

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

#### Feb 20, 2024 – 05:08 AM EST

PDB ID	:	4LL7
Title	:	Structure of She3p amino terminus.
Authors	:	Shi, H.; Singh, N.; Esselborn, F.; Blobel, G.
Deposited on	:	2013-07-09
Resolution	:	2.31  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
EDS	:	2.36
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)	:	2.36

# 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 2.31 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	$egin{array}{c} { m Whole \ archive} \ (\#{ m Entries}) \end{array}$	${f Similar\ resolution}\ (\#{ m Entries,\ resolution\ range}({ m \AA}))$
R <sub>free</sub>	130704	5974 (2.34-2.30)
Clashscore	141614	6604 (2.34-2.30)
Ramachandran outliers	138981	6523 (2.34-2.30)
Sidechain outliers	138945	6523 (2.34-2.30)
RSRZ outliers	127900	5855(2.34-2.30)

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	٨	0.0	15%				
1	А	96	36%	53%	8% •		
			23%				
1	В	96	45%	43%	• 8%		
			21%				
1	С	96	46%	41%	7% 6%		
			22%				
1	D	96	48%	38%	9% 5%		
			29%				
1	Ε	96	42%	51%	• 6%		



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Mol	Chain	Length	Quality of chain				
1	F	96	21% 42%	50%	•• 5%		
1	G	96	31% 48%	39%	• 9%		
1	Н	96	34%	55%	5% 5%		

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
2	DY	Е	202	-	-	-	Х
3	SO4	А	209	-	-	Х	Х
3	SO4	В	207	-	-	-	Х
5	DTT	А	212	-	-	Х	Х
7	IPA	F	206	-	-	Х	-
7	IPA	F	208	-	-	-	Х



# 2 Entry composition (i)

There are 8 unique types of molecules in this entry. The entry contains 6422 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.

Mol	Chain	Residues		At	oms			ZeroOcc	AltConf	Trace
1	٨	04	Total	С	Ν	0	S	0	0	0
	A	94	778	480	136	160	2	0	0	0
1	P	<u> </u>	Total	С	Ν	0	S	0	0	0
	D	00	731	452	127	150	2	0	0	0
1	С	00	Total	С	Ν	0	S	0	0	0
	U	90	746	460	129	155	2	0	0	0
1	Л	01	Total	С	Ν	0	S	0	0	0
	D	91	754	466	130	156	2	0		0
1	F	00	Total	С	Ν	0	S	0	0	0
	Ľ	90	746	460	129	155	2		0	0
1	Б	01	Total	С	Ν	0	S	0	0	0
	Ľ	91	754	466	130	156	2	0	0	0
1	С	87	Total	С	Ν	0	S	0	0	0
	I G	01	723	446	126	149	2	0	0	0
1	и	01	Total	С	Ν	0	S	0	0	0
	11	91	754	466	130	156	2		0 0	U

• Molecule 1 is a protein called SWI5-dependent HO expression protein 3.

• Molecule 2 is DYSPROSIUM ION (three-letter code: DY) (formula: Dy).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	А	4	Total Dy 5 5	0	1
2	В	3	Total Dy 3 3	0	0
2	С	3	Total Dy 5 5	0	2
2	D	3	Total Dy 3 3	0	0
2	Ε	5	Total Dy 6 6	0	1
2	F	3	Total Dy 3 3	0	0



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Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	G	2	$\begin{array}{cc} \text{Total} & \text{Dy} \\ 2 & 2 \end{array}$	0	0
2	Н	3	Total Dy 3 3	0	0



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf	
3	Λ	1	Total O S	0	0	
5	Л	1	5 4 1	0	0	
ગ	Δ	1	Total O S	0	0	
0	11	1	5 4 1	0	0	
3	Δ	1	Total O S	0	0	
0	11	I	5 4 1	0	0	
3	А	1	Total O S	0	0	
0	11	I	5 4 1	0		
3	А	1	Total O S	0	0	
		1	5 4 1	0		
3	А	1	Total O S	0	0	
		1	5 4 1	0	0	
3	В	1	Total O S	0	0	
	D	Ŧ	5 4 1	0	0	
3	В	1	Total O S	0	0	
	D	L	5 4 1	0	0	
3	В	1	Total O S	0	0	
0	D	1	5 4 1	0		



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Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	В	1	$\begin{array}{ccc} \text{Total} & \text{O} & \text{S} \\ 5 & 4 & 1 \end{array}$	0	0
3	С	1	$\begin{array}{ccc} \text{Total} & \text{O} & \text{S} \\ 5 & 4 & 1 \end{array}$	0	0
3	С	1	$\begin{array}{ccc} \text{Total} & \text{O} & \text{S} \\ 5 & 4 & 1 \end{array}$	0	0
3	С	1	$\begin{array}{ccc} \text{Total} & \text{O} & \text{S} \\ 5 & 4 & 1 \end{array}$	0	0
3	С	1	$\begin{array}{ccc} \text{Total} & \text{O} & \text{S} \\ 5 & 4 & 1 \end{array}$	0	0
3	С	1	$\begin{array}{ccc} \text{Total} & \text{O} & \text{S} \\ 5 & 4 & 1 \end{array}$	0	0
3	С	1	$\begin{array}{ccc} \text{Total} & \text{O} & \text{S} \\ 5 & 4 & 1 \end{array}$	0	0
3	С	1	$\begin{array}{ccc} \text{Total} & \text{O} & \text{S} \\ 5 & 4 & 1 \end{array}$	0	0
3	D	1	$\begin{array}{ccc} \text{Total} & \text{O} & \text{S} \\ 5 & 4 & 1 \end{array}$	0	0
3	D	1	$\begin{array}{ccc} \text{Total} & \text{O} & \text{S} \\ 5 & 4 & 1 \end{array}$	0	0
3	Е	1	$\begin{array}{ccc} \text{Total} & \text{O} & \text{S} \\ 5 & 4 & 1 \end{array}$	0	0
3	F	1	$\begin{array}{ccc} \text{Total} & \text{O} & \text{S} \\ 5 & 4 & 1 \end{array}$	0	0
3	G	1	$\begin{array}{ccc} \text{Total} & \text{O} & \text{S} \\ 5 & 4 & 1 \end{array}$	0	0
3	G	1	$\begin{array}{ccc} \text{Total} & \text{O} & \text{S} \\ 5 & 4 & 1 \end{array}$	0	0
3	G	1	$\begin{array}{ccc} \text{Total} & \text{O} & \text{S} \\ 5 & 4 & 1 \end{array}$	0	0
3	G	1	$\begin{array}{ccc} \text{Total} & \text{O} & \text{S} \\ 5 & 4 & 1 \end{array}$	0	0
3	G	1	$\begin{array}{ccc} \text{Total} & \text{O} & \text{S} \\ 5 & 4 & 1 \end{array}$	0	0
3	G	1	$\begin{array}{ccc} \text{Total} & \text{O} & \text{S} \\ 5 & 4 & 1 \end{array}$	0	0
3	Н	1	$\begin{array}{ccc} \text{Total} & \text{O} & \text{S} \\ 5 & 4 & 1 \end{array}$	0	0
3	Н	1	$\begin{array}{ccc} \text{Total} & \text{O} & \text{S} \\ 5 & 4 & 1 \end{array}$	0	0

<sup>•</sup> Molecule 4 is PLATINUM (II) ION (three-letter code: PT) (formula: Pt).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	А	1	Total Pt 1 1	0	0
4	В	1	Total Pt 1 1	0	0
4	С	1	Total Pt 1 1	0	0
4	D	1	Total Pt 1 1	0	0
4	Ε	1	Total Pt 1 1	0	0
4	G	1	Total Pt 1 1	0	0

• Molecule 5 is 2,3-DIHYDROXY-1,4-DITHIOBUTANE (three-letter code: DTT) (formula:  $C_4H_{10}O_2S_2$ ).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
5	А	1	Total 8	$\begin{array}{c} \mathrm{C} \\ 4 \end{array}$	O 2	${ m S} { m 2}$	0	0

• Molecule 6 is 1,2-ETHANEDIOL (three-letter code: EDO) (formula:  $C_2H_6O_2$ ).





Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
6	В	1	$\begin{array}{ccc} \text{Total} & \text{C} & \text{O} \\ 4 & 2 & 2 \end{array}$	0	0
6	D	1	$\begin{array}{ccc} \text{Total} & \text{C} & \text{O} \\ 4 & 2 & 2 \end{array}$	0	0
6	D	1	$\begin{array}{ccc} \text{Total} & \text{C} & \text{O} \\ 4 & 2 & 2 \end{array}$	0	0
6	Е	1	$\begin{array}{ccc} \text{Total}  \text{C}  \text{O} \\ 4  2  2 \end{array}$	0	0
6	Е	1	$\begin{array}{ccc} \text{Total} & \text{C} & \text{O} \\ 4 & 2 & 2 \end{array}$	0	0
6	F	1	$\begin{array}{ccc} \text{Total} & \text{C} & \text{O} \\ 4 & 2 & 2 \end{array}$	0	0
6	Н	1	$\begin{array}{ccc} \text{Total} & \text{C} & \text{O} \\ 4 & 2 & 2 \end{array}$	0	0

• Molecule 7 is ISOPROPYL ALCOHOL (three-letter code: IPA) (formula: C<sub>3</sub>H<sub>8</sub>O).





Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
7	С	1	$\begin{array}{ccc} \text{Total}  \text{C}  \text{O} \\ 4  3  1 \end{array}$	0	0
7	D	1	$\begin{array}{ccc} \text{Total}  \text{C}  \text{O} \\ 4  3  1 \end{array}$	0	0
7	Е	1	$\begin{array}{ccc} \text{Total}  \text{C}  \text{O} \\ 4  3  1 \end{array}$	0	0
7	F	1	$\begin{array}{ccc} \text{Total}  \text{C}  \text{O} \\ 4  3  1 \end{array}$	0	0
7	F	1	$\begin{array}{ccc} \text{Total} & \text{C} & \text{O} \\ 4 & 3 & 1 \end{array}$	0	0
7	F	1	$\begin{array}{ccc} \text{Total}  \text{C}  \text{O} \\ 4  3  1 \end{array}$	0	0

• Molecule 8 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
8	А	20	TotalO2020	0	0
8	В	34	Total O 34 34	0	0
8	С	30	Total O 30 30	0	0
8	D	17	Total O 17 17	0	0
8	Е	26	Total O 26 26	0	0
8	F	20	$\begin{array}{cc} \text{Total} & \text{O} \\ 20 & 20 \end{array}$	0	0



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Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
8	G	21	Total O 21 21	0	0
8	Н	27	$\begin{array}{cc} \text{Total} & \text{O} \\ 27 & 27 \end{array}$	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: SWI5-dependent HO expression protein 3

• Molecule 1: SWI5-dependent HO expression protein 3









 $\bullet$  Molecule 1: SWI5-dependent HO expression protein 3



• Molecule 1: SWI5-dependent HO expression protein 3



• Molecule 1: SWI5-dependent HO expression protein 3



# 4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 1	Depositor
Cell constants	28.07Å $49.58$ Å $149.95$ Å	Denesitor
a, b, c, $\alpha$ , $\beta$ , $\gamma$	$89.96^{\circ}$ $84.67^{\circ}$ $89.98^{\circ}$	Depositor
$\mathbf{P}_{\text{assolution}}(\hat{\mathbf{A}})$	29.86 - 2.31	Depositor
Resolution (A)	29.86 - 2.31	EDS
% Data completeness	78.7 (29.86-2.31)	Depositor
(in resolution range)	90.1 (29.86-2.31)	EDS
R <sub>merge</sub>	(Not available)	Depositor
R <sub>sym</sub>	(Not available)	Depositor
$< I/\sigma(I) > 1$	$3.00 (at 2.31 \text{\AA})$	Xtriage
Refinement program	CNS	Depositor
B B.	0.231 , $0.264$	Depositor
It, Itfree	0.225 , $0.232$	DCC
$R_{free}$ test set	3438 reflections $(9.98\%)$	wwPDB-VP
Wilson B-factor $(Å^2)$	30.1	Xtriage
Anisotropy	0.681	Xtriage
Bulk solvent $k_{sol}(e/Å^3), B_{sol}(Å^2)$	0.30 , $56.2$	EDS
L-test for $twinning^2$	$< L >=0.53, < L^2>=0.37$	Xtriage
	0.447 for h,-k,h-l	
Estimated twinning fraction	0.447 for -h,k,-l	Xtriage
	$0.458 { m ~for ~-h,-k,-h+l}$	
$F_o, F_c$ correlation	0.94	EDS
Total number of atoms	6422	wwPDB-VP
Average B, all atoms $(Å^2)$	76.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: The analyses of the Patterson function reveals a significant off-origin peak that is 30.00 % of the origin peak, indicating pseudo-translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo-translational symmetry is equal to 1.4094e-03. The detected translational NCS is most likely also responsible for the elevated intensity ratio.

<sup>&</sup>lt;sup>2</sup>Theoretical values of  $\langle |L| \rangle$ ,  $\langle L^2 \rangle$  for a centric 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: PT, DTT, EDO, SO4, DY, IPA

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	Bond angles		
	Unam	RMSZ	# Z  > 5	RMSZ	# Z  > 5	
1	А	0.45	0/781	0.69	2/1041~(0.2%)	
1	В	0.32	0/734	0.55	0/978	
1	С	0.35	0/749	0.52	0/998	
1	D	0.33	0/757	0.58	0/1009	
1	Е	0.34	0/749	0.61	0/998	
1	F	0.33	0/757	0.55	1/1009~(0.1%)	
1	G	0.36	0/726	0.57	0/967	
1	Н	0.34	0/757	0.60	0/1009	
All	All	0.36	0/6010	0.59	3/8009~(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	F	136	LEU	CA-CB-CG	7.22	131.91	115.30
1	А	44	ARG	NE-CZ-NH1	6.21	123.41	120.30
1	А	44	ARG	NE-CZ-NH2	-5.51	117.55	120.30

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.



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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	А	778	0	803	88	0
1	В	731	0	754	77	0
1	С	746	0	765	69	1
1	D	754	0	776	87	0
1	Е	746	0	765	64	0
1	F	754	0	776	82	0
1	G	723	0	743	72	0
1	Н	754	0	776	63	1
2	А	5	0	0	0	0
2	В	3	0	0	0	0
2	С	5	0	0	0	1
2	D	3	0	0	0	0
2	Е	6	0	0	0	0
2	F	3	0	0	0	0
2	G	2	0	0	0	0
2	Н	3	0	0	0	1
3	А	30	0	0	2	0
3	В	20	0	0	0	0
3	С	35	0	0	1	0
3	D	10	0	0	1	0
3	Ε	5	0	0	0	0
3	F	5	0	0	1	0
3	G	30	0	0	0	0
3	Н	10	0	0	0	0
4	А	1	0	0	0	0
4	В	1	0	0	0	0
4	С	1	0	0	0	0
4	D	1	0	0	0	0
4	Ε	1	0	0	0	0
4	G	1	0	0	0	0
5	А	8	0	10	9	0
6	В	4	0	6	0	0
6	D	8	0	12	1	0
6	Е	8	0	12	1	0
6	F	4	0	6	2	0
6	Н	4	0	6	2	0
7	С	4	0	8	0	0
7	D	4	0	8	3	0
7	E	4	0	8	1	0
7	F	12	0	24	8	0
8	A	20	0	0	0	0
8	B	34	0	0	5	0
8	С	30	0	0	2	0



• • • • • •											
Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes					
8	D	17	0	0	0	0					
8	Ε	26	0	0	1	0					
8	F	20	0	0	2	0					
8	G	21	0	0	2	0					
8	Н	27	0	0	1	0					
All	All	6422	0	6258	433	2					

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 35.

All (433) 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:121:ASN:HB3	5:A:212:DTT:O2	1.42	1.15
1:F:63:LEU:HB3	1:G:63:LEU:HB3	1.38	1.06
1:F:56:LEU:HD23	1:G:56:LEU:HB2	1.34	1.05
1:A:56:LEU:HD23	1:C:56:LEU:HB3	1.39	1.02
1:C:92:LYS:HG2	1:G:127:LYS:NZ	1.74	1.01
1:A:65:THR:HA	1:A:68:GLN:HG3	1.44	0.99
1:A:121:ASN:CB	5:A:212:DTT:O2	2.15	0.95
1:C:96:GLU:HG3	1:G:127:LYS:HE2	1.49	0.94
1:A:69:ASN:HD21	1:A:70:LEU:HG	1.34	0.92
1:F:53:ILE:HG23	1:G:56:LEU:HD11	1.51	0.92
1:G:53:ILE:HD12	1:G:53:ILE:H	1.35	0.92
1:F:70:LEU:HB2	1:G:70:LEU:HD13	1.50	0.92
1:B:56:LEU:HD23	1:D:56:LEU:CB	2.00	0.91
1:B:56:LEU:CD2	1:D:56:LEU:HB2	2.00	0.91
1:B:56:LEU:HD23	1:D:56:LEU:HB2	1.52	0.91
1:E:84:LEU:HD13	1:H:84:LEU:HD23	1.54	0.89
1:A:81:GLU:O	1:A:85:LEU:HG	1.73	0.88
1:C:92:LYS:HG2	1:G:127:LYS:HZ3	1.31	0.88
1:A:77:ALA:HA	1:A:80:LYS:NZ	1.89	0.87
1:A:69:ASN:ND2	1:A:70:LEU:HG	1.89	0.87
1:F:70:LEU:HD22	1:G:74:LEU:HD11	1.56	0.86
1:C:57:THR:HA	1:C:60:ASN:ND2	1.91	0.85
1:E:58:LYS:O	1:E:62:GLN:HG2	1.77	0.85
1:G:84:LEU:O	1:G:88:LEU:HD13	1.77	0.85
1:A:77:ALA:HA	1:A:80:LYS:HZ3	1.44	0.83
1:B:70:LEU:HB2	1:D:70:LEU:HD23	1.59	0.82
1:C:61:LEU:O	1:C:64:THR:HG22	1.79	0.82
1:B:131:ASP:OD1	1:E:92:LYS:HE3	1.80	0.82



