

# Full wwPDB X-ray Structure Validation Report (i)

#### Aug 14, 2023 – 09:35 PM EDT

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 https://www.wwpdb.org/validation/2017/XrayValidationReportHelp with specific help available everywhere you see the (i) 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 (1)) were used in the production of this report:

MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
$\mathrm{EDS}$	:	2.35
buster-report	:	1.1.7(2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.35

# 1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:  $X\text{-}RAY \, DIFFRACTION$ 

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	$\begin{array}{c} {\rm Whole \ archive} \\ (\#{\rm Entries}) \end{array}$	${f Similar\ resolution}\ (\#{ m Entries,\ resolution\ range}({ m \AA}))$		
R <sub>free</sub>	130704	1094 (3.10-3.10)		
Clashscore	141614	1184 (3.10-3.10)		
Ramachandran outliers	138981	1141 (3.10-3.10)		
Sidechain outliers	138945	1141 (3.10-3.10)		
RSRZ outliers	127900	1067 (3.10-3.10)		

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 <=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	А	840	40%	47%	8% 5%			
2	Y	156	47%	33%	10% • 9%			
3	Z	156	47%	45%	8% •			

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	А	996	-	-	Х	-



# 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	
1	А	802	Total 6301	C 4020	N 1075	0 1168	S 38	0	0	0

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

Mol	Chain	Residues	Atoms			ZeroOcc	AltConf	Trace		
2	Y	142	Total 1064	$\begin{array}{c} \mathrm{C} \\ 665 \end{array}$	N 173	0 217	S 9	0	0	0

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

Mol	Chain	Residues		At	$\mathbf{oms}$			ZeroOcc	AltConf	Trace
3	Ζ	155	Total 1207	$\begin{array}{c} \mathrm{C} \\ 767 \end{array}$	N 190	0 243	${f S} {f 7}$	0	0	0

• Molecule 4 is SULFATE ION (three-letter code: SO4) (formula:  $O_4S$ ).





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

• Molecule 5 is ADENOSINE-5'-DIPHOSPHATE (three-letter code: ADP) (formula:  $C_{10}H_{15}N_5O_{10}P_2$ ).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf		
5	А	1	Total 27	C 10	N 5	O 10	Р 2	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 CALCIUM ION (three-letter code: CA) (formula: Ca).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
7	Ζ	1	Total Ca 1 1	0	0

• Molecule 8 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
8	А	1	Total O 1 1	0	0



# 3 Residue-property plots (i)

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: Myosin heavy chain, striated muscle







## 4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants	84.05Å 50.94Å 161.59Å	Depositor
a, b, c, $\alpha$ , $\beta$ , $\gamma$	$90.00^{\circ}$ $98.36^{\circ}$ $90.00^{\circ}$	Depositor
Bosolution(Å)	43.44 - 3.10	Depositor
Resolution (A)	43.43 - 3.04	EDS
% Data completeness	84.6 (43.44-3.10)	Depositor
(in resolution range)	81.5(43.43-3.04)	EDS
R <sub>merge</sub>	(Not available)	Depositor
$R_{sym}$	0.07	Depositor
$< I/\sigma(I) > 1$	$2.30 (at 3.06 \text{\AA})$	Xtriage
Refinement program	CNS 1.0	Depositor
P. P.	0.233 , $0.269$	Depositor
II, II, <i>free</i>	0.217 , $0.240$	DCC
$R_{free}$ test set	1310 reflections $(5.88\%)$	wwPDB-VP
Wilson B-factor $(Å^2)$	79.7	Xtriage
Anisotropy	0.414	Xtriage
Bulk solvent $k_{sol}(e/A^3), B_{sol}(A^2)$	0.28 , 74.9	EDS
L-test for $twinning^2$	$ < L >=0.47, < L^2>=0.30$	Xtriage
Estimated twinning fraction	No twinning to report.	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.

<sup>&</sup>lt;sup>2</sup>Theoretical 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.



<sup>&</sup>lt;sup>1</sup>Intensities estimated from amplitudes.

# 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: SO4, ADP, MG, CA

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).

Mal	Chain	Bond	lengths	Bo	ond angles
WIOI	Unam	RMSZ	# Z  > 5	RMSZ	# Z  > 5
1	А	0.31	0/6431	0.67	2/8689~(0.0%)
2	Y	0.32	0/1079	0.77	1/1448~(0.1%)
3	Ζ	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	$Observed(^{o})$	$Ideal(^{o})$
1	А	566	GLY	N-CA-C	-7.17	95.17	113.10
1	А	834	LYS	N-CA-C	6.95	129.77	111.00
2	Υ	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	А	6301	0	6170	438	0
2	Y	1064	0	990	68	0
3	Ζ	1207	0	1127	76	0
4	А	5	0	0	3	0
5	А	27	0	12	5	0



Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes	
6	Y	1	0	0	0	0	
7	Ζ	1	0	0	0	0	
8	А	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	Clash
Atom-1	Atom-2	distance (Å)	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:HG3	1:A:128:ARG:NH1	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
1:A:796:LYS:HD3	3:Z:152:PRO:HB3	1.58	0.84
3:Z:69:LEU:HB3	3:Z:70:PRO:HD3	1.59	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	5: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:401:PRO:HG3	1:A:603:ASN:HD21	1.46	0.80
1:A:522:LEU:HD11	1:A:562:PHE:HB2	1.64	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:180:ALA:HA	1:A:672:ILE:HG23	1.64	0.79



