEU:HD13	2.20	0.40
1:A:38:ILE:HG12	1:A:465:ALA:CB	2.49	0.40
1:A:69:MET:HE1	1:A:111:LEU:N	2.37	0.40
1:A:376:LEU:O	1:A:377:LEU:C	2.64	0.40
1:A:462:SER:HB3	1:A:865:GLN:HE22	1.84	0.40
1:A:697:GLN:O	1:A:698:ALA:C	2.65	0.40
1:A:487:ILE:O	1:A:491:ALA:HB2	2.21	0.40
1:A:872:GLN:O	1:A:874:PRO:CD	2.68	0.40
1:A:41:PRO:HD2	1:A:94:PHE:O	2.22	0.40
1:A:156:ASP:CG	1:A:182:TYR:CD2	3.00	0.40
1:A:631:LEU:HD13	1:A:637:ARG:CZ	2.51	0.40
1:A:682:PHE:CZ	1:A:857:TYR:HB2	2.57	0.40
1:A:873:ALA:O	1:A:876:LEU:HB2	2.22	0.40
1:A:921:LEU:CD2	1:A:1005:THR:OG1	2.69	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	1043/1049 (99%)	870 (83%)	143 (14%)	30 (3%)	3	19

All (30) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	74	ASN
1	A	300	LEU
1	A	459	PHE
1	A	579	PRO
1	A	618	ALA
1	A	620	ARG
1	A	669	PRO
1	A	671	ILE
1	A	867	ARG
1	A	1034	SER
1	A	1043	SER
1	A	538	THR
1	A	672	VAL
1	A	299	ALA
1	A	301	ASP
1	A	439	GLN
1	A	634	TRP
1	A	678	THR
1	A	713	LEU
1	A	992	SER
1	A	995	ALA
1	A	84	SER
1	A	330	THR
1	A	308	ALA
1	A	994	GLY
1	A	2	PRO
1	A	113	LEU
1	A	957	GLY
1	A	460	GLY
1	A	1040	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	851/855 (100%)	766 (90%)	85 (10%)	7	25

All (85) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	15	ILE
1	A	18	ILE
1	A	27	ILE
1	A	53	ASP
1	A	60	THR
1	A	62	THR
1	A	81	ASN
1	A	83	ASP
1	A	85	THR
1	A	93	THR
1	A	98	THR
1	A	107	VAL
1	A	122	VAL
1	A	145	THR
1	A	152	GLU
1	A	158	VAL
1	A	164	ASP
1	A	167	SER
1	A	194	ASN
1	A	199	THR
1	A	225	VAL
1	A	250	LEU
1	A	262	LEU
1	A	270	LEU
1	A	274	ASN
1	A	291	ILE
1	A	300	LEU
1	A	319	SER
1	A	321	LEU
1	A	330	THR
1	A	341	VAL
1	A	348	ILE
1	A	359	LEU
1	A	362	PHE
1	A	372	VAL
1	A	376	LEU

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Mol	Chain	Res	Type
1	A	379	THR
1	A	389	SER
1	A	405	LEU
1	A	414	GLU
1	A	425	LEU
1	A	445	ILE
1	A	452	VAL
1	A	474	ILE
1	A	495	THR
1	A	528	THR
1	A	538	THR
1	A	542	LEU
1	A	564	LEU
1	A	626	ILE
1	A	649	MET
1	A	671	ILE
1	A	673	GLU
1	A	683	GLU
1	A	687	GLN
1	A	695	LEU
1	A	713	LEU
1	A	716	VAL
1	A	722	GLU
1	A	776	GLU
1	A	801	PHE
1	A	805	SER
1	A	828	LEU
1	A	830	GLN
1	A	853	THR
1	A	872	GLN
1	A	887	CYS
1	A	904	VAL
1	A	917	THR
1	A	919	ARG
1	A	921	LEU
1	A	929	VAL
1	A	934	THR
1	A	935	ILE
1	A	946	VAL
1	A	962	GLU
1	A	972	LEU
1	A	980	LEU

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Mol	Chain	Res	Type
1	A	1007	VAL
1	A	1017	LEU
1	A	1030	ARG
1	A	1036	LYS
1	A	1038	GLU
1	A	1040	ILE
1	A	1041	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (15) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	191	ASN
1	A	210	GLN
1	A	213	GLN
1	A	254	ASN
1	A	284	GLN
1	A	298	ASN
1	A	391	ASN
1	A	577	GLN
1	A	613	ASN
1	A	687	GLN
1	A	733	GLN
1	A	830	GLN
1	A	865	GLN
1	A	872	GLN
1	A	1042	HIS

5.3.3 RNA ⓘ

There are no RNA molecules 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 oligosaccharides in this entry.