		Interatomic	Clash
Atom-1	Atom-2	distance (Å)	overlap (Å)
1:G:53:ILE:HD12	1:G:53:ILE:N	1.95	0.80
1:D:69:ASN:OD1	1:D:70:LEU:HD13	1.80	0.80
1:F:86:GLU:O	1:F:90:LEU:HD13	1.80	0.80
1:B:63:LEU:HB3	1:D:63:LEU:HB3	1.64	0.80
1:F:66:GLN:HA	1:F:69:ASN:ND2	1.96	0.79
1:D:64:THR:HG22	1:D:68:GLN:HE21	1.46	0.79
1:G:83:LYS:HB3	8:G:305:HOH:O	1.81	0.78
1:A:45:VAL:HG23	1:A:46:ILE:HG13	1.63	0.78
1:C:131:ASP:OD1	1:G:92:LYS:HG3	1.83	0.78
1:H:59:THR:O	1:H:63:LEU:HD13	1.84	0.77
1:D:92:LYS:HE3	1:H:131:ASP:OD1	1.85	0.77
1:G:50:HIS:HA	1:G:53:ILE:HD13	1.67	0.77
1:B:127:LYS:HE3	1:E:96:GLU:HB2	1.68	0.76
1:C:96:GLU:CG	1:G:127:LYS:HE2	2.15	0.76
1:D:66:GLN:HA	1:D:69:ASN:HD21	1.50	0.75
1:D:109:LEU:HD11	1:H:109:LEU:HD11	1.67	0.75
1:G:53:ILE:H	1:G:53:ILE:CD1	1.99	0.75
1:F:97:ASN:HA	7:F:206:IPA:H13	1.67	0.74
1:A:43:SER:N	1:A:45:VAL:HG22	2.02	0.74
1:B:70:LEU:HB3	1:D:70:LEU:HB3	1.70	0.74
1:B:74:LEU:HD21	1:D:73:LYS:HB3	1.67	0.74
1:B:74:LEU:HD11	1:D:73:LYS:HB2	1.69	0.74
1:C:109:LEU:HD21	1:G:109:LEU:HD11	1.69	0.74
1:E:72:SER:HA	1:E:75:GLU:OE1	1.87	0.73
1:E:56:LEU:HD13	1:H:57:THR:HG22	1.70	0.73
1:F:60:ASN:OD1	1:G:60:ASN:HA	1.86	0.73
1:A:86:GLU:O	1:A:90:LEU:HD12	1.88	0.73
1:H:132:GLN:HA	1:H:135:LYS:HE3	1.71	0.73
1:A:121:ASN:HB3	5:A:212:DTT:HO2	1.53	0.72
1:B:124:ASN:O	1:B:128:GLU:HG3	1.89	0.72
1:C:59:THR:O	1:C:63:LEU:HG	1.89	0.72
1:F:124:ASN:O	1:F:128:GLU:HG3	1.90	0.72
1:H:53:ILE:O	1:H:57:THR:HG23	1.90	0.71
1:H:84:LEU:O	1:H:88:LEU:HG	1.89	0.71
1:B:60:ASN:OD1	1:D:63:LEU:HD22	1.90	0.71
1:C:84:LEU:O	1:C:88:LEU:HG	1.91	0.71
1:H:50:HIS:O	1:H:53:ILE:HG22	1.91	0.71
1:B:56:LEU:HD23	1:D:56:LEU:HB3	1.73	0.70
1:A:56:LEU:HB3	1:C:56:LEU:HD23	1.73	0.70
1:F:66:GLN:HA	1:F:69:ASN:HD21	1.56	0.70
1:B:56:LEU:HD21	1:D:57:THR:N	2.05	0.70



	hi o	Interatomic	Clash
Atom-1	Atom-2	distance (Å)	overlap (Å)
1:A:69:ASN:HD22	1:A:70:LEU:N	1.88	0.70
1:E:56:LEU:HD13	1:H:57:THR:CG2	2.22	0.70
1:F:53:ILE:HG12	1:G:53:ILE:HG13	1.74	0.70
1:C:104:ARG:HD2	3:C:209:SO4:O2	1.92	0.70
1:E:73:LYS:HA	1:E:76:LEU:HD12	1.72	0.70
1:A:82:SER:HA	1:A:85:LEU:HD12	1.74	0.69
1:A:64:THR:O	1:A:68:GLN:HG2	1.91	0.69
1:H:81:GLU:O	1:H:85:LEU:HG	1.92	0.69
1:B:67:SER:HB2	1:D:66:GLN:HB3	1.74	0.69
1:C:101:ILE:HG21	7:F:208:IPA:H32	1.73	0.69
1:B:64:THR:OG1	1:D:63:LEU:HD21	1.93	0.69
1:F:63:LEU:HD22	1:G:60:ASN:OD1	1.93	0.68
1:F:107:LYS:O	1:F:111:GLU:HG3	1.93	0.68
1:B:136:LEU:HD23	1:B:136:LEU:H	1.59	0.68
1:C:57:THR:HA	1:C:60:ASN:HD21	1.58	0.68
1:B:85:LEU:HD12	8:B:311:HOH:O	1.93	0.68
1:C:66:GLN:O	1:C:70:LEU:HG	1.94	0.68
1:B:56:LEU:CD2	1:D:56:LEU:CB	2.67	0.67
1:H:63:LEU:O	1:H:66:GLN:HB3	1.94	0.67
1:A:49:LEU:HD21	1:C:49:LEU:HB2	1.77	0.67
1:A:127:LYS:HG3	1:F:95:ASN:ND2	2.08	0.67
1:A:46:ILE:O	1:A:49:LEU:HB3	1.95	0.67
1:D:90:LEU:O	1:D:94:GLU:HG3	1.95	0.67
1:F:96:GLU:HG3	7:F:206:IPA:H32	1.76	0.67
1:B:74:LEU:HD21	1:D:73:LYS:CB	2.23	0.67
1:H:47:GLU:HG2	1:H:48:SER:N	2.08	0.67
1:C:92:LYS:HZ2	1:C:92:LYS:HB3	1.60	0.66
1:F:121:ASN:O	1:F:125:GLU:HG2	1.95	0.66
1:A:130:MET:HE2	1:A:133:LEU:HD12	1.77	0.66
1:F:119:LEU:HB2	7:F:208:IPA:H31	1.77	0.66
1:E:136:LEU:HD12	1:F:122:ARG:CD	2.26	0.66
1:A:94:GLU:HB3	1:G:126:GLN:NE2	2.11	0.66
1:H:78:GLN:O	1:H:81:GLU:N	2.29	0.66
1:B:74:LEU:HD11	1:D:73:LYS:CB	2.26	0.65
1:B:134:SER:OG	1:E:85:LEU:HD11	1.97	0.65
1:F:97:ASN:CA	7:F:206:IPA:H13	2.27	0.65
1:H:54:ASP:O	1:H:58:LYS:HG3	1.96	0.65
1:E:66:GLN:O	1:E:70:LEU:HG	1.97	0.64
1:A:71:LEU:O	1:A:75:GLU:HG3	1.98	0.64
1:C:49:LEU:HD23	1:C:52:GLN:NE2	2.11	0.64
1:B:53:ILE:HG23	1:D:56:LEU:HD11	1.79	0.64



Interatomic Clash				
Atom-1	Atom-2	distance (Å)	overlap (Å)	
1:B:56:LEU:HD21	1:D:56:LEU:C	2.18	0.64	
1:A:73:LYS:O	1:A:76:LEU:N	2.30	0.64	
1:A:109:LEU:HD11	1:F:109:LEU:HD11	1.81	0.63	
1:E:136:LEU:HD12	1:F:122:ARG:HD2	1.80	0.63	
1:F:49:LEU:HD22	1:G:53:ILE:HD11	1.80	0.63	
1:B:49:LEU:HB3	1:D:49:LEU:HD21	1.80	0.63	
1:G:50:HIS:CA	1:G:53:ILE:HD13	2.27	0.63	
1:H:132:GLN:HG3	1:H:135:LYS:HE3	1.79	0.63	
1:A:69:ASN:ND2	1:A:70:LEU:N	2.46	0.63	
1:C:131:ASP:OD1	1:G:92:LYS:HE3	1.99	0.63	
1:E:132:GLN:OE1	1:F:118:GLU:HG3	1.99	0.62	
1:D:78:GLN:O	1:D:81:GLU:HB3	1.99	0.62	
1:A:84:LEU:HD13	1:C:84:LEU:CD2	2.30	0.62	
1:D:97:ASN:HB2	6:D:207:EDO:H11	1.81	0.62	
1:H:132:GLN:HG3	1:H:135:LYS:CE	2.29	0.62	
1:A:98:LEU:HD21	1:G:122:ARG:HD2	1.82	0.62	
1:F:63:LEU:HD21	1:G:64:THR:OG1	1.99	0.62	
1:A:49:LEU:HD21	1:C:49:LEU:CB	2.30	0.61	
1:F:128:GLU:HA	1:F:131:ASP:OD2	1.99	0.61	
1:B:82:SER:HA	8:B:311:HOH:O	2.00	0.61	
1:F:104:ARG:HH11	6:F:205:EDO:H22	1.65	0.61	
1:B:127:LYS:HG2	1:E:95:ASN:HD22	1.64	0.61	
1:C:84:LEU:CD1	1:F:133:LEU:HD21	2.30	0.61	
1:A:54:ASP:O	1:A:58:LYS:HG3	2.01	0.61	
1:A:84:LEU:HD13	1:C:84:LEU:HD23	1.83	0.61	
1:B:109:LEU:HD11	1:E:109:LEU:HD11	1.81	0.61	
1:B:49:LEU:HB3	1:D:49:LEU:CD2	2.31	0.61	
1:G:70:LEU:O	1:G:74:LEU:HG	2.00	0.60	
1:C:96:GLU:HG3	1:G:127:LYS:CE	2.28	0.60	
1:A:45:VAL:HG23	1:A:46:ILE:H	1.66	0.60	
1:F:47:GLU:HG3	1:F:48:SER:N	2.16	0.60	
1:D:62:GLN:HA	1:D:65:THR:HG23	1.84	0.59	
1:E:125:GLU:OE1	1:E:125:GLU:HA	2.00	0.59	
1:B:127:LYS:O	1:B:127:LYS:HD3	2.02	0.59	
1:D:127:LYS:HE2	1:H:96:GLU:OE1	2.01	0.59	
1:A:60:ASN:O	1:A:64:THR:HG23	2.02	0.59	
1:A:121:ASN:O	5:A:212:DTT:O3	2.18	0.59	
1:A:77:ALA:HA	1:A:80:LYS:HZ1	1.67	0.59	
1:D:112:LEU:HD22	1:D:116:TYR:CE2	2.37	0.59	
1:E:59:THR:O	1:E:63:LEU:HD13	2.03	0.59	
1:F:70:LEU:HD12	1:G:70:LEU:HB2	1.84	0.59	



