



Full wwPDB X-ray Structure Validation Report ⓘ

Jan 31, 2016 – 10:07 PM GMT

PDB ID : 1S5G
Title : Structure of Scallop myosin S1 reveals a novel nucleotide conformation
Authors : Risal, D.; Gourinath, S.; Himmel, D.M.; Szent-Gyorgyi, A.G.; Cohen, C.
Deposited on : 2004-01-20
Resolution : 3.10 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

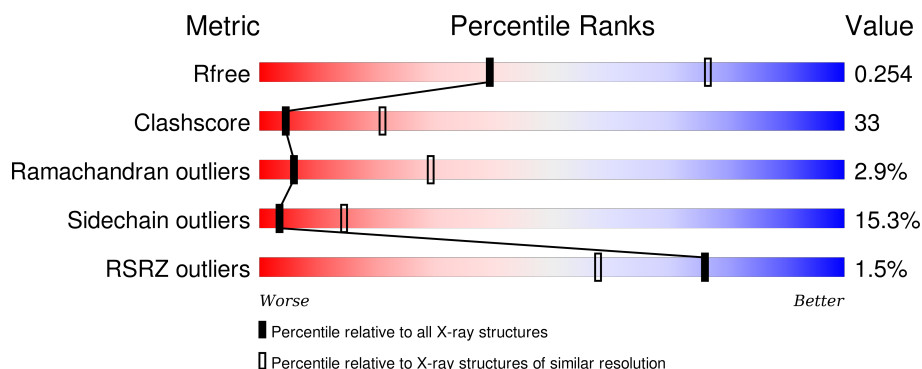
1 Overall quality at a glance ⓘ

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 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}	91344	1114 (3.14-3.06)
Clashscore	102246	1222 (3.14-3.06)
Ramachandran outliers	100387	1174 (3.14-3.06)
Sidechain outliers	100360	1174 (3.14-3.06)
RSRZ outliers	91569	1119 (3.14-3.06)

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	840	<div> <div>8%</div> <div>40%</div> <div>47%</div> <div>8%</div> <div>5%</div> </div>
2	Y	156	<div> <div>8%</div> <div>47%</div> <div>33%</div> <div>10%</div> <div>9%</div> </div>
3	Z	156	<div> <div>47%</div> <div>45%</div> <div>8%</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
4	SO4	A	996	-	-	X	X
5	CA	Z	998	-	-	-	X

2 Entry composition [i](#)

There are 8 unique types of molecules in this entry. The entry contains 8607 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 Myosin heavy chain, striated muscle.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	802	6301	4020	1075	1168	38	0	0	0

- Molecule 2 is a protein called Myosin regulatory light chain, striated adductor muscle.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
2	Y	142	1064	665	173	217	9	0	0	0

- Molecule 3 is a protein called Myosin essential light chain, striated adductor muscle.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
3	Z	155	1207	767	190	243	7	0	0	0

- Molecule 4 is SULFATE ION (three-letter code: SO4) (formula: O₄S).



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

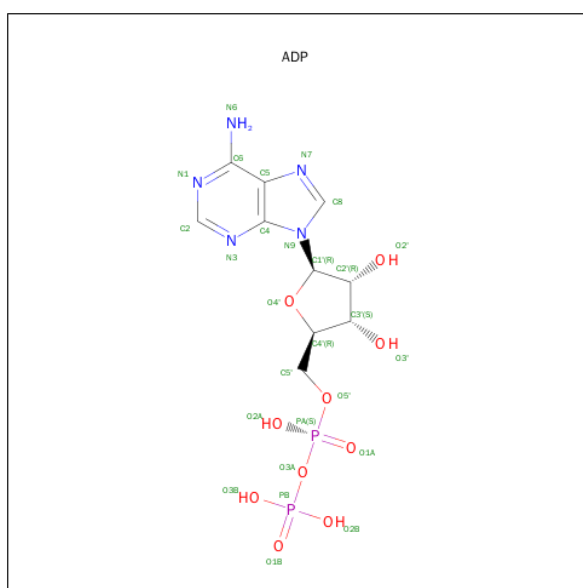
- Molecule 5 is CALCIUM ION (three-letter code: CA) (formula: Ca).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	Z	1	Total Ca 1 1	0	0

- Molecule 6 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
6	Y	1	Total Mg 1 1	0	0

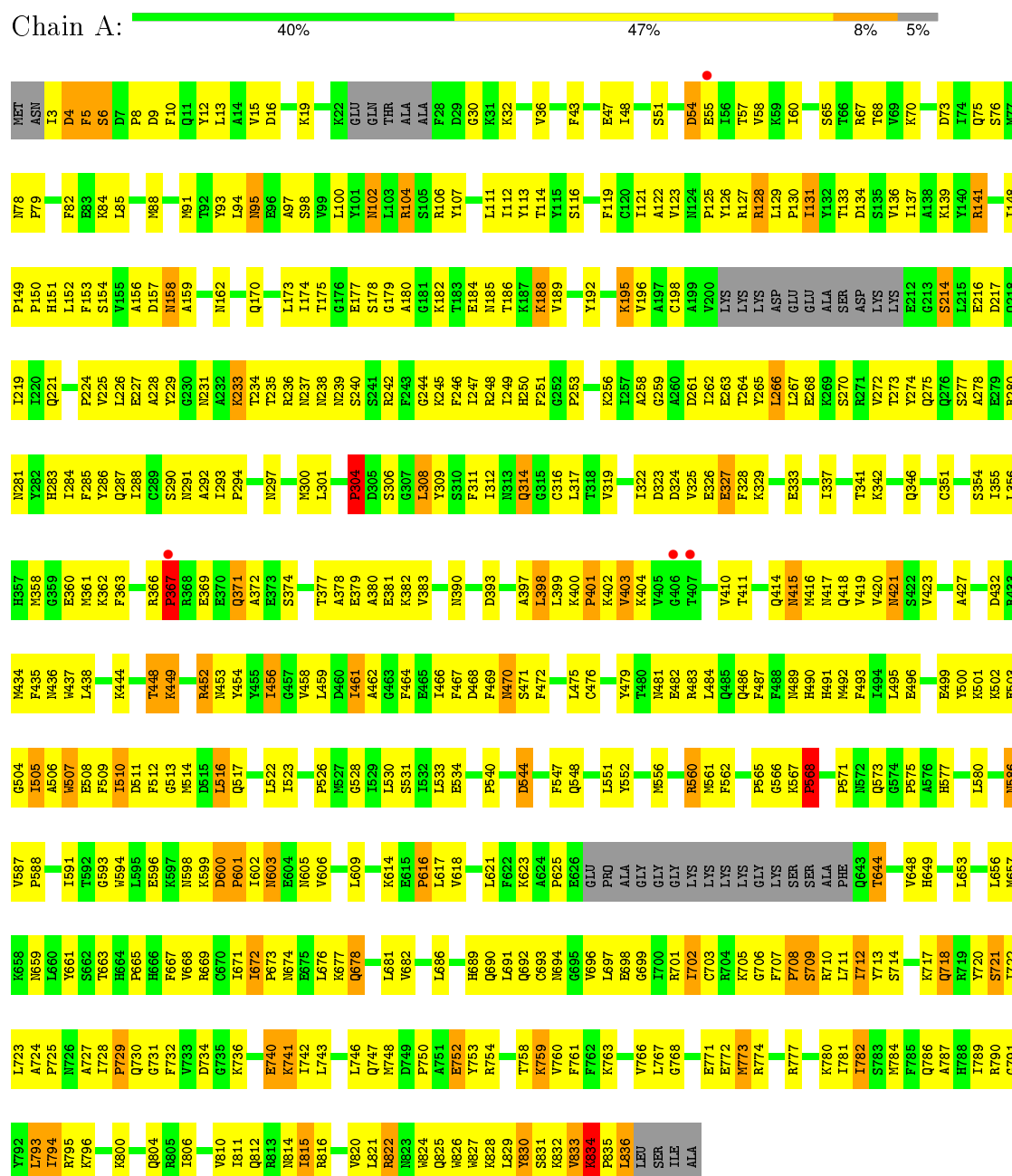
- Molecule 7 is ADENOSINE-5'-DIPHOSPHATE (three-letter code: ADP) (formula: C₁₀H₁₅N₅O₁₀P₂).