5.6 Ligand geometry

Of 1 ligands modelled in this entry, 1 is monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

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	1045/1049 (99%)	0.75	121 (11%) 9 10	25, 52, 83, 110	19 (1%)

All (121) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	867	ARG	9.1
1	A	866	GLU	8.2
1	A	632	LYS	7.7
1	A	436	GLY	5.9
1	A	31	PRO	5.7
1	A	631	LEU	5.5
1	A	715	SER	4.9
1	A	868	LEU	4.9
1	A	877	TYR	4.9
1	A	869	SER	4.9
1	A	305	ALA	4.4
1	A	302	THR	4.4
1	A	293	LEU	4.0
1	A	633	ASP	4.0
1	A	404	LEU	4.0
1	A	676	THR	3.8
1	A	421	ALA	3.6
1	A	70	ASN	3.6
1	A	297	ALA	3.6
1	A	295	THR	3.5
1	A	622	GLN	3.5
1	A	840	ALA	3.4
1	A	630	SER	3.3
1	A	425	LEU	3.2
1	A	672	VAL	3.2
1	A	459	PHE	3.2
1	A	291	ILE	3.2

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Mol	Chain	Res	Type	RSRZ
1	A	635	ALA	3.1
1	A	388	PHE	3.1
1	A	470	PHE	3.1
1	A	685	ILE	3.1
1	A	461	GLY	3.0
1	A	870	GLY	3.0
1	A	892	TYR	3.0
1	A	627	ALA	2.9
1	A	816	LEU	2.9
1	A	113	LEU	2.9
1	A	7	ASP	2.8
1	A	855	VAL	2.8
1	A	429	GLU	2.8
1	A	624	THR	2.8
1	A	679	GLY	2.8
1	A	1043	SER	2.8
1	A	469	GLN	2.8
1	A	830	GLN	2.8
1	A	294	ALA	2.7
1	A	887	CYS	2.7
1	A	167	SER	2.7
1	A	456	MET	2.7
1	A	505	HIS	2.7
1	A	880	SER	2.7
1	A	714	THR	2.7
1	A	296	GLY	2.6
1	A	829	GLY	2.6
1	A	75	LEU	2.6
1	A	430	ALA	2.6
1	A	813	SER	2.6
1	A	304	ALA	2.6
1	A	629	VAL	2.6
1	A	860	THR	2.6
1	A	681	ASP	2.6
1	A	427	PRO	2.6
1	A	713	LEU	2.6
1	A	708	LYS	2.6
1	A	407	ASP	2.5
1	A	401	ALA	2.5
1	A	65	ILE	2.5
1	A	390	ILE	2.5
1	A	886	LEU	2.5

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Mol	Chain	Res	Type	RSRZ
1	A	301	ASP	2.5
1	A	424	GLY	2.5
1	A	848	ALA	2.5
1	A	900	SER	2.5
1	A	8	ARG	2.5
1	A	872	GLN	2.5
1	A	563	PHE	2.4
1	A	623	ASN	2.4
1	A	621	GLY	2.4
1	A	337	ILE	2.4
1	A	300	LEU	2.4
1	A	879	ILE	2.4
1	A	680	PHE	2.4
1	A	876	LEU	2.4
1	A	287	SER	2.4
1	A	432	ARG	2.3
1	A	112	GLN	2.3
1	A	1041	GLU	2.3
1	A	493	CYS	2.3
1	A	804	PHE	2.3
1	A	67	GLN	2.3
1	A	383	LEU	2.3
1	A	338	HIS	2.3
1	A	687	GLN	2.3
1	A	32	VAL	2.3
1	A	677	ALA	2.2
1	A	839	GLU	2.2
1	A	197	GLN	2.2
1	A	1033	PHE	2.2
1	A	80	SER	2.2
1	A	462	SER	2.2
1	A	1040	ILE	2.2
1	A	871	ASN	2.2
1	A	693	GLU	2.1
1	A	448	VAL	2.1
1	A	465	ALA	2.1
1	A	107	VAL	2.1
1	A	853	THR	2.1
1	A	494	ALA	2.1
1	A	171	GLY	2.1
1	A	992	SER	2.1
1	A	335	ILE	2.1

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Mol	Chain	Res	Type	RSRZ
1	A	671	ILE	2.1
1	A	873	ALA	2.1
1	A	891	LEU	2.0
1	A	1042	HIS	2.0
1	A	678	THR	2.0
1	A	857	TYR	2.0
1	A	890	ALA	2.0
1	A	58	GLN	2.0
1	A	663	VAL	2.0
1	A	561	SER	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 oligosaccharides in this entry.

6.4 Ligands [i](#)

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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
2	NI	A	1201	1/1	0.99	0.22	24,24,24,24	1

6.5 Other polymers [i](#)

There are no such residues in this entry.