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Atom-1	Atom-2	distance (Å)	overlap (Å)
1:A:567:LYS:HB3	1:A:568:PRO:HD2	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:HG12	1:A:833:VAL:O	1.90	0.71
1:A:459:LEU:HD11	1:A:461:ILE:HD11	1.73	0.70
1:A:603:ASN:HD22	1:A:605:ASN:HB3	1.56	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:70:LYS:O	1:A:73:ASP:HB2	1.91	0.70
1:A:746:LEU:CD2	1:A:773:MET:HE1	2.21	0.70
1:A:414:GLN:HB2	1:A:418:GLN:HB2	1.74	0.69
1:A:672:ILE:H	1:A:672:ILE:HD13	1.56	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	5: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:221:GLN:O	1:A:224:PRO:HD2	1.93	0.68
1:A:244:GLY:HA3	1:A:461:ILE:HG23	1.76	0.68



	louo pugom	Interatomic	Clash
Atom-1	Atom-2	distance (Å)	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:363:PHE:HD2	1:A:374:SER:HA	1.60	0.67
1:A:694:ASN:ND2	1:A:696:VAL:HG13	2.10	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:HH11	1:A:822:ARG:CG	2.08	0.66
2:Y:18:GLN:O	2:Y:21:LYS:HB3	1.96	0.66
3:Z:42:ILE:C	3:Z:44:PRO:HD3	2.17	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:N	1:A:586:ASN:HD22	1.95	0.64
1:A:470:ASN:N	1:A:470:ASN:ND2	2.39	0.63
1:A:746:LEU:HD21	1:A:773:MET:HE1	1.79	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: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: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: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:5:PHE:CG	1:A:6:SER:N	2.62	0.62



	louo pugom	Interatomic	Clash
Atom-1	Atom-2	distance (Å)	overlap (Å)
1:A:568:PRO:HA	1:A:573:GLN:OE1	2.00	0.62
2:Y:35:VAL:CG1	2:Y:39:ASP:HB3	2.22	0.62
1:A:170:GLN:O	1:A:456:ILE:HA	1.99	0.61
1:A:691:LEU:HD22	1:A:696:VAL:HG21	1.81	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:286:TYR:HE2	1:A:317:LEU:HD23	1.64	0.61
1:A:371:GLN:HG3	1:A:372:ALA:N	2.15	0.61
1:A:410:VAL:HG12	1:A:411:THR:N	2.16	0.61
1:A:577:HIS:ND1	1:A:591:ILE:HG12	2.14	0.61
1:A:690:GLN:O	1:A:694:ASN:HB2	2.01	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:826:TRP:HZ2	2:Y:59:MET:SD	2.24	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:HD2	1:A:830:TYR:C	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:264:THR:HG21	1:A:435:PHE:HE1	1.66	0.59
1:A:351:CYS:SG	1:A:617:LEU:HD23	2.41	0.59
2:Y:122:LYS:H	2:Y:122:LYS:HD2	1.67	0.59
1:A:698:GLU:O	1:A:702:ILE:HG23	2.03	0.59
1:A:784:MET:HE1	3:Z:79:GLU:CB	2.31	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:288:ILE:HD12	1:A:300:MET:SD	2.43	0.58
1:A:522:LEU:HD13	1:A:580:LEU:HD11	1.85	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:170:GLN:HB2	1:A:456:ILE:HB	1.86	0.58
1:A:239:ASN:CB	5:A:995:ADP:O2A	2.49	0.58
1:A:674:ASN:ND2	1:A:681:LEU:HB3	2.18	0.58



		Interatomic	Clash
Atom-1	Atom-2	distance $(\text{\AA})$	overlap (Å)
2:Y:122:LYS:HD2	2:Y:122:LYS:N	2.18	0.58
1:A:696:VAL:HG23	1:A:697:LEU:H	1.67	0.58
1:A:499:GLU:HG2	1:A:710:ARG:NH1	2.19	0.58
3:Z:69:LEU:HB3	3:Z:70:PRO:CD	2.31	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:156:ALA:O	1:A:159:ALA:HB3	2.05	0.57
1:A:297:ASN:N	1:A:297:ASN:HD22	2.02	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:267:LEU:HD12	1:A:268:GLU:N	2.18	0.57
1:A:112:ILE:O	1:A:122:ALA:HA	2.04	0.57
1:A:397:ALA:O	1:A:401:PRO:HG3	2.04	0.57
1:A:174:ILE:HD13	1:A:668:VAL:HB	1.86	0.57
1:A:240:SER:OG	1:A:242:ARG:HD3	2.05	0.57
1:A:724:ALA:N	1:A:725:PRO:HD3	2.20	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: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:60:ILE:HD12	1:A:60:ILE:N	2.20	0.56
1:A:128:ARG:HD2	1:A:128:ARG:H	1.71	0.56
1:A:184:GLU:O	1:A:188:LYS:HD2	2.05	0.56
1:A:248:ARG:C	1:A:249:ILE:HD12	2.26	0.56
1:A:264:THR:HG21	1:A:435:PHE:CE1	2.41	0.56
1:A:456:ILE:O	1:A:456:ILE:HG13	2.05	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:151:HIS:ND1	1:A:152:LEU:N	2.53	0.56
1:A:293:ILE:HG22	1:A:293:ILE:O	2.05	0.56
1:A:702:ILE:O	1:A:705:LYS:HG2	2.05	0.56
1:A:742:ILE:O	1:A:746:LEU:HB2	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:214:SER:O	1:A:217:ASP:HB2	2.03	0.56
1:A:249:ILE:HG22	1:A:251:PHE:CE1	2.40	0.56
1:A:741:LYS:O	1:A:741:LYS:HD3	2.05	0.56



	ti a	Interatomic	Clash
Atom-1	Atom-2	distance (Å)	overlap (Å)
1:A:811:ILE:HD11	2:Y:93:PHE:N	2.21	0.56
1:A:830:TYR:HD1	2:Y:76:PHE:CE2	2.24	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:390:ASN:HB3	1:A:393:ASP:HB2	1.87	0.55
1:A:728:ILE:HG22	1:A:729:PRO:O	2.06	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:CG	3:Z:31:PHE:O	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:HD12	1:A:173:LEU:N	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:15:VAL:HG12	1:A:16:ASP:N	2.23	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:728:ILE:O	1:A:729:PRO:C	2.46	0.54
1:A:806:ILE:O	1:A:810:VAL:HG23	2.07	0.54
3:Z:101:ILE:HG22	3:Z:141:TYR:HD1	1.73	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:198:CYS:O	1:A:256:LYS:HD2	2.09	0.53
1:A:829:LEU:HD21	2:Y:40:ILE:HG23	1.90	0.53
3:Z:120:GLU:O	3:Z:124:GLU:HB2	2.08	0.53
1:A:216:GLU:HA	1:A:219:ILE:HD13	1.91	0.53
1:A:692:GLN:HA	1:A:697:LEU:HD12	1.90	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
1:A:505:ILE:CD1	1:A:754:ARG:HB3	2.38	0.53
1:A:707:PHE:CZ	1:A:754:ARG:HD2	2.44	0.53
1:A:741:LYS:HD3	1:A:741:LYS:C	2.29	0.53