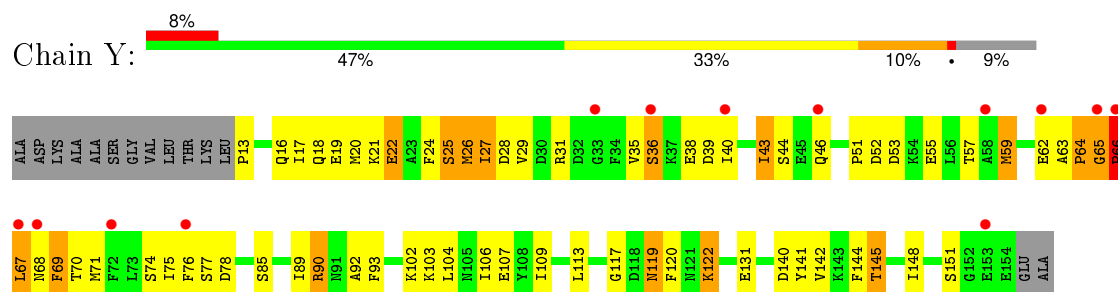
3 Residue-property plots

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: Myosin heavy chain, striated muscle



- Molecule 2: Myosin regulatory light chain, striated adductor muscle



- Molecule 3: Myosin essential light chain, striated adductor muscle



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	84.05Å 50.94Å 161.59Å 90.00° 98.36° 90.00°	Depositor
Resolution (Å)	43.44 – 3.10 43.43 – 3.04	Depositor EDS
% Data completeness (in resolution range)	84.6 (43.44-3.10) 81.5 (43.43-3.04)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.07	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.30 (at 3.06Å)	Xtriage
Refinement program	CNS 1.0	Depositor
R, R_{free}	0.233 , 0.269 0.224 , 0.254	Depositor DCC
R_{free} test set	1259 reflections (5.91%)	DCC
Wilson B-factor (Å ²)	79.7	Xtriage
Anisotropy	0.414	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.28 , 74.9	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.47$, $\langle L^2 \rangle = 0.30$	Xtriage
Outliers	0 of 22273 reflections	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	8607	wwPDB-VP
Average B, all atoms (Å ²)	80.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.67% 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: MG, CA, ADP, SO4

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	A	0.31	0/6431	0.67	2/8689 (0.0%)
2	Y	0.32	0/1079	0.77	1/1448 (0.1%)
3	Z	0.32	0/1232	0.63	0/1661
All	All	0.31	0/8742	0.67	3/11798 (0.0%)

There are no bond length outliers.

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	566	GLY	N-CA-C	-7.17	95.17	113.10
1	A	834	LYS	N-CA-C	6.95	129.77	111.00
2	Y	65	GLY	N-CA-C	-6.53	96.78	113.10

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	6301	0	6170	438	0
2	Y	1064	0	990	68	0
3	Z	1207	0	1127	76	0
4	A	5	0	0	3	0
5	Z	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
6	Y	1	0	0	0	0
7	A	27	0	12	5	0
8	A	1	0	0	0	0
All	All	8607	0	8299	550	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 33.

All (550) 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:128:ARG:HH11	1:A:128:ARG:HG3	0.95	1.08
1:A:148:ILE:HG13	1:A:149:PRO:HD2	1.36	1.08
2:Y:35:VAL:HG13	2:Y:39:ASP:HB3	1.33	1.05
1:A:128:ARG:NH1	1:A:128:ARG:HG3	1.75	0.96
1:A:822:ARG:CB	1:A:822:ARG:HH11	1.81	0.92
1:A:468:ASP:HB3	1:A:573:GLN:HA	1.53	0.91
1:A:723:LEU:HD23	1:A:746:LEU:HD11	1.51	0.91
3:Z:52:VAL:HG21	3:Z:75:LEU:HD21	1.51	0.89
1:A:253:PRO:HG3	1:A:453:ASN:ND2	1.89	0.87
1:A:48:ILE:HA	1:A:58:VAL:HG12	1.56	0.87
1:A:319:VAL:HB	1:A:322:ILE:HB	1.57	0.87
3:Z:5:GLN:HA	3:Z:8:ILE:HD12	1.57	0.86
1:A:448:THR:H	1:A:452:ARG:HH22	1.21	0.86
1:A:523:ILE:HD11	1:A:580:LEU:HD21	1.58	0.86
1:A:128:ARG:HH11	1:A:128:ARG:CG	1.86	0.85
1:A:292:ALA:HB2	1:A:325:VAL:HG13	1.59	0.84
3:Z:69:LEU:HB3	3:Z:70:PRO:HD3	1.59	0.84
1:A:796:LYS:HD3	3:Z:152:PRO:HB3	1.58	0.84
1:A:55:GLU:HG3	1:A:68:THR:HG21	1.60	0.83
1:A:784:MET:HE1	3:Z:79:GLU:HB3	1.61	0.82
1:A:291:ASN:HD22	1:A:304:PRO:HG2	1.44	0.82
1:A:290:SER:HB2	1:A:325:VAL:HG22	1.61	0.82
1:A:239:ASN:HB3	7:A:995:ADP:O2A	1.79	0.81
1:A:507:TRP:CG	1:A:508:GLU:N	2.49	0.81
1:A:717:LYS:HG3	1:A:718:GLN:N	1.95	0.80
1:A:522:LEU:HD11	1:A:562:PHE:HB2	1.64	0.80
1:A:401:PRO:HG3	1:A:603:ASN:HD21	1.46	0.80
1:A:470:ASN:N	1:A:470:ASN:HD22	1.79	0.80
1:A:603:ASN:HB3	1:A:606:VAL:H	1.47	0.79
1:A:567:LYS:HB3	1:A:568:PRO:HD2	1.64	0.79