Interatomic Clash				
Atom-1	Atom-2	distance (Å)	overlap (Å)	
1:D:66:GLN:HA	1:D:69:ASN:ND2	2.17	0.59	
1:A:59:THR:O	1:A:63:LEU:HD13	2.03	0.58	
1:A:114:LYS:O	1:A:118:GLU:HG3	2.03	0.58	
1:C:134:SER:O	1:C:135:LYS:HB2	2.04	0.58	
1:E:67:SER:O	1:E:71:LEU:HG	2.04	0.58	
1:A:45:VAL:HG23	1:A:46:ILE:N	2.18	0.58	
1:B:63:LEU:HD21	1:D:64:THR:OG1	2.04	0.58	
1:E:79:SER:O	1:E:83:LYS:HD3	2.04	0.57	
1:C:92:LYS:HD2	1:G:131:ASP:HA	1.86	0.57	
1:A:66:GLN:O	1:A:70:LEU:HD12	2.04	0.57	
1:A:92:LYS:HE3	1:F:131:ASP:OD1	2.03	0.57	
1:B:108:LYS:HD3	1:H:112:LEU:HD13	1.86	0.57	
1:F:56:LEU:CD2	1:G:56:LEU:HB2	2.23	0.57	
1:B:110:LYS:HA	1:E:113:GLU:OE1	2.05	0.57	
1:A:135:LYS:HE3	1:B:118:GLU:OE1	2.05	0.57	
1:B:92:LYS:NZ	1:E:131:ASP:OD2	2.38	0.57	
1:D:49:LEU:HD23	1:D:49:LEU:O	2.05	0.57	
1:G:64:THR:O	1:G:68:GLN:HG3	2.05	0.57	
1:H:104:ARG:HH12	6:H:206:EDO:H22	1.69	0.57	
1:E:74:LEU:O	1:E:77:ALA:HB3	2.04	0.57	
1:A:113:GLU:OE2	1:F:110:LYS:HA	2.04	0.56	
1:B:74:LEU:HG	1:D:74:LEU:HD22	1.87	0.56	
1:D:132:GLN:HA	1:D:132:GLN:NE2	2.20	0.56	
1:F:53:ILE:CG1	1:G:53:ILE:HG13	2.34	0.56	
1:E:60:ASN:HB2	1:H:60:ASN:OD1	2.05	0.56	
1:B:113:GLU:HB3	1:E:113:GLU:OE1	2.06	0.56	
1:A:88:LEU:HD13	1:F:133:LEU:HD22	1.88	0.56	
1:A:121:ASN:HA	5:A:212:DTT:O3	2.06	0.56	
1:E:63:LEU:HA	1:E:66:GLN:HG3	1.86	0.56	
1:D:92:LYS:CE	1:H:131:ASP:HA	2.36	0.55	
1:B:53:ILE:HG23	1:D:56:LEU:CD1	2.36	0.55	
1:B:108:LYS:HD3	1:H:112:LEU:CD1	2.36	0.55	
1:H:135:LYS:HB3	1:H:136:LEU:HD23	1.89	0.55	
1:A:66:GLN:O	1:A:69:ASN:ND2	2.38	0.55	
1:F:63:LEU:HB3	1:G:63:LEU:CB	2.26	0.55	
1:A:49:LEU:HD23	1:C:49:LEU:HD12	1.89	0.55	
1:A:70:LEU:HD13	1:C:70:LEU:HD12	1.88	0.55	
1:F:64:THR:OG1	1:G:63:LEU:HD21	2.06	0.55	
1:A:96:GLU:HG2	1:F:127:LYS:HE3	1.87	0.55	
1:E:56:LEU:HD12	1:H:53:ILE:HG13	1.87	0.55	
1:D:132:GLN:O	1:D:136:LEU:HD12	2.07	0.55	



		Interatomic	Clash
Atom-1	Atom-2	distance (Å)	overlap (Å)
1:D:63:LEU:O	1:D:66:GLN:HB2	2.08	0.54
1:D:135:LYS:NZ	1:D:135:LYS:HB3	2.22	0.54
1:E:73:LYS:HA	1:E:76:LEU:CD1	2.38	0.54
1:A:56:LEU:HD23	1:C:56:LEU:CB	2.26	0.54
1:B:84:LEU:HD21	1:D:84:LEU:HD22	1.88	0.54
1:D:132:GLN:HA	1:D:132:GLN:HE21	1.72	0.54
1:A:53:ILE:HD13	1:C:53:ILE:HD13	1.89	0.54
1:B:53:ILE:CD1	1:D:53:ILE:HG12	2.38	0.54
1:H:118:GLU:O	1:H:122:ARG:HG3	2.08	0.54
1:A:70:LEU:HB2	1:C:70:LEU:HD13	1.90	0.54
1:C:80:LYS:HD2	1:C:80:LYS:N	2.23	0.53
1:C:91:LEU:HD23	1:F:130:MET:CE	2.39	0.53
1:B:60:ASN:O	1:D:63:LEU:HD23	2.08	0.53
1:B:127:LYS:HG2	1:E:95:ASN:ND2	2.23	0.53
1:A:125:GLU:HB2	5:A:212:DTT:H11	1.91	0.53
1:H:84:LEU:HG	1:H:88:LEU:HD11	1.91	0.53
1:A:112:LEU:HG	3:A:209:SO4:O4	2.08	0.53
1:A:130:MET:HG2	1:G:91:LEU:HD13	1.91	0.53
1:C:92:LYS:HB3	1:C:92:LYS:NZ	2.22	0.53
1:D:69:ASN:OD1	1:D:70:LEU:N	2.41	0.53
8:C:327:HOH:O	1:F:95:ASN:HB2	2.09	0.52
1:F:70:LEU:CD1	1:G:70:LEU:HB2	2.39	0.52
1:F:136:LEU:C	1:F:136:LEU:HD13	2.30	0.52
1:G:128:GLU:O	1:G:132:GLN:HG2	2.10	0.52
1:F:60:ASN:OD1	1:G:63:LEU:HD22	2.09	0.52
1:A:56:LEU:HB3	1:C:56:LEU:CD2	2.38	0.52
1:E:82:SER:O	1:E:86:GLU:HG3	2.09	0.52
1:F:114:LYS:HE2	8:F:314:HOH:O	2.09	0.52
1:E:132:GLN:HB2	8:E:321:HOH:O	2.09	0.52
1:F:67:SER:HA	1:G:70:LEU:HD12	1.92	0.52
1:D:110:LYS:HE2	8:H:325:HOH:O	2.09	0.52
1:E:70:LEU:N	1:E:70:LEU:HD23	2.24	0.52
5:A:212:DTT:H41	1:B:110:LYS:HZ2	1.75	0.52
1:B:63:LEU:HD23	1:D:64:THR:N	2.24	0.52
1:C:49:LEU:HD23	1:C:52:GLN:HE22	1.73	0.52
1:C:60:ASN:OD1	1:C:61:LEU:N	2.43	0.52
3:D:204:SO4:O3	7:E:210:IPA:H11	2.10	0.51
1:F:58:LYS:O	1:F:62:GLN:HG2	2.09	0.51
1:E:84:LEU:O	1:E:88:LEU:HG	2.10	0.51
1:A:51:ASP:HA	1:A:54:ASP:OD2	2.10	0.51
1:A:96:GLU:OE1	1:A:96:GLU:HA	2.11	0.51



		Interatomic	Clash
Atom-1	Atom-2	distance (Å)	overlap (Å)
1:A:127:LYS:HG3	1:F:95:ASN:HD22	1.73	0.51
1:D:46:ILE:HG22	1:D:46:ILE:O	2.10	0.51
1:E:62:GLN:O	1:E:65:THR:OG1	2.29	0.51
1:E:71:LEU:O	1:E:75:GLU:HG3	2.11	0.51
1:F:70:LEU:HB3	1:G:70:LEU:HB3	1.92	0.51
1:A:69:ASN:HD22	1:A:70:LEU:H	1.59	0.51
1:A:112:LEU:HD22	1:A:116:TYR:CE2	2.46	0.51
1:B:91:LEU:HD23	1:H:130:MET:CE	2.41	0.51
1:C:69:ASN:O	1:C:73:LYS:HG2	2.11	0.51
1:F:128:GLU:O	1:F:132:GLN:HG2	2.11	0.51
1:B:70:LEU:HB2	1:D:70:LEU:CD2	2.36	0.51
1:C:104:ARG:NH1	8:C:322:HOH:O	2.44	0.51
1:E:60:ASN:N	1:H:60:ASN:HD21	2.08	0.51
1:E:89:ASN:HA	1:E:92:LYS:HB3	1.93	0.51
1:F:56:LEU:HD21	1:G:57:THR:OG1	2.11	0.51
1:A:121:ASN:OD1	5:A:212:DTT:H42	2.11	0.50
1:H:99:ASN:O	1:H:103:GLU:HG3	2.11	0.50
1:B:57:THR:O	1:B:61:LEU:HG	2.11	0.50
1:E:135:LYS:HG3	1:E:136:LEU:H	1.75	0.50
1:B:70:LEU:CB	1:D:70:LEU:HB3	2.41	0.50
1:D:83:LYS:O	1:D:87:ASN:ND2	2.45	0.50
1:E:135:LYS:HG3	1:E:136:LEU:N	2.27	0.50
1:G:124:ASN:O	1:G:128:GLU:HG3	2.12	0.49
1:C:101:ILE:O	1:C:105:LYS:HG2	2.12	0.49
1:H:101:ILE:O	1:H:105:LYS:HG2	2.12	0.49
1:D:49:LEU:O	1:D:53:ILE:HG13	2.13	0.49
1:E:61:LEU:HD23	1:E:61:LEU:O	2.13	0.49
1:F:107:LYS:HE2	8:F:319:HOH:O	2.12	0.49
1:H:127:LYS:O	1:H:127:LYS:HD3	2.12	0.49
1:F:63:LEU:HD23	1:G:60:ASN:O	2.12	0.49
1:A:80:LYS:CE	1:C:81:GLU:OE2	2.61	0.49
1:B:73:LYS:HG2	1:D:74:LEU:HD11	1.94	0.49
1:B:77:ALA:O	1:B:80:LYS:HB3	2.13	0.49
1:F:53:ILE:HG23	1:G:56:LEU:CD1	2.33	0.49
1:C:78:GLN:HA	1:C:78:GLN:NE2	2.27	0.49
1:F:100:SER:OG	6:F:205:EDO:H21	2.13	0.49
1:F:133:LEU:C	1:F:133:LEU:HD23	2.33	0.49
1:B:91:LEU:HD23	1:H:130:MET:HE1	1.94	0.48
1:H:78:GLN:O	1:H:80:LYS:N	2.46	0.48
1:H:135:LYS:C	1:H:136:LEU:HD23	2.33	0.48
1:B:53:ILE:HG12	1:D:53:ILE:HG12	1.95	0.48