		Interatomic	Clash	
Atom-1	Atom-2	distance (Å)	overlap (Å)	
2:Y:36:SER:N	2:Y:39:ASP:HB2	2.23	0.53	
1:A:128:ARG:HH21	5:A:995:ADP:H2'	1.74	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: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:128:ARG:NH2	5:A:995:ADP:H2'	2.24	0.53	
1:A:491:HIS:NE2	1:A:495:LEU:HD11	2.24	0.52	
1:A:707:PHE:HE2	1:A:763:LYS:HG2	1.75	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:106:ARG:HB3	1:A:111:LEU:HB2	1.90	0.52	
1:A:746:LEU:HD22	1:A:773:MET:HE1	1.92	0.52	
2:Y:13:PRO:HB3	2:Y:17:ILE:HD11	1.92	0.52	
1:A:723:LEU:HD11	1:A:774:ARG:HA	1.91	0.52	
2:Y:39:ASP:O	2:Y:43:ILE:HG22	2.10	0.52	
3:Z:42:ILE:HG22	3:Z:44:PRO:CD	2.39	0.51	
1:A:448:THR:N	1:A:452:ARG:HH22	2.00	0.51	
1:A:721:SER:HA	1:A:742:ILE:HD11	1.92	0.51	
1:A:195:LYS:O	1:A:195:LYS:HG3	2.09	0.51	
1:A:481:ASN:HA	1:A:484:LEU:HB2	1.92	0.51	
1:A:707:PHE:CB	1:A:761:PHE:HB3	2.40	0.51	
1:A:355:ILE:HG22	1:A:355:ILE:O	2.09	0.51	
1:A:490:HIS:O	1:A:493:PHE:HB3	2.10	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:591:ILE:HA	1:A:594:TRP:CE2	2.46	0.50	
1:A:603:ASN:C	1:A:605:ASN:H	2.13	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:4:ASP:HB3	1:A:10:PHE:CE2	2.46	0.50	



		Interatomic	Clash	
Atom-1	Atom-2	distance (Å)	overlap (Å)	
1:A:758:THR:HG23	1:A:759:LYS:CD	2.41	0.50	
1:A:100:LEU:HD12	1:A:100:LEU:O	2.12	0.50	
1:A:178:SER:O	1:A:236:ARG:HG2	2.12	0.50	
1:A:277:SER:O	1:A:278:ALA:HB3	2.12	0.50	
1:A:707:PHE:CE2	1:A:763:LYS:HG2	2.47	0.50	
3:Z:33:LEU:HA	3:Z:68:PHE:CZ	2.46	0.50	
1:A:603:ASN:CB	1:A:606:VAL:HG23	2.42	0.49	
2:Y:62:GLU:O	2:Y:75:ILE:HG23	2.12	0.49	
3:Z:44:PRO:HB3	3:Z:75:LEU:HD12	1.92	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:54:ASP:O	1:A:70:LYS:HA	2.13	0.49	
1:A:78:ASN:HD22	1:A:98:SER:HB2	1.76	0.49	
1:A:728:ILE:C	1:A:729:PRO:O	2.48	0.49	
2:Y:65:GLY:O	2:Y:71:MET:HG2	2.12	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:3:ILE:HG22	1:A:4:ASP:H	1.78	0.49	
1:A:300:MET:O	1:A:301:LEU:HB2	2.11	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	
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:796:LYS:HB2	3:Z:152:PRO:CG	2.42	0.48	
1:A:829:LEU:HD11	2:Y:44:SER:HB2	1.95	0.48	
3:Z:17:LEU:O	3:Z:20:PHE:HB3	2.14	0.48	
1:A:134:ASP:HA	1:A:137:ILE:HD12	1.95	0.48	
1:A:233:LYS:HE3	1:A:316:CYS:SG	2.53	0.48	
1:A:815:ILE:HG21	2:Y:120:PHE:CE2	2.47	0.48	
1:A:113:TYR:CD2	1:A:151:HIS:HA	2.49	0.48	
1:A:466:ILE:HG23	1:A:587:VAL:HG13	1.94	0.48	
2:Y:27:ILE:HG23	2:Y:35:VAL:CG2	2.43	0.48	
2:Y:67:LEU:HG	2:Y:67:LEU:O	2.13	0.48	
3:Z:43:ASN:N	3:Z:44:PRO:HD3	2.29	0.48	
3:Z:4:SER:O	3:Z:8:ILE:HG13	2.13	0.48	



		Interatomic	Clash	
Atom-1	Atom-2	distance (Å)	overlap (Å)	
3:Z:107:ARG:NH1	3:Z:107:ARG:HB2	2.28	0.48	
1:A:244:GLY:HA3	1:A:265:TYR:HB2	1.96	0.48	
1:A:410:VAL:CG1	1:A:411:THR:N	2.77	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:182:LYS:HE3	1:A:462:ALA:HA	1.96	0.47	
1:A:780:LYS:HE2	1:A:784:MET:CE	2.44	0.47	
1:A:78:ASN:ND2	1:A:98:SER:HB2	2.29	0.47	
1:A:773:MET:HE3	1:A:773:MET:HB3	1.79	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:43:PHE:CD1	1:A:97:ALA:HB2	2.49	0.47	
1:A:228:ALA:O	1:A:284:ILE:HB	2.13	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:237:ASN:OD1	1:A:238:ASN:N	2.47	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:275:GLN:OE1	1:A:312:ILE:HA	2.14	0.47	
3:Z:70:PRO:O	3:Z:73:GLU:HG3	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:125:PRO:O	1:A:126:TYR:HB2	2.14	0.47	
1:A:141:ARG:HD2	1:A:196:VAL:HG12	1.97	0.47	
1:A:672:ILE:HD13	1:A:672:ILE:N	2.28	0.47	
1:A:736:LYS:O	1:A:740:GLU:HB2	2.15	0.47	
1:A:787:ALA:HB1	3:Z:44:PRO:O	2.14	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:361:MET:CE	1:A:380:ALA:HA	2.45	0.46	
1:A:567:LYS:HB3	1:A:568:PRO:CD	2.39	0.46	
1:A:360:GLU:O	1:A:379:GLU:HG3	2.15	0.46	
1:A:438:LEU:HD23	1:A:438:LEU:O	2.16	0.46	
1:A:245:LYS:HE3	1:A:247:ILE:HB	1.98	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:36:VAL:O	1:A:43:PHE:HA	2.16	0.46	
1:A:177:GLU:HB2	1:A:672:ILE:CD1	2.45	0.46	
1:A:467:PHE:C	1:A:470:ASN:HD21	2.19	0.46	