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:180:ALA:HA	1:A:672:ILE:HG23	1.64	0.79
1:A:148:ILE:HG13	1:A:149:PRO:CD	2.12	0.79
1:A:836:LEU:HD22	2:Y:26:MET:SD	2.23	0.78
1:A:182:LYS:HG2	4:A:996:SO4:O2	1.83	0.78
1:A:822:ARG:HH11	1:A:822:ARG:HB2	1.48	0.78
1:A:157:ASP:HB2	1:A:192:TYR:OH	1.85	0.77
1:A:829:LEU:O	1:A:833:VAL:HG23	1.85	0.76
1:A:186:THR:HG23	1:A:458:VAL:HG11	1.67	0.75
1:A:123:VAL:HG12	1:A:673:PRO:HG3	1.68	0.75
1:A:509:PHE:O	1:A:510:ILE:HG23	1.87	0.75
2:Y:21:LYS:O	2:Y:24:PHE:HB3	1.87	0.74
1:A:796:LYS:CD	3:Z:152:PRO:HB3	2.18	0.74
1:A:107:TYR:HA	1:A:111:LEU:O	1.86	0.74
1:A:55:GLU:HG3	1:A:68:THR:CG2	2.19	0.73
1:A:834:LYS:HA	1:A:836:LEU:HD23	1.69	0.73
1:A:287:GLN:HB3	1:A:328:PHE:HB2	1.70	0.73
1:A:227:GLU:HA	1:A:231:ASN:OD1	1.88	0.72
1:A:707:PHE:CE1	1:A:754:ARG:HD2	2.23	0.72
3:Z:42:ILE:HG22	3:Z:44:PRO:HD3	1.71	0.72
1:A:112:ILE:HD13	1:A:125:PRO:HG3	1.71	0.71
2:Y:40:ILE:O	2:Y:43:ILE:HG23	1.90	0.71
1:A:833:VAL:O	1:A:833:VAL:HG12	1.90	0.71
1:A:603:ASN:HD22	1:A:605:ASN:HB3	1.56	0.70
1:A:459:LEU:HD11	1:A:461:ILE:HD11	1.73	0.70
1:A:13:LEU:HD21	1:A:131:ILE:CG2	2.21	0.70
1:A:727:ALA:O	1:A:729:PRO:HD3	1.91	0.70
1:A:448:THR:H	1:A:452:ARG:NH2	1.90	0.70
1:A:746:LEU:CD2	1:A:773:MET:HE1	2.21	0.70
1:A:70:LYS:O	1:A:73:ASP:HB2	1.91	0.70
1:A:672:ILE:H	1:A:672:ILE:HD13	1.56	0.69
1:A:414:GLN:HB2	1:A:418:GLN:HB2	1.74	0.69
3:Z:31:PHE:CD2	3:Z:58:MET:HG2	2.27	0.69
1:A:694:ASN:HD22	1:A:696:VAL:HG13	1.57	0.69
1:A:378:ALA:O	1:A:382:LYS:HG3	1.93	0.69
1:A:128:ARG:HA	7:A:995:ADP:H2	1.57	0.68
1:A:758:THR:HG23	1:A:759:LYS:HD3	1.75	0.68
1:A:707:PHE:HB3	1:A:761:PHE:HB3	1.74	0.68
2:Y:63:ALA:O	2:Y:65:GLY:N	2.24	0.68
3:Z:69:LEU:O	3:Z:73:GLU:HG2	1.94	0.68
1:A:244:GLY:HA3	1:A:461:ILE:HG23	1.76	0.68
1:A:221:GLN:O	1:A:224:PRO:HD2	1.93	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:377:THR:O	1:A:381:GLU:HG3	1.94	0.68
1:A:291:ASN:HB2	1:A:304:PRO:HB3	1.74	0.67
1:A:694:ASN:ND2	1:A:696:VAL:HG13	2.10	0.67
1:A:363:PHE:HD2	1:A:374:SER:HA	1.60	0.67
1:A:280:ARG:HG2	1:A:316:CYS:O	1.95	0.67
1:A:800:LYS:O	1:A:804:GLN:HG3	1.95	0.66
1:A:468:ASP:CB	1:A:573:GLN:HA	2.25	0.66
1:A:812:GLN:O	1:A:816:ARG:HG3	1.95	0.66
1:A:106:ARG:HG2	1:A:111:LEU:HD12	1.77	0.66
1:A:834:LYS:O	1:A:834:LYS:HD3	1.96	0.66
1:A:822:ARG:CG	1:A:822:ARG:HH11	2.08	0.66
3:Z:42:ILE:C	3:Z:44:PRO:HD3	2.17	0.66
2:Y:18:GLN:O	2:Y:21:LYS:HB3	1.96	0.66
1:A:717:LYS:HG3	1:A:718:GLN:H	1.61	0.65
1:A:229:TYR:CZ	1:A:284:ILE:HG12	2.30	0.65
2:Y:27:ILE:HG22	2:Y:28:ASP:N	2.11	0.65
2:Y:35:VAL:CG1	2:Y:40:ILE:HG13	2.26	0.65
3:Z:71:ALA:O	3:Z:75:LEU:HD23	1.97	0.65
1:A:342:LYS:O	1:A:346:GLN:HG3	1.96	0.65
1:A:522:LEU:HD12	1:A:561:MET:HB2	1.78	0.65
1:A:711:LEU:O	1:A:759:LYS:HB2	1.97	0.65
2:Y:70:THR:HG22	2:Y:70:THR:O	1.98	0.65
1:A:292:ALA:C	1:A:293:ILE:HD12	2.18	0.64
1:A:398:LEU:HD21	1:A:423:VAL:HG22	1.79	0.64
1:A:13:LEU:HD21	1:A:131:ILE:HG21	1.78	0.64
1:A:789:ILE:HG23	3:Z:125:ILE:HD12	1.80	0.64
1:A:123:VAL:CG1	1:A:673:PRO:HG3	2.28	0.64
1:A:586:ASN:HD22	1:A:586:ASN:N	1.95	0.64
1:A:746:LEU:HD21	1:A:773:MET:HE1	1.79	0.63
1:A:470:ASN:N	1:A:470:ASN:ND2	2.39	0.63
2:Y:75:ILE:O	2:Y:75:ILE:HG22	1.98	0.63
2:Y:35:VAL:HG13	2:Y:39:ASP:CB	2.20	0.63
3:Z:31:PHE:HD2	3:Z:58:MET:HG2	1.61	0.63
1:A:686:LEU:O	1:A:690:GLN:HG3	1.98	0.63
1:A:690:GLN:O	1:A:694:ASN:N	2.32	0.63
1:A:79:PRO:HD2	1:A:82:PHE:CD1	2.33	0.63
1:A:354:SER:O	1:A:358:MET:HG3	1.98	0.63
1:A:267:LEU:HD12	1:A:268:GLU:H	1.62	0.63
1:A:469:PHE:C	1:A:470:ASN:HD22	2.01	0.62
2:Y:27:ILE:HG23	2:Y:35:VAL:HG21	1.82	0.62
1:A:568:PRO:HA	1:A:573:GLN:OE1	2.00	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:5:PHE:CG	1:A:6:SER:N	2.62	0.62
2:Y:35:VAL:CG1	2:Y:39:ASP:HB3	2.22	0.62
1:A:691:LEU:HD22	1:A:696:VAL:HG21	1.81	0.61
1:A:170:GLN:O	1:A:456:ILE:HA	1.99	0.61
1:A:154:SER:O	1:A:158:ASN:HB2	2.00	0.61
1:A:781:ILE:HG21	3:Z:85:ASP:O	2.01	0.61
1:A:128:ARG:HD2	1:A:128:ARG:N	2.16	0.61
3:Z:142:GLU:O	3:Z:146:LYS:HG2	2.01	0.61
1:A:410:VAL:HG12	1:A:411:THR:N	2.16	0.61
1:A:371:GLN:HG3	1:A:372:ALA:N	2.15	0.61
1:A:577:HIS:ND1	1:A:591:ILE:HG12	2.14	0.61
1:A:286:TYR:HE2	1:A:317:LEU:HD23	1.64	0.61
1:A:690:GLN:O	1:A:694:ASN:HB2	2.01	0.61
1:A:826:TRP:HZ2	2:Y:59:MET:SD	2.24	0.61
1:A:479:TYR:O	1:A:482:GLU:HB3	2.01	0.61
1:A:676:LEU:HD12	1:A:681:LEU:CD2	2.31	0.61
1:A:186:THR:HG23	1:A:458:VAL:CG1	2.31	0.60
1:A:119:PHE:CE1	1:A:696:VAL:HA	2.36	0.60
1:A:830:TYR:C	1:A:830:TYR:HD2	2.05	0.60
1:A:113:TYR:O	1:A:150:PRO:HB2	2.02	0.60
3:Z:111:THR:O	3:Z:116:ARG:HG2	2.02	0.60
1:A:781:ILE:HG21	3:Z:89:ALA:HB2	1.83	0.60
1:A:292:ALA:CB	1:A:325:VAL:HG13	2.29	0.60
2:Y:24:PHE:CG	2:Y:69:PHE:HB2	2.37	0.60
1:A:351:CYS:SG	1:A:617:LEU:HD23	2.41	0.59
1:A:264:THR:HG21	1:A:435:PHE:HE1	1.66	0.59
2:Y:122:LYS:HD2	2:Y:122:LYS:H	1.67	0.59
1:A:784:MET:HE1	3:Z:79:GLU:CB	2.31	0.59
1:A:698:GLU:O	1:A:702:ILE:HG23	2.03	0.59
1:A:399:LEU:C	1:A:401:PRO:HD3	2.23	0.59
1:A:133:THR:O	1:A:137:ILE:HG13	2.03	0.59
1:A:522:LEU:HD13	1:A:580:LEU:HD11	1.85	0.58
1:A:288:ILE:HD12	1:A:300:MET:SD	2.43	0.58
1:A:483:ARG:HB3	1:A:657:MET:HE2	1.85	0.58
1:A:486:GLN:HE22	1:A:517:GLN:HG2	1.67	0.58
1:A:88:MET:HA	1:A:91:MET:HG3	1.85	0.58
1:A:533:LEU:HD11	1:A:594:TRP:HB3	1.85	0.58
1:A:244:GLY:CA	1:A:461:ILE:HG23	2.33	0.58
1:A:239:ASN:CB	7:A:995:ADP:O2A	2.49	0.58
1:A:170:GLN:HB2	1:A:456:ILE:HB	1.86	0.58
1:A:674:ASN:ND2	1:A:681:LEU:HB3	2.18	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:Y:122:LYS:N	2:Y:122:LYS:HD2	2.18	0.58
1:A:696:VAL:HG23	1:A:697:LEU:H	1.67	0.58
3:Z:69:LEU:HB3	3:Z:70:PRO:CD	2.31	0.58
1:A:499:GLU:HG2	1:A:710:ARG:NH1	2.19	0.58
1:A:180:ALA:CA	1:A:672:ILE:HG23	2.33	0.57
1:A:791:GLY:O	1:A:795:ARG:HB2	2.03	0.57
2:Y:144:PHE:O	2:Y:148:ILE:HG12	2.04	0.57
1:A:192:TYR:O	1:A:196:VAL:HG22	2.04	0.57
1:A:262:ILE:HG22	1:A:263:GLU:N	2.19	0.57
1:A:489:ASN:HB3	1:A:512:PHE:CB	2.35	0.57
1:A:511:ASP:OD1	1:A:513:GLY:N	2.36	0.57
1:A:297:ASN:N	1:A:297:ASN:HD22	2.02	0.57
1:A:156:ALA:O	1:A:159:ALA:HB3	2.05	0.57
1:A:267:LEU:HD12	1:A:268:GLU:N	2.18	0.57
1:A:397:ALA:O	1:A:401:PRO:HG3	2.04	0.57
1:A:112:ILE:O	1:A:122:ALA:HA	2.04	0.57
1:A:240:SER:OG	1:A:242:ARG:HD3	2.05	0.57
1:A:830:TYR:HD1	2:Y:76:PHE:HE2	1.53	0.57
3:Z:105:GLU:O	3:Z:108:HIS:HB3	2.05	0.57
1:A:174:ILE:HD13	1:A:668:VAL:HB	1.86	0.57
1:A:724:ALA:N	1:A:725:PRO:HD3	2.20	0.57
1:A:603:ASN:C	1:A:605:ASN:N	2.58	0.57
1:A:272:VAL:HA	1:A:281:ASN:HD21	1.70	0.56
1:A:830:TYR:C	1:A:830:TYR:CD2	2.77	0.56
1:A:128:ARG:HD2	1:A:128:ARG:H	1.71	0.56
1:A:248:ARG:C	1:A:249:ILE:HD12	2.26	0.56
1:A:523:ILE:HD11	1:A:580:LEU:CD2	2.33	0.56
2:Y:63:ALA:HB1	2:Y:66:PRO:O	2.05	0.56
1:A:456:ILE:HG13	1:A:456:ILE:O	2.05	0.56
1:A:264:THR:HG21	1:A:435:PHE:CE1	2.41	0.56
1:A:184:GLU:O	1:A:188:LYS:HD2	2.05	0.56
1:A:60:ILE:N	1:A:60:ILE:HD12	2.20	0.56
1:A:742:ILE:O	1:A:746:LEU:HB2	2.05	0.56
1:A:293:ILE:O	1:A:293:ILE:HG22	2.05	0.56
1:A:151:HIS:ND1	1:A:152:LEU:N	2.53	0.56
1:A:702:ILE:O	1:A:705:LYS:HG2	2.05	0.56
3:Z:12:LYS:HD2	3:Z:16:GLU:OE1	2.06	0.56
3:Z:86:TYR:O	3:Z:89:ALA:HB3	2.05	0.56
1:A:249:ILE:HG22	1:A:251:PHE:CE1	2.40	0.56
1:A:214:SER:O	1:A:217:ASP:HB2	2.03	0.56
1:A:830:TYR:HD1	2:Y:76:PHE:CE2	2.24	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:811:ILE:HD11	2:Y:93:PHE:N	2.21	0.56
1:A:741:LYS:HD3	1:A:741:LYS:O	2.05	0.56
1:A:119:PHE:HE1	1:A:696:VAL:HA	1.69	0.56
1:A:696:VAL:HG23	1:A:697:LEU:N	2.21	0.56
1:A:728:ILE:HG22	1:A:729:PRO:O	2.06	0.55
1:A:390:ASN:HB3	1:A:393:ASP:HB2	1.87	0.55
1:A:227:GLU:O	1:A:231:ASN:HB2	2.06	0.55
1:A:291:ASN:ND2	1:A:304:PRO:HG2	2.18	0.55