	lous pagem	Interatomic	Clash
Atom-1	Atom-2	distance (Å)	overlap (Å)
1:B:76:LEU:C	1:B:76:LEU:HD12	2.34	0.48
1:B:85:LEU:O	1:B:89:ASN:ND2	2.46	0.48
1:E:72:SER:O	1:E:76:LEU:HG	2.14	0.48
1:D:127:LYS:CE	1:H:96:GLU:HB2	2.44	0.48
1:A:56:LEU:CD2	1:C:56:LEU:HB3	2.27	0.48
1:B:64:THR:HG22	1:B:68:GLN:HE21	1.78	0.48
1:B:110:LYS:NZ	1:E:117:SER:OG	2.40	0.48
1:C:84:LEU:HD11	1:F:133:LEU:HD21	1.95	0.48
1:A:87:ASN:HA	1:A:90:LEU:HD13	1.95	0.48
1:D:69:ASN:O	1:D:73:LYS:HG2	2.14	0.48
1:D:91:LEU:HD23	1:E:130:MET:HE2	1.95	0.47
1:A:111:GLU:HB2	3:A:209:SO4:O1	2.14	0.47
1:D:70:LEU:O	1:D:74:LEU:HD23	2.14	0.47
1:C:119:LEU:HD22	1:C:123:TYR:CE2	2.49	0.47
1:D:94:GLU:HB3	7:D:209:IPA:C3	2.44	0.47
1:B:76:LEU:HG	1:B:77:ALA:N	2.29	0.47
1:B:59:THR:O	1:B:63:LEU:HD13	2.14	0.47
1:F:56:LEU:HD12	1:F:56:LEU:HA	1.72	0.47
1:D:94:GLU:HA	7:D:209:IPA:H13	1.97	0.47
1:C:61:LEU:HD23	1:C:61:LEU:C	2.35	0.47
1:C:94:GLU:HB3	1:F:126:GLN:NE2	2.28	0.47
1:E:87:ASN:HA	1:E:90:LEU:HD12	1.97	0.47
1:C:113:GLU:OE2	1:G:110:LYS:HA	2.14	0.47
1:D:92:LYS:NZ	1:H:131:ASP:HA	2.30	0.47
1:B:74:LEU:CD2	1:D:73:LYS:HB3	2.40	0.47
1:C:110:LYS:HD3	1:G:113:GLU:CD	2.34	0.47
1:B:64:THR:OG1	1:D:63:LEU:CD2	2.61	0.47
1:A:133:LEU:HD13	1:G:88:LEU:HD12	1.96	0.46
1:D:101:ILE:HG21	6:E:208:EDO:H12	1.97	0.46
1:D:127:LYS:HE2	1:H:96:GLU:HB2	1.97	0.46
1:D:91:LEU:HD23	1:E:130:MET:CE	2.44	0.46
1:D:134:SER:C	1:D:136:LEU:N	2.67	0.46
1:F:97:ASN:O	1:F:101:ILE:HG13	2.15	0.46
1:G:61:LEU:HD13	1:G:61:LEU:C	2.35	0.46
1:A:92:LYS:CE	1:F:131:ASP:OD1	2.63	0.46
1:A:80:LYS:NZ	1:A:80:LYS:HB3	2.30	0.46
1:G:114:LYS:O	1:G:114:LYS:HG3	2.14	0.46
1:H:57:THR:O	1:H:61:LEU:HG	2.16	0.46
1:H:69:ASN:OD1	1:H:70:LEU:HD12	2.16	0.46
1:A:46:ILE:HG22	1:A:50:HIS:CD2	2.51	0.46
1:B:84:LEU:O	1:B:88:LEU:HB2	2.16	0.46



		Interatomic	Clash
Atom-1	Atom-2	distance (Å)	overlap (Å)
1:F:49:LEU:HD22	1:G:53:ILE:CD1	2.45	0.46
1:C:50:HIS:ND1	1:C:50:HIS:C	2.69	0.46
1:A:69:ASN:ND2	1:A:69:ASN:C	2.67	0.46
1:F:60:ASN:HA	1:G:60:ASN:OD1	2.15	0.46
1:H:66:GLN:O	1:H:69:ASN:HB3	2.16	0.46
1:A:73:LYS:O	1:A:74:LEU:C	2.54	0.46
1:E:132:GLN:CG	1:F:121:ASN:OD1	2.64	0.46
1:B:110:LYS:HD2	8:B:313:HOH:O	2.17	0.45
1:B:134:SER:OG	1:E:85:LEU:CD1	2.64	0.45
1:A:72:SER:O	1:A:76:LEU:HG	2.17	0.45
1:B:53:ILE:HD13	1:D:53:ILE:HA	1.99	0.45
1:H:135:LYS:O	1:H:136:LEU:O	2.35	0.45
1:D:127:LYS:NZ	1:H:96:GLU:HB2	2.31	0.45
1:H:78:GLN:O	1:H:79:SER:C	2.55	0.45
1:A:121:ASN:CG	5:A:212:DTT:O2	2.56	0.45
1:E:136:LEU:CD1	1:F:122:ARG:HD2	2.46	0.45
1:C:131:ASP:O	1:C:135:LYS:N	2.49	0.45
1:F:81:GLU:O	1:F:85:LEU:HG	2.17	0.45
8:B:309:HOH:O	1:E:103:GLU:HG2	2.17	0.44
1:C:131:ASP:CG	1:G:92:LYS:HE3	2.37	0.44
1:E:70:LEU:HD13	1:H:71:LEU:CD2	2.47	0.44
1:F:97:ASN:CB	7:F:206:IPA:H13	2.46	0.44
1:E:63:LEU:HG	1:E:66:GLN:OE1	2.17	0.44
1:F:106:ASN:O	1:F:110:LYS:HG3	2.17	0.44
1:A:54:ASP:OD1	1:A:55:MET:N	2.51	0.44
1:E:73:LYS:O	1:E:76:LEU:HB2	2.17	0.44
1:G:135:LYS:HA	1:G:135:LYS:HD3	1.81	0.44
1:A:74:LEU:HD23	1:A:74:LEU:O	2.17	0.44
1:B:56:LEU:HD11	1:D:57:THR:HA	2.00	0.44
1:B:74:LEU:HD11	1:D:73:LYS:HG3	2.00	0.44
1:E:64:THR:HG22	1:E:64:THR:O	2.17	0.44
1:E:70:LEU:HB2	1:H:70:LEU:HD23	1.98	0.44
1:H:73:LYS:O	1:H:76:LEU:N	2.51	0.44
8:B:319:HOH:O	6:H:206:EDO:H12	2.16	0.44
1:E:53:ILE:HD12	1:H:49:LEU:HD11	1.99	0.44
1:B:53:ILE:HD13	1:D:56:LEU:HD12	1.99	0.44
1:E:129:LYS:O	1:E:133:LEU:HB2	2.18	0.44
1:F:97:ASN:HB2	7:F:206:IPA:H13	2.00	0.44
1:G:69:ASN:O	1:G:73:LYS:HG2	2.17	0.44
1:H:91:LEU:O	1:H:95:ASN:HB2	2.18	0.44
1:A:67:SER:HA	1:A:70:LEU:HD12	2.00	0.44



		Interatomic	Clash
Atom-1	Atom-2	distance (Å)	overlap (Å)
1:D:130:MET:O	1:D:133:LEU:HB2	2.18	0.44
1:E:60:ASN:CA	1:H:60:ASN:HD21	2.31	0.44
1:E:70:LEU:HD13	1:H:71:LEU:HD21	2.00	0.44
1:E:87:ASN:O	1:E:90:LEU:HB2	2.18	0.44
1:F:63:LEU:CD2	1:G:60:ASN:O	2.66	0.44
1:F:49:LEU:CD2	1:G:53:ILE:HG12	2.48	0.44
1:G:61:LEU:HD13	1:G:61:LEU:O	2.18	0.44
1:G:85:LEU:HD12	1:G:89:ASN:OD1	2.18	0.44
1:A:63:LEU:O	1:A:66:GLN:HB3	2.18	0.43
1:F:72:SER:O	1:F:76:LEU:HG	2.18	0.43
1:H:107:LYS:O	1:H:111:GLU:HG3	2.18	0.43
1:B:84:LEU:CD2	1:D:84:LEU:HD22	2.48	0.43
1:B:109:LEU:HB2	1:H:112:LEU:HD21	2.01	0.43
1:A:80:LYS:O	1:A:84:LEU:HB2	2.18	0.43
1:C:91:LEU:HD23	1:F:130:MET:HE1	1.99	0.43
1:B:58:LYS:O	1:B:62:GLN:HG2	2.18	0.43
1:C:92:LYS:CG	1:G:127:LYS:NZ	2.65	0.43
1:A:65:THR:CA	1:A:68:GLN:HG3	2.31	0.43
1:C:87:ASN:HB3	1:F:133:LEU:HD12	2.01	0.43
1:D:74:LEU:HD13	1:D:74:LEU:HA	1.92	0.43
1:E:53:ILE:HG12	1:H:53:ILE:HB	2.01	0.43
1:H:50:HIS:HA	1:H:53:ILE:HG22	1.99	0.43
1:E:61:LEU:HD23	1:E:61:LEU:C	2.39	0.43
1:H:83:LYS:HD2	1:H:83:LYS:HA	1.84	0.43
1:D:49:LEU:HD23	1:D:49:LEU:C	2.39	0.43
1:A:49:LEU:CD2	1:C:49:LEU:HD12	2.48	0.43
1:C:48:SER:O	1:C:52:GLN:HG3	2.19	0.42
1:D:105:LYS:NZ	1:E:115:ASP:OD2	2.46	0.42
1:E:56:LEU:HB2	1:H:56:LEU:CD2	2.49	0.42
1:C:92:LYS:HE2	1:G:131:ASP:OD1	2.20	0.42
1:D:80:LYS:HE3	1:D:80:LYS:HB2	1.70	0.42
1:H:59:THR:C	1:H:63:LEU:HD13	2.39	0.42
1:A:85:LEU:HG	1:A:85:LEU:H	1.68	0.42
1:A:46:ILE:HG22	1:A:50:HIS:NE2	2.34	0.42
1:B:55:MET:O	1:B:59:THR:HG23	2.20	0.42
1:C:92:LYS:HG3	1:G:130:MET:HG3	2.01	0.42
1:C:94:GLU:HB2	3:F:204:SO4:O2	2.19	0.42
1:G:62:GLN:O	1:G:66:GLN:HG2	2.19	0.42
1:G:110:LYS:HD2	8:G:310:HOH:O	2.20	0.42
1:A:47:GLU:HA	1:A:50:HIS:HD2	1.84	0.42
1:D:132:GLN:NE2	1:D:132:GLN:CA	2.81	0.42



