

Full wwPDB X-ray Structure Validation Report (i)

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PDB ID	:	8T7F
Title	:	Structure of the S1 variant of Fab F1
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Deposited on	:	2023-06-20
Resolution	:	3.50 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
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)	:	2.36

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 3.50 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.



Motric	Whole archive	Similar resolution
	$(\# { m Entries})$	$(\# { m Entries}, { m resolution} { m range}({ m \AA}))$
R_{free}	130704	1659 (3.60-3.40)
Clashscore	141614	1036 (3.58-3.42)
Ramachandran outliers	138981	1005 (3.58-3.42)
Sidechain outliers	138945	1006 (3.58-3.42)
RSRZ outliers	127900	1559 (3.60-3.40)

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	237	64%	30%	• 5%
1	С	237	63%	32%	5%
1	D	237	67%	27%	5%
1	F	237	70%	25%	5%
1	Ι	237	% 64%	29%	• 5%



Mol	Chain	Length	Quality of chain		
1	K	237	69%	24%	• 5%
2	В	216	55%	38%	• 6%
2	Е	216	59%	37%	••
2	G	216	61%	35%	••
2	Н	216	67%	28%	•••
2	J	216	69%	27%	••
2	L	216	63%	28%	• 7%



2 Entry composition (i)

There are 4 unique types of molecules in this entry. The entry contains 18965 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		Ate	oms			ZeroOcc	AltConf	Trace
1	C	226	Total	С	Ν	Ο	\mathbf{S}	0	0	0
1		220	1677	1067	278	326	6	0	0	0
1	Δ	226	Total	С	Ν	Ο	S	0	0	0
1	Л	220	1659	1052	274	327	6	0	0	0
1	П	224	Total	С	Ν	Ο	S	0	0	0
1	D		1662	1057	274	325	6	0	0	0
1	F	225	Total	С	Ν	Ο	S	0	0	0
1	Ľ	220	1658	1055	274	323	6	0	0	0
1	т	224	Total	С	Ν	Ο	S	0	0	0
1		224	1648	1049	272	321	6	0	0	0
1	K	224	Total	С	Ν	Ο	S	0	0	0
		224	1648	1051	272	319	6	0	U	

• Molecule 1 is a protein called S1 variant of Fab F1 heavy chain.

• Molecule 2 is a protein called S1 variant of Fab F1 light chain.

Mol	Chain	Residues		At	oms			ZeroOcc	AltConf	Trace
2	С	210	Total	С	Ν	Ο	S	0	0	0
	G	210	1559	976	260	318	5	0	0	0
2	В	202	Total	С	Ν	0	S	0	0	0
	D	202	1458	920	234	299	5	0	0	0
2	F	209	Total	С	Ν	0	S	0	0	0
	Ľ		1535	968	253	309	5	0	0	0
2	Ц	207	Total	С	Ν	Ο	S	0	0	0
	11	201	1476	928	245	298	5	0	0	0
9	т	200	Total	С	Ν	Ο	S	0	0	0
	J	209	1500	946	244	305	5	0	0	0
9	т	200	Total	С	Ν	Ο	S	0	0	0
		200	1445	908	238	294	5	0	U	0

• Molecule 3 is 4-(2-HYDROXYETHYL)-1-PIPERAZINE ETHANESULFONIC ACID (three-letter code: EPE) (formula: C₈H₁₈N₂O₄S) (labeled as "Ligand of Interest" by depositor).





Mol	Chain	Residues	Atoms			ZeroOcc	AltConf		
3	С	1	Total	С	Ν	0	\mathbf{S}	0	0
0	3 0	T	15	8	2	4	1	0	0
3	Л	1	Total	С	Ν	0	\mathbf{S}	0	0
			15	8	2	4	1		U

• Molecule 4 is SULFATE ION (three-letter code: SO4) (formula: O_4S) (labeled as "Ligand of Interest" by depositor).



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



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



3 Residue-property plots (i)

• Molecule 1: S1 variant of Fab F1 heavy chain

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.