1:A:753:TYR:O	1:A:754:ARG:HG3	2.07	0.55
3:Z:31:PHE:O	3:Z:31:PHE:CG	2.59	0.55
1:A:231:ASN:HA	1:A:240:SER:O	2.06	0.55
1:A:593:GLY:O	1:A:596:GLU:HG2	2.07	0.55
1:A:173:LEU:N	1:A:173:LEU:HD12	2.22	0.54
1:A:432:ASP:OD1	1:A:436:ASN:ND2	2.41	0.54
2:Y:55:GLU:HA	2:Y:59:MET:CE	2.38	0.54
3:Z:10:ASP:O	3:Z:13:ASP:HB2	2.07	0.54
2:Y:106:ILE:HG23	2:Y:107:GLU:N	2.23	0.54
2:Y:131:GLU:O	2:Y:131:GLU:HG3	2.07	0.54
1:A:665:PRO:HB3	1:A:667:PHE:CZ	2.42	0.54
3:Z:88:GLU:O	3:Z:92:THR:HG23	2.08	0.54
1:A:15:VAL:HG12	1:A:16:ASP:N	2.23	0.54
1:A:728:ILE:O	1:A:729:PRO:C	2.46	0.54
3:Z:101:ILE:HG22	3:Z:141:TYR:HD1	1.73	0.54
1:A:806:ILE:O	1:A:810:VAL:HG23	2.07	0.54
1:A:79:PRO:HD2	1:A:82:PHE:HD1	1.72	0.54
2:Y:122:LYS:H	2:Y:122:LYS:CD	2.19	0.54
1:A:9:ASP:HB3	1:A:136:VAL:HG22	1.90	0.53
1:A:262:ILE:HG22	1:A:263:GLU:H	1.72	0.53
1:A:829:LEU:HD21	2:Y:40:ILE:HG23	1.90	0.53
1:A:198:CYS:O	1:A:256:LYS:HD2	2.09	0.53
3:Z:120:GLU:O	3:Z:124:GLU:HB2	2.08	0.53
1:A:692:GLN:HA	1:A:697:LEU:HD12	1.90	0.53
1:A:216:GLU:HA	1:A:219:ILE:HD13	1.91	0.53
3:Z:40:LEU:HD12	3:Z:72:TYR:CE1	2.43	0.53
1:A:484:LEU:O	1:A:487:PHE:HB3	2.09	0.53
1:A:614:LYS:O	1:A:616:PRO:HD3	2.08	0.53
1:A:287:GLN:HB3	1:A:328:PHE:CB	2.37	0.53
1:A:599:LYS:O	1:A:601:PRO:HD3	2.08	0.53
2:Y:36:SER:N	2:Y:39:ASP:HB2	2.23	0.53
1:A:707:PHE:CZ	1:A:754:ARG:HD2	2.44	0.53
1:A:505:ILE:CD1	1:A:754:ARG:HB3	2.38	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:741:LYS:HD3	1:A:741:LYS:C	2.29	0.53
1:A:128:ARG:HH21	7:A:995:ADP:H2'	1.74	0.53
1:A:834:LYS:HA	1:A:836:LEU:CD2	2.38	0.53
2:Y:22:GLU:O	2:Y:25:SER:HB2	2.09	0.53
1:A:275:GLN:NE2	1:A:281:ASN:HD22	2.07	0.53
1:A:499:GLU:O	1:A:502:LYS:HB3	2.09	0.53
1:A:736:LYS:O	1:A:740:GLU:N	2.35	0.53
1:A:128:ARG:NH2	7:A:995:ADP:H2'	2.24	0.53
1:A:707:PHE:HE2	1:A:763:LYS:HG2	1.75	0.52
1:A:491:HIS:NE2	1:A:495:LEU:HD11	2.24	0.52
1:A:789:ILE:HG12	3:Z:125:ILE:HD13	1.91	0.52
1:A:291:ASN:HB2	1:A:304:PRO:CB	2.40	0.52
1:A:414:GLN:HE21	1:A:419:VAL:HG22	1.74	0.52
1:A:547:PHE:CZ	1:A:551:LEU:HD11	2.44	0.52
1:A:746:LEU:HD22	1:A:773:MET:HE1	1.92	0.52
1:A:106:ARG:HB3	1:A:111:LEU:HB2	1.90	0.52
2:Y:13:PRO:HB3	2:Y:17:ILE:HD11	1.92	0.52
2:Y:39:ASP:O	2:Y:43:ILE:HG22	2.10	0.52
1:A:723:LEU:HD11	1:A:774:ARG:HA	1.91	0.52
3:Z:42:ILE:HG22	3:Z:44:PRO:CD	2.39	0.51
1:A:721:SER:HA	1:A:742:ILE:HD11	1.92	0.51
1:A:448:THR:N	1:A:452:ARG:HH22	2.00	0.51
1:A:707:PHE:CB	1:A:761:PHE:HB3	2.40	0.51
1:A:481:ASN:HA	1:A:484:LEU:HB2	1.92	0.51
1:A:195:LYS:HG3	1:A:195:LYS:O	2.09	0.51
1:A:490:HIS:O	1:A:493:PHE:HB3	2.10	0.51
1:A:355:ILE:HG22	1:A:355:ILE:O	2.09	0.51
1:A:185:ASN:O	1:A:189:VAL:HG23	2.10	0.51
1:A:363:PHE:CD2	1:A:374:SER:HA	2.43	0.51
1:A:600:ASP:O	1:A:602:ILE:HG12	2.11	0.51
1:A:259:GLY:HA3	1:A:452:ARG:HH12	1.76	0.51
3:Z:30:ALA:C	3:Z:32:LYS:H	2.14	0.51
2:Y:102:LYS:O	2:Y:103:LYS:HG3	2.11	0.51
1:A:134:ASP:O	1:A:137:ILE:HB	2.11	0.51
1:A:475:LEU:HD23	1:A:475:LEU:C	2.30	0.51
1:A:603:ASN:C	1:A:605:ASN:H	2.13	0.50
1:A:591:ILE:HA	1:A:594:TRP:CE2	2.46	0.50
1:A:13:LEU:HD21	1:A:131:ILE:HG23	1.94	0.50
1:A:489:ASN:N	1:A:489:ASN:HD22	2.10	0.50
1:A:500:TYR:HB3	1:A:506:ALA:HA	1.94	0.50
1:A:758:THR:HG23	1:A:759:LYS:CD	2.41	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:4:ASP:HB3	1:A:10:PHE:CE2	2.46	0.50
1:A:100:LEU:O	1:A:100:LEU:HD12	2.12	0.50
1:A:707:PHE:CE2	1:A:763:LYS:HG2	2.47	0.50
1:A:277:SER:O	1:A:278:ALA:HB3	2.12	0.50
3:Z:33:LEU:HA	3:Z:68:PHE:CZ	2.46	0.50
1:A:178:SER:O	1:A:236:ARG:HG2	2.12	0.50
1:A:603:ASN:CB	1:A:606:VAL:HG23	2.42	0.49
3:Z:44:PRO:HB3	3:Z:75:LEU:HD12	1.92	0.49
2:Y:62:GLU:O	2:Y:75:ILE:HG23	2.12	0.49
1:A:227:GLU:CD	1:A:239:ASN:HD21	2.14	0.49
1:A:489:ASN:HB3	1:A:512:PHE:HB2	1.93	0.49
1:A:618:VAL:HA	1:A:621:LEU:HD12	1.94	0.49
1:A:728:ILE:C	1:A:729:PRO:O	2.48	0.49
1:A:54:ASP:O	1:A:70:LYS:HA	2.13	0.49
2:Y:65:GLY:O	2:Y:71:MET:HG2	2.12	0.49
1:A:78:ASN:HD22	1:A:98:SER:HB2	1.76	0.49
1:A:104:ARG:HB3	1:A:682:VAL:HG11	1.95	0.49
1:A:221:GLN:C	1:A:224:PRO:HD2	2.32	0.49
3:Z:131:LEU:HG	3:Z:139:VAL:HG11	1.94	0.49
1:A:657:MET:O	1:A:661:TYR:HD2	1.95	0.49
1:A:503:GLU:O	1:A:505:ILE:HG22	2.12	0.49
1:A:746:LEU:O	1:A:747:GLN:HB2	2.12	0.49
1:A:300:MET:O	1:A:301:LEU:HB2	2.11	0.49
1:A:3:ILE:HG22	1:A:4:ASP:H	1.78	0.49
3:Z:134:ASP:OD1	3:Z:136:GLU:N	2.46	0.49
2:Y:55:GLU:HA	2:Y:59:MET:HE3	1.95	0.49
2:Y:109:ILE:O	2:Y:113:LEU:HG	2.12	0.49
1:A:274:TYR:O	1:A:275:GLN:HG3	2.13	0.48
1:A:699:GLY:O	1:A:703:CYS:HB2	2.13	0.48
1:A:829:LEU:HD11	2:Y:44:SER:HB2	1.95	0.48
1:A:796:LYS:HB2	3:Z:152:PRO:CG	2.42	0.48
3:Z:17:LEU:O	3:Z:20:PHE:HB3	2.14	0.48
1:A:233:LYS:HE3	1:A:316:CYS:SG	2.53	0.48
1:A:134:ASP:HA	1:A:137:ILE:HD12	1.95	0.48
1:A:815:ILE:HG21	2:Y:120:PHE:CE2	2.47	0.48
2:Y:27:ILE:HG23	2:Y:35:VAL:CG2	2.43	0.48
3:Z:43:ASN:N	3:Z:44:PRO:HD3	2.29	0.48
1:A:466:ILE:HG23	1:A:587:VAL:HG13	1.94	0.48
1:A:113:TYR:CD2	1:A:151:HIS:HA	2.49	0.48
2:Y:67:LEU:O	2:Y:67:LEU:HG	2.13	0.48
3:Z:4:SER:O	3:Z:8:ILE:HG13	2.13	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:Z:107:ARG:NH1	3:Z:107:ARG:HB2	2.28	0.48
1:A:410:VAL:CG1	1:A:411:THR:N	2.77	0.48
1:A:244:GLY:HA3	1:A:265:TYR:HB2	1.96	0.48
1:A:453:ASN:HB3	1:A:454:TYR:CD1	2.49	0.48
1:A:671:ILE:HG23	1:A:690:GLN:CD	2.34	0.48
1:A:489:ASN:HB3	1:A:512:PHE:HB3	1.96	0.48
1:A:648:VAL:HG12	1:A:649:HIS:N	2.29	0.48
1:A:780:LYS:HE2	1:A:784:MET:CE	2.44	0.47
1:A:182:LYS:HE3	1:A:462:ALA:HA	1.96	0.47
1:A:773:MET:HE3	1:A:773:MET:HB3	1.79	0.47
1:A:78:ASN:ND2	1:A:98:SER:HB2	2.29	0.47
1:A:180:ALA:HA	1:A:672:ILE:CG2	2.41	0.47
1:A:811:ILE:HD11	2:Y:92:ALA:C	2.35	0.47
1:A:228:ALA:O	1:A:284:ILE:HB	2.13	0.47
1:A:43:PHE:CD1	1:A:97:ALA:HB2	2.49	0.47
1:A:261:ASP:C	1:A:261:ASP:OD1	2.53	0.47
1:A:284:ILE:HG23	1:A:285:PHE:N	2.29	0.47
1:A:411:THR:O	1:A:411:THR:HG22	2.15	0.47
1:A:415:ASN:OD1	1:A:418:GLN:HG3	2.15	0.47
1:A:237:ASN:OD1	1:A:238:ASN:N	2.47	0.47
3:Z:70:PRO:O	3:Z:73:GLU:HG3	2.14	0.47
1:A:275:GLN:OE1	1:A:312:ILE:HA	2.14	0.47
3:Z:100:PHE:HA	3:Z:139:VAL:O	2.14	0.47
3:Z:106:LEU:HD11	3:Z:110:LEU:HD11	1.95	0.47
1:A:787:ALA:HB1	3:Z:44:PRO:O	2.14	0.47
1:A:672:ILE:N	1:A:672:ILE:HD13	2.28	0.47
1:A:141:ARG:HD2	1:A:196:VAL:HG12	1.97	0.47
1:A:125:PRO:O	1:A:126:TYR:HB2	2.14	0.47
1:A:736:LYS:O	1:A:740:GLU:HB2	2.15	0.47
1:A:371:GLN:HE22	1:A:414:GLN:N	2.12	0.47
1:A:790:ARG:O	1:A:794:ILE:HG12	2.14	0.47
1:A:567:LYS:HB3	1:A:568:PRO:CD	2.39	0.46
1:A:361:MET:CE	1:A:380:ALA:HA	2.45	0.46
1:A:438:LEU:O	1:A:438:LEU:HD23	2.16	0.46
1:A:360:GLU:O	1:A:379:GLU:HG3	2.15	0.46
1:A:816:ARG:O	1:A:820:VAL:HG23	2.15	0.46
3:Z:45:ARG:O	3:Z:48:ASP:HB2	2.15	0.46
1:A:245:LYS:HE3	1:A:247:ILE:HB	1.98	0.46
3:Z:11:LEU:HD23	3:Z:69:LEU:HD13	1.98	0.46
1:A:467:PHE:C	1:A:470:ASN:HD21	2.19	0.46
1:A:177:GLU:HB2	1:A:672:ILE:CD1	2.45	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:36:VAL:O	1:A:43:PHE:HA	2.16	0.46
1:A:552:TYR:HA	1:A:556:MET:HB2	1.97	0.46
1:A:323:ASP:O	1:A:325:VAL:N	2.48	0.46
1:A:790:ARG:NH1	3:Z:46:ASN:OD1	2.48	0.46
2:Y:102:LYS:HA	2:Y:141:TYR:OH	2.16	0.46
1:A:822:ARG:CB	1:A:822:ARG:NH1	2.63	0.46
1:A:12:TYR:HB2	1:A:131:ILE:CD1	2.45	0.46
1:A:361:MET:CE	1:A:383:VAL:HG21	2.46	0.46
1:A:403:VAL:CG1	1:A:404:LYS:N	2.79	0.46
1:A:782:ILE:O	1:A:786:GLN:HG3	2.16	0.46
3:Z:108:HIS:O	3:Z:112:ALA:HB3	2.16	0.46
1:A:266:LEU:HG	1:A:649:HIS:CE1	2.51	0.46
1:A:449:LYS:HA	1:A:449:LYS:HD2	1.53	0.46
1:A:414:GLN:HB2	1:A:418:GLN:CB	2.44	0.45
1:A:95:ASN:ND2	1:A:98:SER:H	2.14	0.45
1:A:358:MET:HA	1:A:361:MET:HE3	1.99	0.45
3:Z:35:ASP:HA	3:Z:38:ARG:HH11	1.80	0.45
1:A:308:LEU:O	1:A:308:LEU:HD12	2.16	0.45