		Interatomic	Clash	
Atom-1	Atom-2	distance (Å)	overlap (Å)	
3:Z:11:LEU:HD23	3:Z:69:LEU:HD13	1.98	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: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:822:ARG:CB	1:A:822:ARG:NH1	2.63	0.46	
1:A:782:ILE:O	1:A:786:GLN:HG3	2.16	0.46	
1:A:266:LEU:HG	1:A:649:HIS:CE1	2.51	0.46	
1:A:449:LYS:HD2	1:A:449:LYS:HA	1.53	0.46	
3:Z:108:HIS:O	3:Z:112:ALA:HB3	2.16	0.46	
1:A:95:ASN:ND2	1:A:98:SER:H	2.14	0.45	
1:A:308:LEU:HD12	1:A:308:LEU:O	2.16	0.45	
1:A:358:MET:HA	1:A:361:MET:HE3	1.99	0.45	
1:A:414:GLN:HB2	1:A:418:GLN:CB	2.44	0.45	
3:Z:35:ASP:HA	3:Z:38:ARG:HH11	1.80	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:784:MET:CE	3:Z:79:GLU:HB3	2.41	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: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:822:ARG:CG	1:A:822:ARG:NH1	2.74	0.45	
1:A:85:LEU:N	1:A:102:ASN:HD21	2.15	0.45	
1:A:507:TRP:CH2	1:A:706:GLY:HA2	2.52	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	
1:A:487:PHE:CZ	1:A:665:PRO:HG3	2.52	0.45	
1:A:544:ASP:OD1	1:A:544:ASP:N	2.42	0.45	
1:A:811:ILE:HG23	2:Y:93:PHE:CZ	2.51	0.45	
2:Y:93:PHE:HB3	2:Y:141:TYR:CD2	2.51	0.45	
1:A:15:VAL:CG1	1:A:16:ASP:N	2.80	0.45	
1:A:309:TYR:CD2	1:A:356:LEU:HB3	2.52	0.45	
1:A:371:GLN:HE21	1:A:371:GLN:HB2	1.66	0.45	
2:Y:90:ARG:O	2:Y:90:ARG:CG	2.65	0.45	
1:A:84:LYS:HA	1:A:106:ARG:HG3	1.99	0.44	



	loue page	Interatomic	Clash	
Atom-1	Atom-2	distance $(Å)$	overlap (Å)	
1:A:273:THR:HG22	1:A:311:PHE:CE1	2.52	0.44	
1:A:795:ARG:HD3	3:Z:38:ARG:O	2.16	0.44	
1:A:245:LYS:HE2	1:A:247:ILE:CG2	2.48	0.44	
1:A:355:ILE:HG23	1:A:427:ALA:HB1	1.99	0.44	
1:A:663:THR:O	1:A:665:PRO:HD3	2.17	0.44	
1:A:706:GLY:C	1:A:708:PRO:HD3	2.38	0.44	
1:A:560:ARG:HE	1:A:560:ARG:HB2	1.66	0.44	
1:A:752:GLU:HG3	1:A:766:VAL:HG21	1.98	0.44	
1:A:76:SER:HB3	1:A:93:TYR:CG	2.51	0.44	
1:A:131:ILE:O	1:A:136:VAL:HG11	2.17	0.44	
1:A:828:LYS:NZ	1:A:828:LYS:HB2	2.33	0.44	
3:Z:131:LEU:HG	3:Z:139:VAL:CG1	2.47	0.44	
2:Y:93:PHE:CG	2:Y:141:TYR:HB2	2.53	0.44	
3:Z:4:SER:C	3:Z:6:ASP:N	2.71	0.44	
1:A:825:GLN:OE1	1:A:825:GLN:HA	2.16	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: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	
3:Z:4:SER:OG	3:Z:6:ASP:HB3	2.17	0.44	
1:A:470:ASN:OD1	1:A:587:VAL:HG13	2.18	0.43	
1:A:760:VAL:HG13	1:A:760:VAL:O	2.18	0.43	
1:A:763:LYS:O	1:A:766:VAL:HG23	2.17	0.43	
3:Z:107:ARG:HB2	3:Z:107:ARG:HH11	1.83	0.43	
1:A:377:THR:HG22	1:A:381:GLU:HG3	2.00	0.43	
1:A:468:ASP:HB3	1:A:573:GLN:CA	2.38	0.43	
1:A:491:HIS:CD2	1:A:495:LEU:HD11	2.52	0.43	
1:A:827:TRP:O	1:A:831:SER:N	2.42	0.43	
1:A:250:HIS:CB	1:A:452:ARG:HD3	2.48	0.43	
1:A:251:PHE:HA	1:A:258:ALA:H	1.83	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:N	1:A:586:ASN:ND2	2.64	0.43	
1:A:129:LEU:HA	1:A:130:PRO:HD3	1.78	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:293:ILE:HD11	1:A:329:LYS:HG2	2.01	0.43	
1:A:746:LEU:HD21	1:A:773:MET:CE	2.48	0.43	
1:A:401:PRO:CG	1:A:603:ASN:HD21	2.23	0.43	
1:A:493:PHE:CD1	1:A:511:ASP:HA	2.53	0.43	