		Interatomic	Clash
Atom-1	Atom-2	distance (Å)	overlap (Å)
1:F:70:LEU:HD22	1:G:74:LEU:CD1	2.39	0.42
1:H:110:LYS:O	1:H:113:GLU:HG2	2.19	0.42
1:A:80:LYS:HZ3	1:A:80:LYS:HB3	1.85	0.42
1:B:136:LEU:HD23	1:B:136:LEU:N	2.28	0.42
1:C:113:GLU:OE2	1:G:113:GLU:HB3	2.19	0.42
1:D:127:LYS:HZ1	1:H:96:GLU:HB2	1.85	0.42
1:F:49:LEU:O	1:F:53:ILE:HG13	2.20	0.42
1:F:69:ASN:OD1	1:F:70:LEU:N	2.53	0.42
1:D:91:LEU:CD2	1:E:130:MET:HE2	2.50	0.42
1:B:53:ILE:HD11	1:D:53:ILE:CG1	2.50	0.42
1:C:88:LEU:O	1:C:92:LYS:HB2	2.20	0.42
1:C:79:SER:O	1:C:83:LYS:HG2	2.19	0.41
1:H:46:ILE:O	1:H:49:LEU:HB3	2.20	0.41
1:A:56:LEU:CB	1:C:56:LEU:HD23	2.48	0.41
1:A:65:THR:O	1:A:68:GLN:HB2	2.21	0.41
1:C:92:LYS:HG3	1:G:130:MET:CG	2.50	0.41
1:D:91:LEU:HD12	1:D:91:LEU:HA	1.83	0.41
1:D:94:GLU:HB3	7:D:209:IPA:H33	2.01	0.41
1:F:111:GLU:O	1:F:114:LYS:HB3	2.21	0.41
1:A:88:LEU:HD11	1:C:84:LEU:HD11	2.03	0.41
1:B:91:LEU:HD12	1:B:91:LEU:HA	1.84	0.41
1:F:70:LEU:HB2	1:G:70:LEU:CD1	2.34	0.41
1:D:94:GLU:OE1	1:E:126:GLN:OE1	2.38	0.41
1:B:135:LYS:HD3	1:B:135:LYS:O	2.21	0.41
1:C:92:LYS:HZ2	1:C:92:LYS:CB	2.26	0.41
1:D:55:MET:O	1:D:59:THR:HG23	2.21	0.41
1:F:70:LEU:CB	1:G:70:LEU:HB3	2.51	0.41
1:F:96:GLU:HG3	7:F:206:IPA:C3	2.47	0.41
1:B:105:LYS:HE3	1:H:115:ASP:HB3	2.03	0.40
1:C:134:SER:O	1:C:135:LYS:CB	2.68	0.40
1:F:46:ILE:HG22	1:F:50:HIS:NE2	2.36	0.40
1:G:76:LEU:HD23	1:G:76:LEU:C	2.41	0.40
1:A:61:LEU:O	1:A:65:THR:HG23	2.21	0.40
1:F:56:LEU:HD22	1:G:53:ILE:HG23	2.03	0.40
1:G:134:SER:HB2	1:G:135:LYS:H	1.70	0.40
1:H:126:GLN:OE1	1:H:129:LYS:NZ	2.52	0.40

All (2) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.



Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:113:GLU:OE1	2:C:201[B]:DY:DY[1_565]	2.03	0.17
1:C:125:GLU:OE2	2:H:202:DY:DY[1_545]	2.10	0.10

### 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	А	92/96~(96%)	88~(96%)	4~(4%)	0	100 100
1	В	86/96~(90%)	82 (95%)	4(5%)	0	100 100
1	С	88/96~(92%)	88 (100%)	0	0	100 100
1	D	89/96~(93%)	87~(98%)	2(2%)	0	100 100
1	Е	88/96~(92%)	84 (96%)	4 (4%)	0	100 100
1	F	89/96~(93%)	89 (100%)	0	0	100 100
1	G	85/96~(88%)	82~(96%)	2(2%)	1 (1%)	13 13
1	Н	89/96~(93%)	85 (96%)	3(3%)	1 (1%)	14 15
All	All	706/768~(92%)	685~(97%)	19 (3%)	2 (0%)	41 50

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	G	135	LYS
1	Н	79	SER

#### 5.3.2 Protein sidechains (i)

In the following table, the Percentiles column shows the percent side chain 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.



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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles		
1	А	93/94~(99%)	83~(89%)	10 (11%)		6	7
1	В	87/94~(93%)	78~(90%)	9 (10%)		7	8
1	С	89/94~(95%)	76~(85%)	13~(15%)		3	3
1	D	90/94~(96%)	77~(86%)	13 (14%)		3	3
1	Ε	89/94~(95%)	85~(96%)	4 (4%)	6 4	27	38
1	F	90/94~(96%)	84~(93%)	6~(7%)	-	16	21
1	G	86/94~(92%)	79~(92%)	7 (8%)	1	11	14
1	Н	90/94~(96%)	81 (90%)	9 (10%)		7	8
All	All	714/752~(95%)	643 (90%)	71 (10%)		8	9

All (71) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	А	69	ASN
1	А	70	LEU
1	А	80	LYS
1	А	84	LEU
1	А	85	LEU
1	А	94	GLU
1	А	96	GLU
1	А	102	PHE
1	А	130	MET
1	А	131	ASP
1	В	66	GLN
1	В	75	GLU
1	В	76	LEU
1	В	79	SER
1	В	80	LYS
1	В	88	LEU
1	В	91	LEU
1	В	95	ASN
1	В	102	PHE
1	С	50	HIS
1	С	80	LYS
1	С	82	SER
1	С	91	LEU
1	С	92	LYS
1	С	95	ASN
1	С	96	GLU
1	С	100	SER



Mol	Chain	Res	Type
1	С	102	PHE
1	С	107	LYS
1	С	109	LEU
1	С	119	LEU
1	С	130	MET
1	D	54	ASP
1	D	70	LEU
1	D	78	GLN
1	D	84	LEU
1	D	85	LEU
1	D	86	GLU
1	D	91	LEU
1	D	102	PHE
1	D	112	LEU
1	D	132	GLN
1	D	133	LEU
1	D	135	LYS
1	D	136	LEU
1	Ε	54	ASP
1	Ε	102	PHE
1	Е	131	ASP
1	Е	134	SER
1	F	49	LEU
1	F	61	LEU
1	F	72	SER
1	F	74	LEU
1	F	102	PHE
1	F	136	LEU
1	G	53	ILE
1	G	65	THR
1	G	90	LEU
1	G	95	ASN
1	G	102	PHE
1	G	114	LYS
1	G	122	ARG
1	H	47	GLU
1	Н	50	HIS
1	H	68	GLN
1	H	72	SER
1	Н	90	LEU
1	Н	100	SER
1	Н	102	PHE



Continued from previous page...

Mol	Chain	Res	Type
1	Н	132	GLN
1	Н	135	LYS

Sometimes side chains can be flipped to improve hydrogen bonding and reduce clashes. All (24) such side chains are listed below:

Mol	Chain	Res	Type
1	А	50	HIS
1	А	60	ASN
1	А	69	ASN
1	А	95	ASN
1	А	132	GLN
1	В	66	GLN
1	В	68	GLN
1	В	95	ASN
1	В	121	ASN
1	В	126	GLN
1	С	52	GLN
1	С	78	GLN
1	С	95	ASN
1	С	126	GLN
1	D	68	GLN
1	D	87	ASN
1	D	126	GLN
1	D	132	GLN
1	Е	95	ASN
1	Е	126	GLN
1	F	95	ASN
1	F	126	GLN
1	G	95	ASN
1	Н	87	ASN