1:A:784:MET:CE	3:Z:79:GLU:HB3	2.41	0.45
1:A:275:GLN:HB2	1:A:314:GLN:HB2	1.98	0.45
1:A:653:LEU:CD2	1:A:657:MET:HG2	2.46	0.45
1:A:653:LEU:HD23	1:A:653:LEU:O	2.17	0.45
1:A:815:ILE:HD11	2:Y:144:PHE:CE1	2.51	0.45
1:A:505:ILE:HG23	1:A:505:ILE:O	2.16	0.45
1:A:822:ARG:CG	1:A:822:ARG:NH1	2.74	0.45
1:A:179:GLY:HA2	4:A:996:SO4:O4	2.16	0.45
1:A:377:THR:HG22	1:A:381:GLU:CG	2.46	0.45
1:A:393:ASP:HB3	1:A:609:LEU:HD13	1.97	0.45
1:A:507:TRP:CH2	1:A:706:GLY:HA2	2.52	0.45
1:A:85:LEU:N	1:A:102:ASN:HD21	2.15	0.45
1:A:548:GLN:HG3	1:A:552:TYR:HE1	1.82	0.45
2:Y:24:PHE:CD2	2:Y:69:PHE:HB2	2.52	0.45
2:Y:93:PHE:HB3	2:Y:141:TYR:CD2	2.51	0.45
1:A:811:ILE:HG23	2:Y:93:PHE:CZ	2.51	0.45
1:A:487:PHE:CZ	1:A:665:PRO:HG3	2.52	0.45
1:A:544:ASP:N	1:A:544:ASP:OD1	2.42	0.45
1:A:371:GLN:HE21	1:A:371:GLN:HB2	1.66	0.45
1:A:15:VAL:CG1	1:A:16:ASP:N	2.80	0.45
2:Y:90:ARG:CG	2:Y:90:ARG:O	2.65	0.45
1:A:309:TYR:CD2	1:A:356:LEU:HB3	2.52	0.45
1:A:84:LYS:HA	1:A:106:ARG:HG3	1.99	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:795:ARG:HD3	3:Z:38:ARG:O	2.16	0.44
1:A:273:THR:HG22	1:A:311:PHE:CE1	2.52	0.44
1:A:355:ILE:HG23	1:A:427:ALA:HB1	1.99	0.44
1:A:245:LYS:HE2	1:A:247:ILE:CG2	2.48	0.44
1:A:706:GLY:C	1:A:708:PRO:HD3	2.38	0.44
1:A:663:THR:O	1:A:665:PRO:HD3	2.17	0.44
1:A:752:GLU:HG3	1:A:766:VAL:HG21	1.98	0.44
1:A:560:ARG:HE	1:A:560:ARG:HB2	1.66	0.44
1:A:131:ILE:O	1:A:136:VAL:HG11	2.17	0.44
3:Z:131:LEU:HG	3:Z:139:VAL:CG1	2.47	0.44
1:A:828:LYS:NZ	1:A:828:LYS:HB2	2.33	0.44
1:A:76:SER:HB3	1:A:93:TYR:CG	2.51	0.44
3:Z:4:SER:C	3:Z:6:ASP:N	2.71	0.44
2:Y:93:PHE:CG	2:Y:141:TYR:HB2	2.53	0.44
2:Y:117:GLY:HA2	3:Z:20:PHE:CE1	2.53	0.44
3:Z:106:LEU:O	3:Z:110:LEU:HG	2.17	0.44
1:A:825:GLN:HA	1:A:825:GLN:OE1	2.16	0.44
3:Z:4:SER:OG	3:Z:6:ASP:HB3	2.17	0.44
1:A:75:GLN:OE1	1:A:95:ASN:ND2	2.51	0.44
1:A:811:ILE:HD12	2:Y:93:PHE:CD1	2.53	0.44
1:A:763:LYS:O	1:A:766:VAL:HG23	2.17	0.43
1:A:470:ASN:OD1	1:A:587:VAL:HG13	2.18	0.43
3:Z:107:ARG:HH11	3:Z:107:ARG:HB2	1.83	0.43
1:A:760:VAL:HG13	1:A:760:VAL:O	2.18	0.43
1:A:468:ASP:HB3	1:A:573:GLN:CA	2.38	0.43
1:A:377:THR:HG22	1:A:381:GLU:HG3	2.00	0.43
1:A:827:TRP:O	1:A:831:SER:N	2.42	0.43
1:A:491:HIS:CD2	1:A:495:LEU:HD11	2.52	0.43
1:A:251:PHE:HA	1:A:258:ALA:H	1.83	0.43
1:A:250:HIS:CB	1:A:452:ARG:HD3	2.48	0.43
3:Z:31:PHE:CE2	3:Z:58:MET:HG2	2.53	0.43
1:A:500:TYR:HB3	1:A:505:ILE:O	2.18	0.43
1:A:586:ASN:ND2	1:A:586:ASN:N	2.64	0.43
1:A:148:ILE:CG1	1:A:149:PRO:HD2	2.27	0.43
1:A:594:TRP:CD1	1:A:594:TRP:N	2.87	0.43
1:A:676:LEU:C	1:A:678:GLN:N	2.72	0.43
1:A:129:LEU:HA	1:A:130:PRO:HD3	1.78	0.43
1:A:746:LEU:HD21	1:A:773:MET:CE	2.48	0.43
1:A:293:ILE:HD11	1:A:329:LYS:HG2	2.01	0.43
1:A:401:PRO:CG	1:A:603:ASN:HD21	2.23	0.43
2:Y:76:PHE:C	2:Y:78:ASP:H	2.22	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:493:PHE:CD1	1:A:511:ASP:HA	2.53	0.43
1:A:287:GLN:HE21	1:A:327:GLU:HB3	1.84	0.43
1:A:415:ASN:ND2	1:A:418:GLN:HE21	2.17	0.43
1:A:690:GLN:C	1:A:694:ASN:HB2	2.39	0.43
1:A:824:TRP:CE2	1:A:826:TRP:HD1	2.37	0.43
1:A:722:ILE:HD11	3:Z:88:GLU:O	2.18	0.43
3:Z:33:LEU:HA	3:Z:68:PHE:HZ	1.81	0.43
1:A:743:LEU:O	1:A:748:MET:HB2	2.18	0.43
1:A:417:ASN:O	1:A:421:ASN:HB2	2.19	0.43
1:A:814:ASN:ND2	2:Y:89:ILE:HG12	2.34	0.43
1:A:580:LEU:HD12	1:A:580:LEU:HA	1.86	0.42
1:A:126:TYR:CE1	1:A:677:LYS:HA	2.54	0.42
1:A:416:MET:O	1:A:420:VAL:HG13	2.19	0.42
1:A:826:TRP:CZ2	2:Y:59:MET:SD	3.08	0.42
1:A:777:ARG:HD2	1:A:777:ARG:HA	1.88	0.42
1:A:691:LEU:CD2	1:A:696:VAL:HG21	2.47	0.42
3:Z:126:ILE:HG23	3:Z:131:LEU:HB3	2.01	0.42
1:A:766:VAL:C	1:A:768:GLY:N	2.73	0.42
2:Y:19:GLU:HA	2:Y:22:GLU:HB2	2.01	0.42
1:A:720:TYR:O	1:A:742:ILE:HD13	2.20	0.42
1:A:676:LEU:C	1:A:678:GLN:H	2.22	0.42
1:A:516:LEU:HD22	1:A:516:LEU:HA	1.91	0.42
3:Z:101:ILE:HG22	3:Z:141:TYR:CD1	2.54	0.42
1:A:471:SER:OG	1:A:472:PHE:N	2.51	0.42
2:Y:140:ASP:OD1	2:Y:142:VAL:N	2.53	0.42
1:A:225:VAL:HG23	1:A:226:LEU:N	2.33	0.42
3:Z:94:ASP:OD2	3:Z:97:GLY:HA2	2.20	0.42
1:A:752:GLU:HG3	1:A:766:VAL:CG2	2.50	0.42
1:A:398:LEU:HD21	1:A:423:VAL:CG2	2.48	0.42
1:A:16:ASP:HB3	1:A:19:LYS:CB	2.49	0.42
3:Z:44:PRO:CG	3:Z:75:LEU:HD12	2.49	0.42
1:A:402:LYS:CB	1:A:605:ASN:ND2	2.82	0.42
2:Y:67:LEU:HA	2:Y:71:MET:HB3	2.01	0.42
1:A:297:ASN:ND2	1:A:297:ASN:N	2.68	0.42
1:A:828:LYS:O	1:A:832:LYS:HG3	2.19	0.42
1:A:227:GLU:HG2	1:A:231:ASN:ND2	2.35	0.42
1:A:246:PHE:HB3	1:A:263:GLU:HB2	2.02	0.42
1:A:811:ILE:H	1:A:811:ILE:HG12	1.62	0.42
2:Y:103:LYS:N	2:Y:141:TYR:HE1	2.18	0.42
1:A:483:ARG:HB3	1:A:657:MET:CE	2.50	0.42
1:A:794:ILE:HD12	3:Z:35:ASP:OD2	2.20	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:712:ILE:HA	1:A:759:LYS:CB	2.50	0.42
1:A:768:GLY:O	1:A:771:GLU:HB2	2.19	0.41
1:A:587:VAL:HA	1:A:588:PRO:HD3	1.80	0.41
1:A:712:ILE:O	1:A:714:SER:N	2.53	0.41
1:A:496:GLU:OE1	1:A:496:GLU:HA	2.20	0.41
1:A:177:GLU:HB2	1:A:672:ILE:HD11	2.02	0.41
1:A:283:HIS:O	1:A:287:GLN:HG3	2.20	0.41
1:A:786:GLN:HE21	3:Z:110:LEU:HA	1.85	0.41
1:A:179:GLY:CA	4:A:996:SO4:O4	2.68	0.41
1:A:157:ASP:HB2	1:A:192:TYR:CZ	2.53	0.41
3:Z:3:LEU:CD2	3:Z:7:GLU:HG2	2.50	0.41
3:Z:4:SER:C	3:Z:6:ASP:H	2.24	0.41
3:Z:57:LYS:HG2	3:Z:58:MET:N	2.36	0.41
1:A:234:THR:O	1:A:236:ARG:N	2.52	0.41
1:A:656:LEU:O	1:A:659:ASN:N	2.49	0.41
3:Z:93:PHE:CE2	3:Z:109:VAL:HG22	2.55	0.41
1:A:434:MET:O	1:A:437:TRP:HB3	2.20	0.41
2:Y:35:VAL:HG11	2:Y:40:ILE:HG13	2.02	0.41
2:Y:21:LYS:HB2	2:Y:69:PHE:CE1	2.55	0.41
1:A:821:LEU:HD11	1:A:827:TRP:CE3	2.56	0.41
1:A:401:PRO:O	1:A:411:THR:HA	2.20	0.41
1:A:131:ILE:HG22	1:A:151:HIS:HE2	1.86	0.41
1:A:728:ILE:O	1:A:729:PRO:O	2.39	0.41
1:A:486:GLN:HA	1:A:516:LEU:HD12	2.02	0.41
1:A:367:PRO:HB2	1:A:369:GLU:HG2	2.03	0.41
1:A:767:LEU:O	1:A:771:GLU:HG2	2.20	0.41
1:A:400:LYS:N	1:A:401:PRO:HD3	2.36	0.41
1:A:287:GLN:HB3	1:A:328:PHE:CG	2.56	0.41
1:A:598:ASN:ND2	1:A:644:THR:OG1	2.54	0.41
2:Y:36:SER:C	2:Y:38:GLU:H	2.24	0.41
1:A:771:GLU:O	1:A:774:ARG:HB3	2.19	0.41
1:A:250:HIS:O	1:A:258:ALA:N	2.49	0.41
1:A:796:LYS:HB2	3:Z:152:PRO:HG2	2.02	0.41
1:A:153:PHE:HB3	1:A:192:TYR:CE2	2.56	0.41
2:Y:90:ARG:HG2	2:Y:90:ARG:O	2.20	0.41
1:A:369:GLU:HG2	1:A:369:GLU:H	1.68	0.41
1:A:780:LYS:HG2	1:A:784:MET:CE	2.51	0.41
2:Y:22:GLU:C	2:Y:24:PHE:H	2.24	0.41
1:A:327:GLU:HA	1:A:327:GLU:OE1	2.21	0.41
2:Y:93:PHE:HD1	2:Y:104:LEU:HD11	1.86	0.41
3:Z:134:ASP:OD1	3:Z:134:ASP:C	2.59	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:32:LYS:O	1:A:47:GLU:HA	2.21	0.41
1:A:175:THR:OG1	1:A:669:ARG:HD3	2.21	0.41
1:A:121:ILE:H	1:A:121:ILE:HG13	1.56	0.41
2:Y:27:ILE:HD12	2:Y:27:ILE:HA	1.91	0.40
2:Y:35:VAL:HG12	2:Y:35:VAL:O	2.20	0.40
1:A:12:TYR:HE2	1:A:127:ARG:NH2	2.19	0.40
2:Y:75:ILE:O	2:Y:75:ILE:CG2	2.67	0.40
3:Z:101:ILE:HD11	3:Z:105:GLU:CG	2.51	0.40
1:A:333:GLU:O	1:A:337:ILE:HG13	2.21	0.40
1:A:530:LEU:O	1:A:534:GLU:HG3	2.21	0.40
1:A:707:PHE:CE2	1:A:763:LYS:HE2	2.56	0.40
1:A:708:PRO:HB2	1:A:709:SER:H	1.72	0.40
1:A:689:HIS:O	1:A:692:GLN:HB3	2.21	0.40
1:A:793:LEU:O	1:A:794:ILE:C	2.59	0.40
3:Z:3:LEU:HD22	3:Z:7:GLU:HG2	2.04	0.40
3:Z:118:SER:O	3:Z:121:ASP:N	2.53	0.40
3:Z:143:ASP:O	3:Z:147:LYS:HG2	2.22	0.40
1:A:464:PHE:HE2	1:A:466:ILE:HG12	1.86	0.40
1:A:78:ASN:HA	1:A:79:PRO:HD3	1.95	0.40
2:Y:142:VAL:O	2:Y:145:THR:HB	2.21	0.40
1:A:286:TYR:OH	1:A:312:ILE:HB	2.21	0.40
1:A:88:MET:HG2	1:A:102:ASN:OD1	2.21	0.40
1:A:242:ARG:HD2	1:A:242:ARG:HA	1.72	0.40
1:A:505:ILE:HD11	1:A:754:ARG:HB3	2.02	0.40
1:A:824:TRP:HE3	1:A:827:TRP:HB2	1.87	0.40
2:Y:55:GLU:HA	2:Y:59:MET:HE2	2.03	0.40
1:A:337:ILE:HG22	1:A:337:ILE:O	2.20	0.40
1:A:30:GLY:HA3	1:A:772:GLU:OE2	2.21	0.40