	, and pagein	Interatomic	Clash overlap (Å)	
Atom-1	Atom-2	distance (Å)		
2:Y:76:PHE:C	2:Y:78:ASP:H	2.22	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:722:ILE:HD11	3:Z:88:GLU:O	2.18	0.43	
1:A:743:LEU:O	1:A:748:MET:HB2	2.18	0.43	
1:A:824:TRP:CE2	1:A:826:TRP:HD1	2.37	0.43	
3:Z:33:LEU:HA	3:Z:68:PHE:HZ	1.81	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: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:580:LEU:HD12	1:A:580:LEU:HA	1.86	0.42	
1:A:777:ARG:HA	1:A:777:ARG:HD2	1.88	0.42	
1:A:826:TRP:CZ2	2:Y:59:MET:SD	3.08	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:225:VAL:HG23	1:A:226:LEU:N	2.33	0.42	
1:A:471:SER:OG	1:A:472:PHE:N	2.51	0.42	
1:A:516:LEU:HD22	1:A:516:LEU:HA	1.91	0.42	
1:A:676:LEU:C	1:A:678:GLN:H	2.22	0.42	
1:A:720:TYR:O	1:A:742:ILE:HD13	2.20	0.42	
2:Y:140:ASP:OD1	2:Y:142:VAL:N	2.53	0.42	
3:Z:94:ASP:OD2	3:Z:97:GLY:HA2	2.20	0.42	
3:Z:101:ILE:HG22	3:Z:141:TYR:CD1	2.54	0.42	
1:A:16:ASP:HB3	1:A:19:LYS:CB	2.49	0.42	
1:A:398:LEU:HD21	1:A:423:VAL:CG2	2.48	0.42	
1:A:752:GLU:HG3	1:A:766:VAL:CG2	2.50	0.42	
1:A:297:ASN:N	1:A:297:ASN:ND2	2.68	0.42	
1:A:402:LYS:CB	1:A:605:ASN:ND2	2.82	0.42	
1:A:828:LYS:O	1:A:832:LYS:HG3	2.19	0.42	
2:Y:67:LEU:HA	2:Y:71:MET:HB3	2.01	0.42	
3:Z:44:PRO:CG	3:Z:75:LEU:HD12	2.49	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	



		Interatomic	Clash	
Atom-1	Atom-2	distance (Å)	overlap (Å)	
1:A:712:ILE:HA	1:A:759:LYS:CB	2.50	0.42	
1:A:496:GLU:HA	1:A:496:GLU:OE1	2.20	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:768:GLY:O	1:A:771:GLU:HB2	2.19	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:157:ASP:HB2	1:A:192:TYR:CZ	2.53	0.41	
1:A:179:GLY:CA	4:A:996:SO4:O4	2.68	0.41	
3:Z:3:LEU:CD2	3:Z:7:GLU:HG2	2.50	0.41	
1:A:234:THR:O	1:A:236:ARG:N	2.52	0.41	
1:A:434:MET:O	1:A:437:TRP:HB3	2.20	0.41	
1:A:656:LEU:O	1:A:659:ASN:N	2.49	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	
3:Z:93:PHE:CE2	3:Z:109:VAL:HG22	2.55	0.41	
1:A:821:LEU:HD11	1:A:827:TRP:CE3	2.56	0.41	
2:Y:21:LYS:HB2	2:Y:69:PHE:CE1	2.55	0.41	
2:Y:35:VAL:HG11	2:Y:40:ILE:HG13	2.02	0.41	
1:A:131:ILE:HG22	1:A:151:HIS:HE2	1.86	0.41	
1:A:401:PRO:O	1:A:411:THR:HA	2.20	0.41	
1:A:367:PRO:HB2	1:A:369:GLU:HG2	2.03	0.41	
1:A:486:GLN:HA	1:A:516:LEU:HD12	2.02	0.41	
1:A:728:ILE:O	1:A:729:PRO:O	2.39	0.41	
1:A:287:GLN:HB3	1:A:328:PHE:CG	2.56	0.41	
1:A:400:LYS:N	1:A:401:PRO:HD3	2.36	0.41	
1:A:598:ASN:ND2	1:A:644:THR:OG1	2.54	0.41	
1:A:767:LEU:O	1:A:771:GLU:HG2	2.20	0.41	
1:A:153:PHE:HB3	1:A:192:TYR:CE2	2.56	0.41	
1:A:250:HIS:O	1:A:258:ALA:N	2.49	0.41	
1:A:369:GLU:HG2	1:A:369:GLU:H	1.68	0.41	
1:A:771:GLU:O	1:A:774:ARG:HB3	2.19	0.41	
1:A:796:LYS:HB2	3:Z:152:PRO:HG2	2.02	0.41	
2:Y:36:SER:C	2:Y:38:GLU:H	2.24	0.41	
2:Y:90:ARG:O	2:Y:90:ARG:HG2	2.20	0.41	
1:A:32:LYS:O	1:A:47:GLU:HA	2.21	0.41	
1:A:121:ILE:H	1:A:121:ILE:HG13	1.56	0.41	
1:A:175:THR:OG1	1:A:669:ARG:HD3	2.21	0.41	
1:A:327:GLU:OE1	1:A:327:GLU:HA	2.21	0.41	
1:A:780:LYS:HG2	1:A:784:MET:CE	2.51	0.41	