### 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 79 ligands modelled in this entry, 36 are monoatomic - leaving 43 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	Trune	Chain	Deg	<b>Board Link</b> Bond lengths		$_{ m gths}$	B	ond ang	gles	
WIOI	туре	Unain	nes	LIIIK	Counts	RMSZ	# Z >2	Counts	RMSZ	# Z >2
6	EDO	E	208	-	3,3,3	0.41	0	$2,\!2,\!2$	0.35	0
3	SO4	С	208	-	4,4,4	0.15	0	$6,\!6,\!6$	0.13	0
3	SO4	Н	204	-	4,4,4	0.25	0	$6,\!6,\!6$	0.10	0
3	SO4	С	206	-	4,4,4	0.26	0	$6,\!6,\!6$	0.07	0
7	IPA	D	209	-	3,3,3	0.56	0	3,3,3	0.31	0
6	EDO	F	205	-	3,3,3	0.49	0	2,2,2	0.20	0
3	SO4	Е	206	-	4,4,4	0.25	0	$6,\!6,\!6$	0.07	0
5	DTT	А	212	-	7,7,7	1.98	2 (28%)	$4,\!8,\!8$	3.07	2 (50%)
7	IPA	F	208	-	3,3,3	0.51	0	3,3,3	0.37	0
3	SO4	G	203	-	4,4,4	0.26	0	$6,\!6,\!6$	0.06	0
3	SO4	Н	205	-	4,4,4	0.12	0	$6,\!6,\!6$	0.14	0
3	SO4	В	204	-	4,4,4	0.26	0	$6,\!6,\!6$	0.06	0
3	SO4	А	205	-	4,4,4	0.26	0	$6,\!6,\!6$	0.08	0
3	SO4	С	209	-	4,4,4	0.14	0	$6,\!6,\!6$	0.13	0
3	SO4	F	204	-	4,4,4	0.25	0	$6,\!6,\!6$	0.07	0
7	IPA	F	207	-	3,3,3	0.58	0	3,3,3	0.31	0
3	SO4	А	210	-	4,4,4	0.26	0	$6,\!6,\!6$	0.05	0
3	SO4	G	206	-	4,4,4	0.24	0	$6,\!6,\!6$	0.07	0
3	SO4	В	206	-	4,4,4	0.29	0	$6,\!6,\!6$	0.07	0
7	IPA	F	206	-	3,3,3	0.57	0	$3,\!3,\!3$	0.36	0
3	SO4	G	205	-	4,4,4	0.26	0	$6,\!6,\!6$	0.05	0
3	SO4	D	205	-	4,4,4	0.25	0	$6,\!6,\!6$	0.06	0
3	SO4	A	208	-	4,4,4	0.26	0	6,6,6	0.04	0
3	SO4	С	204	-	4,4,4	0.27	0	6,6,6	0.04	0
6	EDO	В	209	-	3,3,3	0.50	0	2,2,2	0.27	0
3	SO4	С	205	-	4,4,4	0.27	0	6,6,6	0.06	0
6	EDO	D	207	-	3,3,3	0.45	0	2,2,2	0.34	0



Mal	Tuno	Chain	Dog	Link	B	ond leng	$\operatorname{gths}$	E	ond ang	gles
	туре	Ullalli	nes		Counts	RMSZ	# Z >2	Counts	RMSZ	# Z >2
6	EDO	Н	206	-	3,3,3	0.48	0	$2,\!2,\!2$	0.28	0
7	IPA	С	212	-	3,3,3	0.68	0	$3,\!3,\!3$	0.29	0
3	SO4	С	207	-	4,4,4	0.27	0	$6,\!6,\!6$	0.06	0
3	SO4	G	208	-	4,4,4	0.16	0	$6,\!6,\!6$	0.06	0
3	SO4	G	204	2	4,4,4	0.27	0	$6,\!6,\!6$	0.05	0
7	IPA	Е	210	-	3,3,3	0.60	0	$3,\!3,\!3$	0.33	0
3	SO4	А	206	-	4,4,4	0.28	0	$6,\!6,\!6$	0.08	0
3	SO4	D	204	-	4,4,4	0.27	0	$6,\!6,\!6$	0.06	0
3	SO4	А	207	-	4,4,4	0.26	0	$6,\!6,\!6$	0.06	0
3	SO4	В	205	-	4,4,4	0.29	0	$6,\!6,\!6$	0.06	0
3	SO4	В	207	-	4,4,4	0.27	0	$6,\!6,\!6$	0.04	0
6	EDO	Е	209	-	3,3,3	0.49	0	$2,\!2,\!2$	0.32	0
6	EDO	D	208	-	3,3,3	0.45	0	$2,\!2,\!2$	0.34	0
3	SO4	С	210	-	4,4,4	0.16	0	$\overline{6,\!6,\!6}$	0.13	0
3	SO4	G	207	-	4,4,4	0.27	0	$6,\!6,\!6$	0.05	0
3	SO4	A	209	-	4,4,4	0.25	0	$6,\!6,\!6$	0.07	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
6	EDO	Е	208	-	-	0/1/1/1	-
6	EDO	В	209	-	-	0/1/1/1	-
6	EDO	Е	209	-	-	1/1/1/1	-
6	EDO	D	208	-	-	1/1/1/1	-
6	EDO	D	207	-	-	0/1/1/1	-
6	EDO	F	205	-	-	0/1/1/1	-
6	EDO	Н	206	-	-	1/1/1/1	-
5	DTT	А	212	-	-	0/8/8/8	-

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	$\mathrm{Ideal}(\mathrm{\AA})$
5	А	212	DTT	O2-C2	-2.93	1.37	1.43
5	А	212	DTT	C1-C2	2.80	1.59	1.51

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	$Observed(^{o})$	$Ideal(^{o})$
5	А	212	DTT	O3-C3-C2	-5.24	98.96	109.72



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Mol	Chain	Res	Type	Atoms	Z	$Observed(^{o})$	$Ideal(^{o})$
5	А	212	DTT	C3-C4-S4	-2.40	107.48	114.47

There are no chirality outliers.

All (3) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
6	D	208	EDO	O1-C1-C2-O2
6	Н	206	EDO	O1-C1-C2-O2
6	Е	209	EDO	O1-C1-C2-O2

There are no ring outliers.

13 monomers are involved in 31 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
6	Е	208	EDO	1	0
7	D	209	IPA	3	0
6	F	205	EDO	2	0
5	А	212	DTT	9	0
7	F	208	IPA	2	0
3	С	209	SO4	1	0
3	F	204	SO4	1	0
7	F	206	IPA	6	0
6	D	207	EDO	1	0
6	Н	206	EDO	2	0
7	Е	210	IPA	1	0
3	D	204	SO4	1	0
3	А	209	SO4	2	0

## 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	<RSRZ $>$	#RSR	#RSRZ>2		$OWAB(Å^2)$	Q<0.9
1	А	94/96~(97%)	0.96	14 (14%)	2	3	20, 73, 127, 144	0
1	В	88/96~(91%)	1.46	22~(25%)	0	1	20, 76, 150, 154	0
1	С	90/96~(93%)	1.37	20~(22%)	0	1	22, 71, 136, 156	0
1	D	91/96~(94%)	1.11	21~(23%)	0	1	17, 74, 143, 148	0
1	Е	90/96~(93%)	1.48	28~(31%)	0	0	20, 69, 136, 154	0
1	F	91/96~(94%)	1.21	20~(21%)	0	1	19, 72, 147, 156	0
1	G	87/96~(90%)	1.61	30 (34%)	0	0	20, 71, 143, 155	0
1	Н	91/96~(94%)	0.97	12 (13%)	3	4	21, 75, 134, 140	0
All	All	722/768~(94%)	1.27	167 (23%)	0	1	17, 75, 142, 156	0

All (167) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	С	70	LEU	12.0
1	F	46	ILE	11.8
1	Е	85	LEU	9.3
1	В	133	LEU	9.0
1	В	74	LEU	8.2
1	G	50	HIS	7.1
1	В	71	LEU	7.1
1	G	136	LEU	7.0
1	В	61	LEU	6.9
1	Е	75	GLU	6.9
1	G	74	LEU	6.8
1	С	74	LEU	6.6
1	Е	70	LEU	6.5
1	В	49	LEU	6.4
1	Е	49	LEU	6.1
1	G	64	THR	5.9



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Mol	Chain	Res	Type	RSRZ
1	С	49	LEU	5.9
1	G	65	THR	5.9
1	С	52	GLN	5.8
1	F	74	LEU	5.8
1	Е	62	GLN	5.3
1	G	76	LEU	5.3
1	D	136	LEU	5.3
1	G	68	GLN	5.1
1	D	46	ILE	5.1
1	Е	48	SER	5.0
1	В	55	MET	5.0
1	Н	74	LEU	5.0
1	В	134	SER	4.9
1	G	70	LEU	4.8
1	А	136	LEU	4.7
1	Е	88	LEU	4.6
1	D	55	MET	4.5
1	G	58	LYS	4.5
1	С	84	LEU	4.5
1	D	52	GLN	4.4
1	G	133	LEU	4.4
1	G	61	LEU	4.4
1	А	46	ILE	4.4
1	Н	80	LYS	4.4
1	Е	47	GLU	4.4
1	Е	69	ASN	4.3
1	С	71	LEU	4.3
1	Е	76	LEU	4.2
1	С	133	LEU	4.2
1	В	70	LEU	4.1
1	Н	135	LYS	4.1
1	G	135	LYS	4.1
1	D	74	LEU	4.1
1	F	59	THR	4.0
1	В	136	LEU	3.9
1	D	63	LEU	3.9
1	Е	51	ASP	3.9
1	А	74	LEU	3.8
1	С	80	LYS	3.8
1	С	135	LYS	3.8
1	G	63	LEU	3.8
1	А	54	ASP	3.7



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Mol	Chain	Res	Type	RSRZ			
1	Н	55	MET	3.7			
1	F	49	LEU	3.7			
1	F	136	LEU	3.7			
1	А	75	GLU	3.7			
1	С	62	GLN	3.7			
1	С	46	ILE	3.6			
1	G	73	LYS	3.6			
1	А	88	LEU	3.6			
1	G	51	ASP	3.6			
1	В	68	GLN	3.6			
1	В	72	SER	3.5			
1	F	81	GLU	3.5			
1	В	73	LYS	3.5			
1	F	71	LEU	3.5			
1	G	85	LEU	3.5			
1	В	52	GLN	3.5			
1	Е	71	LEU	3.4			
1	F	76	LEU	3.4			
1	F	50	HIS	3.4			
1	С	54	ASP	3.4			
1	F	52	GLN	3.3			
1	D	66	GLN	3.3			
1	Н	51	ASP	3.3			
1	В	64	THR	3.2			
1	F	63	LEU	3.2			
1	G	62	GLN	3.2			
1	G	71	LEU	3.2			
1	А	58	LYS	3.1			
1	С	73	LYS	3.1			
1	D	61	LEU	3.1			
1	Е	59	THR	3.0			
1	Н	133	LEU	3.0			
1	В	62	GLN	3.0			
1	Н	52	GLN	3.0			
1	Е	52	GLN	3.0			
1	Е	73	LYS	3.0			
1	С	69	ASN	2.9			
1	Е	130	MET	2.9			
1	G	66	GLN	2.9			
1	Е	61	LEU	2.9			
1	С	113	GLU	2.9			
1	Е	84	LEU	2.9			