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	794/840 (94%)	660 (83%)	113 (14%)	21 (3%)	7	32
2	Y	140/156 (90%)	111 (79%)	25 (18%)	4 (3%)	6	29
3	Z	153/156 (98%)	136 (89%)	11 (7%)	6 (4%)	4	22
All	All	1087/1152 (94%)	907 (83%)	149 (14%)	31 (3%)	6	29

All (31) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	304	PRO
1	A	625	PRO
1	A	708	PRO
1	A	713	TYR
1	A	834	LYS
2	Y	66	PRO
1	A	65	SER
1	A	235	THR
1	A	324	ASP
1	A	367	PRO
1	A	510	ILE
1	A	528	GLY
1	A	568	PRO
1	A	833	VAL
2	Y	85	SER
3	Z	25	ASP
3	Z	96	GLU
3	Z	116	ARG
3	Z	154	PRO
1	A	266	LEU
1	A	540	PRO
2	Y	119	ASN
3	Z	31	PHE
1	A	116	SER
1	A	793	LEU
1	A	504	GLY
2	Y	64	PRO
3	Z	21	TRP
1	A	366	ARG
1	A	731	GLY
1	A	794	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	666/732 (91%)	572 (86%)	94 (14%)	4	18
2	Y	108/133 (81%)	80 (74%)	28 (26%)	0	2
3	Z	126/132 (96%)	110 (87%)	16 (13%)	5	22
All	All	900/997 (90%)	762 (85%)	138 (15%)	3	14