Atom 1	Atom 2	Interatomic	Clash
Atom-1	Atom-2	distance $(\text{\AA})$	overlap (Å)
2:Y:22:GLU:C	2:Y:24:PHE:H	2.24	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
1:A:12:TYR:HE2	1:A:127:ARG:NH2	2.19	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
2:Y:27:ILE:HD12	2:Y:27:ILE:HA	1.91	0.40
2:Y:35:VAL:O	2:Y:35:VAL:HG12	2.20	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:689:HIS:O	1:A:692:GLN:HB3	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: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:78:ASN:HA	1:A:79:PRO:HD3	1.95	0.40
1:A:464:PHE:HE2	1:A:466:ILE:HG12	1.86	0.40
2:Y:142:VAL:O	2:Y:145:THR:HB	2.21	0.40
1:A:88:MET:HG2	1:A:102:ASN:OD1	2.21	0.40
1:A:286:TYR:OH	1:A:312:ILE:HB	2.21	0.40
1:A:30:GLY:HA3	1:A:772:GLU:OE2	2.21	0.40
1:A:242:ARG:HA	1:A:242:ARG:HD2	1.72	0.40
1:A:337:ILE:O	1:A:337:ILE:HG22	2.20	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

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	Per	centiles
1	А	794/840~(94%)	660 (83%)	113 (14%)	21 (3%)	5	26
2	Y	140/156~(90%)	111 (79%)	25~(18%)	4 (3%)	4	24
3	Z	153/156~(98%)	136 (89%)	11 (7%)	6 (4%)	3	18
All	All	1087/1152 (94%)	907 (83%)	149 (14%)	31 (3%)	4	24

All (31) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	А	304	PRO
1	А	625	PRO
1	А	708	PRO
1	А	713	TYR
1	А	834	LYS
2	Y	66	PRO
1	А	65	SER
1	А	235	THR
1	А	324	ASP
1	А	367	PRO
1	А	510	ILE
1	А	528	GLY
1	А	568	PRO
1	А	833	VAL
2	Y	85	SER
3	Ζ	25	ASP
3	Ζ	96	GLU
3	Ζ	116	ARG
3	Ζ	154	PRO
1	А	266	LEU
1	А	540	PRO
2	Y	119	ASN
3	Ζ	31	PHE
1	А	116	SER
1	A	793	LEU
1	А	504	GLY
2	Y	64	PRO
3	Ζ	21	TRP
1	А	366	ARG
1	А	731	GLY
1	А	794	ILE



#### 5.3.2 Protein sidechains (i)

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 side chain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentile	es
1	А	666/732~(91%)	572~(86%)	94 (14%)	3 15	
2	Y	108/133~(81%)	80 (74%)	28 (26%)	0 1	
3	Z	126/132~(96%)	110 (87%)	16 (13%)	4 18	
All	All	900/997~(90%)	762 (85%)	138 (15%)	2 12	