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Mol	Chain	Res	Type	RSRZ			
1	Е	74	LEU	2.8			
1	D	73	LYS	2.8			
1	G	59	THR	2.8			
1	Е	66	GLN	2.8			
1	D	62	GLN	2.7			
1	В	59	THR	2.7			
1	D	47	GLU	2.7			
1	Ε	50	HIS	2.7			
1	А	61	LEU	2.7			
1	F	73	LYS	2.7			
1	D	70	LEU	2.6			
1	D	76	LEU	2.6			
1	Н	91	LEU	2.6			
1	G	52	GLN	2.6			
1	Н	46	ILE	2.6			
1	Е	133	LEU	2.6			
1	А	55	MET	2.6			
1	F	83	LYS	2.5			
1	С	76	LEU	2.5			
1	С	67	SER	2.5			
1	А	52	GLN	2.5			
1	G	54	ASP	2.5			
1	В	63	LEU	2.5			
1	G	56	LEU	2.5			
1	В	113	GLU	2.4			
1	В	54	ASP	2.4			
1	D	85	LEU	2.4			
1	Е	56	LEU	2.4			
1	С	68	GLN	2.4			
1	Е	131	ASP	2.4			
1	В	60	ASN	2.4			
1	G	86	GLU	2.4			
1	D	131	ASP	2.4			
1	D	71	LEU	2.3			
1	D	134	SER	2.3			
1	G	88	LEU	2.3			
1	G	69	ASN	2.3			
1	D	53	ILE	2.3			
1	Н	128	GLU	2.3			
1	Е	136	LEU	2.3			
1	А	44	ARG	2.3			
1	F	135	LYS	2.3			



Mol	Chain	$\mathbf{Res}$	Type	RSRZ
1	G	75	GLU	2.2
1	F	55	MET	2.2
1	Е	65	THR	2.2
1	D	69	ASN	2.2
1	G	57	THR	2.2
1	Е	55	MET	2.2
1	G	134	SER	2.2
1	Е	58	LYS	2.2
1	А	91	LEU	2.2
1	F	133	LEU	2.2
1	А	43	SER	2.2
1	D	57	THR	2.1
1	С	51	ASP	2.1
1	В	66	GLN	2.1
1	А	70	LEU	2.1
1	Н	136	LEU	2.1
1	F	68	GLN	2.1
1	G	130	MET	2.1
1	С	85	LEU	2.1
1	Н	65	THR	2.1
1	F	67	SER	2.1
1	F	66	GLN	2.0
1	F	48	SER	2.0
1	В	58	LYS	2.0
1	D	135	LYS	2.0

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### 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	$B-factors(A^2)$	Q<0.9
2	DY	Н	201	1/1	0.39	0.28	80,80,80,80	1
5	DTT	А	212	8/8	0.42	0.81	84,87,90,97	0
3	SO4	А	209	5/5	0.48	0.49	110,110,117,117	0
7	IPA	F	206	4/4	0.59	0.33	$50,\!51,\!58,\!66$	0
3	SO4	G	207	5/5	0.61	0.28	149,149,151,151	0
2	DY	Е	202	1/1	0.62	1.07	85,85,85,85	1
4	PT	А	211	1/1	0.64	0.26	105,105,105,105	1
3	SO4	G	205	5/5	0.67	0.20	$153,\!154,\!155,\!155$	0
7	IPA	F	208	4/4	0.70	0.40	74,78,80,80	0
2	DY	В	202	1/1	0.71	0.10	72, 72, 72, 72	1
4	PT	Е	207	1/1	0.72	0.08	88,88,88,88	1
2	DY	Е	203	1/1	0.72	0.09	$79,\!79,\!79,\!79$	1
7	IPA	С	212	4/4	0.74	0.21	44,54,62,68	0
3	SO4	Н	205	5/5	0.74	0.20	83,91,94,100	0
3	SO4	А	210	5/5	0.74	0.21	159,160,160,161	0
7	IPA	F	207	4/4	0.76	0.23	$53,\!66,\!70,\!73$	0
3	SO4	D	205	5/5	0.76	0.36	112,112,115,116	0
3	SO4	С	206	5/5	0.77	0.28	115,117,118,121	0
6	EDO	D	207	4/4	0.77	0.28	72,76,76,77	0
6	EDO	В	209	4/4	0.78	0.27	$63,\!64,\!68,\!73$	0
6	EDO	Е	209	4/4	0.78	0.27	53,74,74,82	0
2	DY	F	203	1/1	0.79	0.17	58,58,58,58	1
3	SO4	А	208	5/5	0.79	0.14	131,131,134,134	0
3	SO4	В	207	5/5	0.79	0.64	121,121,124,124	0
3	SO4	С	208	5/5	0.80	0.25	104,105,107,111	0
3	SO4	F	204	5/5	0.80	0.30	118,118,119,125	0
7	IPA	D	209	4/4	0.80	0.22	$62,\!65,\!65,\!67$	0
7	IPA	Е	210	4/4	0.81	0.25	64,66,70,74	0
2	DY	G	201	1/1	0.81	0.17	84,84,84,84	1
4	PT	С	211	1/1	0.81	0.23	112,112,112,112	1
3	SO4	Е	206	5/5	0.81	0.22	$96,\!97,\!102,\!106$	0
3	SO4	Н	204	5/5	0.82	0.34	91,93,103,106	0
6	EDO	D	208	4/4	0.83	0.22	48,52,53,63	0
2	DY	H	203	1/1	0.83	0.11	70,70,70,70	1
3	SO4	G	206	5/5	0.84	0.26	131,131,132,133	0
3	SO4	А	207	5/5	0.84	0.27	144,144,145,146	0
4	PT	В	208	1/1	0.84	0.14	106,106,106,106	1
3	SO4	С	205	5/5	0.84	0.22	119,122,122,123	0
3	SO4	В	204	5/5	0.85	0.25	122,123,126,127	0
6	EDO	F	205	4/4	0.85	0.24	34,49,54,61	0
2	DY	В	203	1/1	0.86	0.07	67,67,67,67	1
6	EDO	Н	206	4/4	0.86	0.16	44,49,51,56	0
2	DY	D	201	1/1	0.86	0.15	83,83,83,83	1



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Mol	Type	Chain	Res	Atoms	RSCC	RSR	$B-factors(A^2)$	Q<0.9
3	SO4	С	207	5/5	0.86	0.12	79,82,87,88	0
2	DY	F	202	1/1	0.87	0.09	64,64,64,64	1
3	SO4	D	204	5/5	0.87	0.15	104,106,108,108	0
2	DY	Е	204	1/1	0.87	0.13	61,61,61,61	1
2	DY	А	204	1/1	0.88	0.24	71,71,71,71	1
3	SO4	G	208	5/5	0.88	0.14	116,116,118,121	0
3	SO4	G	203	5/5	0.88	0.17	108,108,112,112	0
4	PT	D	206	1/1	0.89	0.21	105,105,105,105	1
3	SO4	В	205	5/5	0.89	0.12	83,84,87,87	0
3	SO4	А	206	5/5	0.89	0.19	83,90,93,94	0
3	SO4	G	204	5/5	0.89	0.24	99,99,102,104	0
3	SO4	С	209	5/5	0.89	0.24	88,89,93,95	0
2	DY	D	202	1/1	0.90	0.09	56, 56, 56, 56	1
2	DY	А	203	1/1	0.90	0.33	71,71,71,71	1
2	DY	F	201	1/1	0.90	0.10	94,94,94,94	1
2	DY	В	201	1/1	0.91	0.16	63,63,63,63	1
4	PT	G	209	1/1	0.91	0.15	86,86,86,86	1
3	SO4	С	210	5/5	0.91	0.34	74,78,81,84	0
2	DY	G	202	1/1	0.92	0.12	55,55,55,55	1
2	DY	А	202	1/1	0.92	0.47	56, 56, 56, 56	1
3	SO4	С	204	5/5	0.92	0.12	108,110,112,112	0
2	DY	Е	205	1/1	0.92	0.10	71,71,71,71	1
6	EDO	Е	208	4/4	0.93	0.35	35,42,50,55	0
3	SO4	В	206	5/5	0.93	0.21	75,78,83,87	0
2	DY	Н	202	1/1	0.94	0.19	$65,\!65,\!65,\!65$	1
2	DY	D	203	1/1	0.94	0.39	33,33,33,33	1
2	DY	С	203	1/1	0.96	0.07	70,70,70,70	1
3	SO4	А	205	5/5	0.96	0.10	61,72,74,76	0
2	DY	С	201[B]	1/1	0.98	0.13	18,18,18,18	1
2	DY	С	201[A]	1/1	0.98	0.13	35,35,35,35	1
2	DY	А	201[B]	1/1	0.99	0.10	18,18,18,18	1
2	DY	С	202[A]	1/1	0.99	0.10	32,32,32,32	1
2	DY	С	202[B]	1/1	0.99	0.10	$17,\!17,\!17,\!17$	1
2	DY	Е	201[A]	1/1	0.99	0.11	29,29,29,29	1
2	DY	Е	201[B]	1/1	0.99	0.11	13,13,13,13	1
2	DY	А	201[A]	1/1	0.99	0.10	33,33,33,33	1

# 6.5 Other polymers (i)

There are no such residues in this entry.