All (138) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	4	ASP
1	A	5	PHE
1	A	6	SER
1	A	8	PRO
1	A	51	SER
1	A	54	ASP
1	A	57	THR
1	A	67	ARG
1	A	94	LEU
1	A	95	ASN
1	A	102	ASN
1	A	104	ARG
1	A	114	THR
1	A	128	ARG
1	A	131	ILE
1	A	139	LYS
1	A	141	ARG
1	A	158	ASN
1	A	162	ASN
1	A	188	LYS
1	A	195	LYS
1	A	214	SER
1	A	233	LYS
1	A	270	SER
1	A	294	PRO
1	A	304	PRO

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Mol	Chain	Res	Type
1	A	306	SER
1	A	308	LEU
1	A	314	GLN
1	A	326	GLU
1	A	327	GLU
1	A	341	THR
1	A	362	LYS
1	A	367	PRO
1	A	371	GLN
1	A	398	LEU
1	A	401	PRO
1	A	403	VAL
1	A	415	ASN
1	A	421	ASN
1	A	444	LYS
1	A	448	THR
1	A	449	LYS
1	A	452	ARG
1	A	456	ILE
1	A	461	ILE
1	A	470	ASN
1	A	476	CYS
1	A	492	MET
1	A	501	LYS
1	A	505	ILE
1	A	507	TRP
1	A	514	MET
1	A	516	LEU
1	A	526	PRO
1	A	531	SER
1	A	544	ASP
1	A	560	ARG
1	A	565	PRO
1	A	568	PRO
1	A	571	PRO
1	A	575	PRO
1	A	586	ASN
1	A	600	ASP
1	A	601	PRO
1	A	603	ASN
1	A	616	PRO
1	A	623	LYS