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

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



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



1         A         644         THR           1         A         672         ILE           1         A         673         GLN           1         A         693         CYS           1         A         701         ARG           1         A         702         ILE           1         A         712         ILE           1         A         721         SER           1         A         729         PRO           1         A         732         PHE           1         A         734         ASP           1         A         740         GLU           1         A         750         PRO           1         A         752         GLU           1         A         752         ILE           1         A         782         ILE           1         A         835 </th <th>Mol</th> <th>Chain</th> <th>Res</th> <th>Type</th>	Mol	Chain	Res	Type
1       A $672$ ILE         1       A $678$ GLN         1       A $693$ CYS         1       A $701$ ARG         1       A $702$ ILE         1       A $702$ ILE         1       A $702$ ILE         1       A $712$ ILE         1       A $712$ ILE         1       A $712$ SER         1       A $729$ PRO         1       A $732$ PHE         1       A $734$ ASP         1       A $740$ GLU         1       A $750$ PRO         1       A $750$ PRO         1       A $752$ GLU         1       A $752$ ILE         1       A $752$ ILE         1       A $752$ ILE         1       A $830$ TYR         1       A $835$ PRO <td>1</td> <td>А</td> <td>644</td> <td>THR</td>	1	А	644	THR
1         A         678         GLN           1         A         693         CYS           1         A         701         ARG           1         A         702         ILE           1         A         702         ILE           1         A         712         ILE           1         A         712         ILE           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         750         PRO           1         A         750         PRO           1         A         752         GLU           1         A         753         MET           1         A         782         ILE           1         A         835         PRO           1         A         836         LEU           2         Y         20 </td <td>1</td> <td>А</td> <td>672</td> <td>ILE</td>	1	А	672	ILE
1         A         693         CYS           1         A         701         ARG           1         A         702         ILE           1         A         709         SER           1         A         712         ILE           1         A         712         SER           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         750         PRO           1         A         750         PRO           1         A         752         GLU           1         A         752         GLU           1         A         753         MET           1         A         830         TYR           1         A         835         PRO           1         A         836         LEU           2         Y         20 </td <td>1</td> <td>А</td> <td>678</td> <td>GLN</td>	1	А	678	GLN
1       A       701       ARG         1       A       702       ILE         1       A       709       SER         1       A       712       ILE         1       A       712       ILE         1       A       721       SER         1       A       729       PRO         1       A       732       PHE         1       A       732       PHE         1       A       732       PHE         1       A       732       PHE         1       A       734       ASP         1       A       740       GLU         1       A       750       PRO         1       A       752       GLU         1       A       752       GLU         1       A       752       ILE         1       A       752       ILE         1       A       782       ILE         1       A       830       TYR         1       A       835       PRO         1       A       836       LEU         2	1	A	693	CYS
1       A       702       ILE         1       A       709       SER         1       A       712       ILE         1       A       712       SER         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       740       GLU         1       A       750       PRO         1       A       752       GLU         1       A       752       GLU         1       A       752       ILE         1       A       752       ILE         1       A       752       ILE         1       A       782       ILE         1       A       835       PRO         1       A       835       PRO         1       A       835       PRO         1       A       836       LEU         2	1	A	701	ARG
1       A       709       SER         1       A       712       ILE         1       A       712       SER         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       740       GLU         1       A       750       PRO         1       A       750       PRO         1       A       752       GLU         1       A       752       GLU         1       A       752       ILE         1       A       752       ILE         1       A       782       ILE         1       A       835       IRO         1       A       835       PRO         1       A       835       PRO         1       A       836       LEU         2       Y       20       MET         2	1	А	702	ILE
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       732       PHE         1       A       734       ASP         1       A       740       GLU         1       A       740       GLU         1       A       750       PRO         1       A       752       GLU         1       A       752       GLU         1       A       759       LYS         1       A       752       ILE         1       A       782       ILE         1       A       835       IRO         1       A       835       PRO         1       A       836       LEU         2       Y       20       MET         2       Y       20       MET         2       Y       26       MET         2 <t< td=""><td>1</td><td>А</td><td>709</td><td>SER</td></t<>	1	А	709	SER
1       A       718       GLN         1       A       721       SER         1       A       729       PRO         1       A       730       GLN         1       A       732       PHE         1       A       732       PHE         1       A       734       ASP         1       A       740       GLU         1       A       740       GLU         1       A       741       LYS         1       A       750       PRO         1       A       759       LYS         1       A       759       LYS         1       A       759       LYS         1       A       782       ILE         1       A       782       ILE         1       A       830       TYR         1       A       835       PRO         1       A       836       LEU         2       Y       20       MET         2       Y       20       MET         2       Y       26       MET         2 <t< td=""><td>1</td><td>А</td><td>712</td><td>ILE</td></t<>	1	А	712	ILE
1       A       721       SER         1       A       729       PRO         1       A       730       GLN         1       A       732       PHE         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       752       GLU         1       A       759       LYS         1       A       759       LYS         1       A       782       ILE         1       A       782       ILE         1       A       835       PRO         1       A       836       LEU         2       Y       20       MET         2       Y       20       MET         2       Y       25       SER         2       Y       26       MET         2       Y       26       MET         2	1	А	718	GLN
1       A       729       PRO         1       A       730       GLN         1       A       732       PHE         1       A       734       ASP         1       A       740       GLU         1       A       740       GLU         1       A       740       GLU         1       A       750       PRO         1       A       752       GLU         1       A       752       GLU         1       A       759       LYS         1       A       773       MET         1       A       773       MET         1       A       782       ILE         1       A       830       TYR         1       A       830       TYR         1       A       835       PRO         1       A       836       LEU         2       Y       20       MET         2       Y       25       SER         2       Y       26       MET         2       Y       26       MET         2 <td< td=""><td>1</td><td>А</td><td>721</td><td>SER</td></td<>	1	А	721	SER
1       A       730       GLN         1       A       732       PHE         1       A       734       ASP         1       A       740       GLU         1       A       740       GLU         1       A       740       GLU         1       A       740       PRO         1       A       750       PRO         1       A       752       GLU         1       A       752       GLU         1       A       753       MET         1       A       773       MET         1       A       782       ILE         1       A       815       ILE         1       A       830       TYR         1       A       835       PRO         1       A       836       LEU         2       Y       20       MET         2       Y       20       MET         2       Y       26       MET         2       Y       26       MET         2       Y       31       ARG         2	1	А	729	PRO
1A732PHE1A734ASP1A740GLU1A741LYS1A750PRO1A752GLU1A759LYS1A773MET1A782ILE1A815ILE1A830TYR1A836LEU2Y16GLN2Y20MET2Y26MET2Y26MET2Y26MET2Y31ARG2Y36SER2Y43ILE2Y51PRO2Y53ASP2Y53ASP2Y59MET	1	А	730	GLN
1A734ASP1A740GLU1A741LYS1A750PRO1A752GLU1A759LYS1A773MET1A782ILE1A815ILE1A830TYR1A835PRO1A836LEU2Y16GLN2Y20MET2Y25SER2Y26MET2Y26MET2Y31ARG2Y36SER2Y46GLN2Y51PRO2Y53ASP2Y53ASP2Y59MET	1	А	732	PHE
1A740GLU1A741LYS1A750PRO1A752GLU1A759LYS1A773MET1A782ILE1A815ILE1A822ARG1A830TYR1A835PRO1A836LEU2Y16GLN2Y20MET2Y25SER2Y26MET2Y26MET2Y31ARG2Y36SER2Y43ILE2Y51PRO2Y53ASP2Y53ASP2Y59MET	1	А	734	ASP
1A741LYS1A750PRO1A752GLU1A759LYS1A773MET1A782ILE1A815ILE1A822ARG1A830TYR1A835PRO1A836LEU2Y16GLN2Y20MET2Y25SER2Y26MET2Y26MET2Y27ILE2Y31ARG2Y36SER2Y43ILE2Y51PRO2Y53ASP2Y53ASP2Y59MET	1	А	740	GLU
1A750PRO1A752GLU1A759LYS1A773MET1A782ILE1A815ILE1A822ARG1A830TYR1A835PRO1A836LEU2Y16GLN2Y20MET2Y25SER2Y26MET2Y26MET2Y31ARG2Y36SER2Y46GLN2Y51PRO2Y53ASP2Y57THR2Y59MET	1	А	741	LYS
1A752GLU1A759LYS1A773MET1A782ILE1A815ILE1A822ARG1A830TYR1A835PRO1A836LEU2Y16GLN2Y20MET2Y25SER2Y26MET2Y27ILE2Y31ARG2Y36SER2Y43ILE2Y51PRO2Y53ASP2Y53ASP2Y59MET	1	А	750	PRO
1A759LYS1A773MET1A782ILE1A815ILE1A822ARG1A830TYR1A835PRO1A836LEU2Y16GLN2Y20MET2Y25SER2Y26MET2Y26MET2Y31ARG2Y36SER2Y46GLN2Y51PRO2Y53ASP2Y57THR2Y59MET	1	А	752	GLU
1A773MET1A782ILE1A815ILE1A822ARG1A830TYR1A835PRO1A836LEU2Y16GLN2Y20MET2Y25SER2Y26MET2Y27ILE2Y26MET2Y31ARG2Y36SER2Y43ILE2Y51PRO2Y53ASP2Y53ASP2Y59MET	1	А	759	LYS
$\begin{array}{c ccccccccccccccccccccccccccccccccccc$	1	А	773	MET
$\begin{array}{c ccccccccccccccccccccccccccccccccccc$	1	А	782	ILE
$\begin{array}{c ccccccccccccccccccccccccccccccccccc$	1	А	815	ILE
$\begin{array}{c ccccccccccccccccccccccccccccccccccc$	1	А	822	ARG
$\begin{array}{c ccccccccccccccccccccccccccccccccccc$	1	А	830	TYR
$\begin{array}{c ccccccccccccccccccccccccccccccccccc$	1	А	835	PRO
$\begin{array}{c ccccccccccccccccccccccccccccccccccc$	1	А	836	LEU
$\begin{array}{c ccccccccccccccccccccccccccccccccccc$	2	Y	16	GLN
$\begin{array}{c ccccccccccccccccccccccccccccccccccc$	2	Y	20	MET
$\begin{array}{c ccccccccccccccccccccccccccccccccccc$	2	Y	22	GLU
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         51         PRO           2         Y         52         ASP           2         Y         53         ASP           2         Y         57         THR           2         Y         59         MET	2	Y	25	SER
$\begin{array}{c ccccccccccccccccccccccccccccccccccc$	2	Y	26	MET
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         53         ASP           2         Y         57         THR           2         Y         59         MET	2	Y	27	ILE
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	2	Y	29	VAL
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	2	Y	31	ARG
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	2	Y	36	SER
2         Y         46         GLN           2         Y         51         PRO           2         Y         52         ASP           2         Y         53         ASP           2         Y         57         THR           2         Y         59         MET	2	Y	43	ILE
2         Y         51         PRO           2         Y         52         ASP           2         Y         53         ASP           2         Y         57         THR           2         Y         59         MET	2	Y	46	GLN
2         Y         52         ASP           2         Y         53         ASP           2         Y         57         THR           2         Y         59         MET	2	Y	51	PRO
2         Y         53         ASP           2         Y         57         THR           2         Y         59         MET	2	Y	52	ASP
2         Y         57         THR           2         Y         59         MET	2	Y	53	ASP
2 Y 59 MET	2	Y	57	THR
	2	Y	59	MET



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	Ζ	10	ASP
3	Ζ	58	MET
3	Ζ	62	SER
3	Ζ	64	PRO
3	Ζ	67	GLU
3	Ζ	68	PHE
3	Ζ	70	PRO
3	Ζ	77	ASP
3	Ζ	79	GLU
3	Ζ	80	GLN
3	Ζ	101	ILE
3	Ζ	107	ARG
3	Z	124	GLU
3	Z	127	LYS
3	Ζ	139	VAL
3	Z	146	LYS

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

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



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

#### 5.3.3 RNA (i)

There are no RNA molecules in this entry.

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

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

#### 5.5 Carbohydrates (i)

There are no monosaccharides in this entry.

#### 5.6 Ligand geometry (i)

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).

Mal	Mol Type Chain Be		Dec	Link	Bo	Bond lengths			Bond angles		
	туре	Chain	nes		Counts	RMSZ	# Z >2	Counts	RMSZ	# Z  > 2	
4	SO4	А	996	-	4,4,4	0.25	0	6,6,6	0.06	0	
5	ADP	А	995	-	24,29,29	1.44	4 (16%)	29,45,45	1.55	2 (6%)	

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
5	ADP	А	995	-	-	6/12/32/32	0/3/3/3

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	$\mathrm{Ideal}(\mathrm{\AA})$
5	А	995	ADP	O4'-C1'	3.31	1.45	1.41
5	А	995	ADP	C2-N3	3.21	1.37	1.32
5	А	995	ADP	C5-N7	-2.43	1.30	1.39
5	А	995	ADP	C4-N3	2.21	1.38	1.35

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	$Observed(^{o})$	$Ideal(^{o})$
5	А	995	ADP	N3-C2-N1	-6.52	118.48	128.68
5	А	995	ADP	O3B-PB-O3A	2.06	111.53	104.64

There are no chirality outliers.

All (6) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
5	А	995	ADP	C5'-O5'-PA-O1A
5	А	995	ADP	C5'-O5'-PA-O2A
5	А	995	ADP	C5'-O5'-PA-O3A
5	А	995	ADP	O4'-C4'-C5'-O5'
5	А	995	ADP	C3'-C4'-C5'-O5'
5	А	995	ADP	PB-O3A-PA-O1A

There are no ring outliers.



]	Mol	Chain	Res	Type	Clashes	Symm-Clashes
	4	А	996	SO4	3	0
	5	А	995	ADP	5	0

2 monomers are involved in 8 short contacts:

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less then 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.



## 5.7 Other polymers (i)

There are no such residues in this entry.

## 5.8 Polymer linkage issues (i)

There are no chain breaks in this entry.



## 6 Fit of model and data (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,  $95^{th}$  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	< <b>RSRZ</b> >	#RSRZ>2	$OWAB(Å^2)$	Q<0.9
1	А	802/840~(95%)	-0.40	3 (0%) 92 84	33, 72, 134, 176	0
2	Y	142/156~(91%)	0.08	11 (7%) 13 5	34, 126, 187, 201	0
3	Z	155/156~(99%)	-0.52	0 100 100	31, 67, 104, 126	0
All	All	1099/1152~(95%)	-0.36	14 (1%) 77 59	31, 72, 161, 201	0

All (14) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	Y	72	PHE	4.1
1	А	406	GLY	3.6
2	Y	68	ASN	3.5
1	А	367	PRO	3.0
2	Y	46	GLN	2.7
2	Y	153	GLU	2.7
2	Y	66	PRO	2.6
2	Y	36	SER	2.5
2	Y	62	GLU	2.5
2	Y	33	GLY	2.4
2	Υ	58	ALA	2.3
1	А	407	THR	2.3
2	Y	40	ILE	2.1
2	Y	67	LEU	2.1

## 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 monosaccharides 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,  $95^{th}$  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	$B-factors(Å^2)$	Q<0.9
6	MG	Y	999	1/1	0.88	0.19	137,137,137,137	0
5	ADP	А	995	27/27	0.89	0.20	53,79,92,102	0
4	SO4	А	996	5/5	0.97	0.26	54,73,84,84	0
7	CA	Z	998	1/1	0.97	0.24	75,75,75,75	0

The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation to approximate a three-dimensional view.





## 6.5 Other polymers (i)

There are no such residues in this entry.