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Mol	Chain	Res	Type
1	A	644	THR
1	A	672	ILE
1	A	678	GLN
1	A	693	CYS
1	A	701	ARG
1	A	702	ILE
1	A	709	SER
1	A	712	ILE
1	A	718	GLN
1	A	721	SER
1	A	729	PRO
1	A	730	GLN
1	A	732	PHE
1	A	734	ASP
1	A	740	GLU
1	A	741	LYS
1	A	750	PRO
1	A	752	GLU
1	A	759	LYS
1	A	773	MET
1	A	782	ILE
1	A	815	ILE
1	A	822	ARG
1	A	830	TYR
1	A	835	PRO
1	A	836	LEU
2	Y	16	GLN
2	Y	20	MET
2	Y	22	GLU
2	Y	25	SER
2	Y	26	MET
2	Y	27	ILE
2	Y	29	VAL
2	Y	31	ARG
2	Y	36	SER
2	Y	43	ILE
2	Y	46	GLN
2	Y	51	PRO
2	Y	52	ASP
2	Y	53	ASP
2	Y	57	THR
2	Y	59	MET

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Mol	Chain	Res	Type
2	Y	64	PRO
2	Y	66	PRO
2	Y	67	LEU
2	Y	68	ASN
2	Y	69	PHE
2	Y	74	SER
2	Y	77	SER
2	Y	90	ARG
2	Y	119	ASN
2	Y	122	LYS
2	Y	145	THR
2	Y	151	SER
3	Z	10	ASP
3	Z	58	MET
3	Z	62	SER
3	Z	64	PRO
3	Z	67	GLU
3	Z	68	PHE
3	Z	70	PRO
3	Z	77	ASP
3	Z	79	GLU
3	Z	80	GLN
3	Z	101	ILE
3	Z	107	ARG
3	Z	124	GLU
3	Z	127	LYS
3	Z	139	VAL
3	Z	146	LYS

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (30) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	33	ASN
1	A	95	ASN
1	A	158	ASN
1	A	291	ASN
1	A	297	ASN
1	A	371	GLN
1	A	414	GLN
1	A	418	GLN
1	A	436	ASN
1	A	453	ASN

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Mol	Chain	Res	Type
1	A	470	ASN
1	A	481	ASN
1	A	485	GLN
1	A	486	GLN
1	A	489	ASN
1	A	491	HIS
1	A	497	GLN
1	A	586	ASN
1	A	598	ASN
1	A	603	ASN
1	A	649	HIS
1	A	659	ASN
1	A	694	ASN
1	A	718	GLN
1	A	769	ASN
1	A	814	ASN
2	Y	16	GLN
2	Y	46	GLN
2	Y	91	ASN
3	Z	5	GLN

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 carbohydrates in this entry.

5.6 Ligand geometry ⓘ

Of 4 ligands modelled in this entry, 2 are monoatomic - leaving 2 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	$\# Z > 2$
7	ADP	A	995	-	22,29,29	1.50	4 (18%)	27,45,45	2.83	3 (11%)
4	SO4	A	996	-	4,4,4	0.16	0	6,6,6	0.10	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
7	ADP	A	995	-	-	0/12/32/32	0/3/3/3
4	SO4	A	996	-	-	0/0/0/0	0/0/0/0

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
7	A	995	ADP	C5-N7	-2.51	1.30	1.39
7	A	995	ADP	C4-N3	2.10	1.38	1.35
7	A	995	ADP	C2-N3	2.87	1.37	1.32
7	A	995	ADP	O4'-C1'	3.56	1.45	1.41

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
7	A	995	ADP	N3-C2-N1	-13.59	118.48	128.89
7	A	995	ADP	C4-C5-N7	-2.08	107.57	109.48
7	A	995	ADP	O3A-PA-O5'	2.02	108.29	102.94

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

2 monomers are involved in 8 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
7	A	995	ADP	5	0
4	A	996	SO4	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 [i](#)

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

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

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	A	802/840 (95%)	-0.39	4 (0%) 91 83	33, 72, 134, 176	0
2	Y	142/156 (91%)	0.11	13 (9%) 11 4	34, 126, 187, 201	0
3	Z	155/156 (99%)	-0.51	0 100 100	31, 67, 104, 126	0
All	All	1099/1152 (95%)	-0.34	17 (1%) 76 58	31, 72, 161, 201	0

All (17) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	Y	72	PHE	4.3
1	A	406	GLY	3.7
2	Y	68	ASN	3.6
1	A	367	PRO	3.1
2	Y	46	GLN	2.8
2	Y	153	GLU	2.8
2	Y	66	PRO	2.7
2	Y	36	SER	2.5
2	Y	62	GLU	2.5
2	Y	33	GLY	2.4
1	A	407	THR	2.4
2	Y	58	ALA	2.3
2	Y	40	ILE	2.1
2	Y	67	LEU	2.1
2	Y	65	GLY	2.0
2	Y	76	PHE	2.0
1	A	55	GLU	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(\AA^2)	Q<0.9
5	CA	Z	998	1/1	0.97	0.24	3.89	75,75,75,75	0
4	SO4	A	996	5/5	0.97	0.26	2.43	54,73,84,84	0
7	ADP	A	995	27/27	0.89	0.20	0.28	53,79,92,102	0
6	MG	Y	999	1/1	0.88	0.19	-1.22	137,137,137,137	0

6.5 Other polymers [i](#)

There are no such residues in this entry.