5%

Chain C: 63% 32%



• Molecule 1: S1 variant of Fab F1 heavy chain





V235 E236 P237 LYS SER CYS ASP LYS LYS THR HIS THR

• Molecule 1: S1 variant of Fab F1 heavy chain





• Molecule 2: S1 variant of Fab F1 light chain



• Molecule 2: S1 variant of Fab F1 light chain





SER

8139 8139 E141 143 E141 143 143 144 144 143 145 144 146 144 147 145 148 145 149 146 146 146 146 146 146 156 156 156 157 156 169 169 176 169 176 176 176 156 176 156 176 178 176 178 176 178 176 178 178 178 178 178 178 178 179 1724 1716 1724 1724 1724 1724 1724 1724 1724 1724 1724

• Molecule 2: S1 variant of Fab F1 light chain







4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants	80.76Å 189.46Å 216.47Å	Depositor
a, b, c, α , β , γ	90.00° 90.00° 90.00°	Depositor
Bosolution (Å)	94.73 - 3.50	Depositor
Resolution (A)	94.73 - 3.50	EDS
% Data completeness	92.9(94.73-3.50)	Depositor
(in resolution range)	92.9(94.73-3.50)	EDS
R _{merge}	0.18	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) > 1$	2.32 (at 3.49 Å)	Xtriage
Refinement program	PHENIX 1.20.1_4487, PHENIX 1.20.1_4487	Depositor
D D.	0.243 , 0.306	Depositor
Π, Π_{free}	0.243 , 0.308	DCC
R_{free} test set	1909 reflections (4.81%)	wwPDB-VP
Wilson B-factor $(Å^2)$	91.7	Xtriage
Anisotropy	0.614	Xtriage
Bulk solvent $k_{sol}(e/Å^3)$, $B_{sol}(Å^2)$	0.27, 44.2	EDS
L-test for $twinning^2$	$ L > = 0.48, < L^2 > = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.91	EDS
Total number of atoms	18965	wwPDB-VP
Average B, all atoms $(Å^2)$	96.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: The largest off-origin peak in the Patterson function is 9.87% of the height of the origin peak. No significant pseudotranslation is detected.

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



¹Intensities 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, EPE

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
	Ullalli	RMSZ	# Z > 5	RMSZ	# Z > 5
1	А	0.32	0/1709	0.60	0/2344
1	С	0.34	0/1727	0.59	0/2366
1	D	0.34	0/1712	0.63	1/2348~(0.0%)
1	F	0.35	0/1708	0.58	0/2344
1	Ι	0.33	0/1698	0.61	0/2331
1	K	0.31	0/1697	0.59	0/2329
2	В	0.33	0/1489	0.62	0/2037
2	Е	0.33	0/1568	0.57	0/2143
2	G	0.36	0/1592	0.62	0/2169
2	Н	0.33	0/1509	0.60	1/2068~(0.0%)
2	J	0.34	0/1534	0.59	0/2104
2	L	0.31	0/1477	0.60	0/2020
All	All	0.33	0/19420	0.60	2/26603~(0.0%)

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	$Observed(^{o})$	$Ideal(^{o})$
2	Н	113	LEU	CA-CB-CG	5.70	128.41	115.30
1	D	40	HIS	CB-CA-C	-5.69	99.03	110.40

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



Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	А	1659	0	1519	60	0
1	С	1677	0	1569	59	0
1	D	1662	0	1544	52	0
1	F	1658	0	1528	46	0
1	Ι	1648	0	1515	51	0
1	Κ	1648	0	1524	54	0
2	В	1458	0	1334	72	0
2	Е	1535	0	1431	53	0
2	G	1559	0	1464	63	0
2	Н	1476	0	1321	52	0
2	J	1500	0	1335	45	0
2	L	1445	0	1312	49	0
3	С	15	0	17	4	0
3	D	15	0	17	1	0
4	D	5	0	0	0	0
4	Κ	5	0	0	0	0
All	All	18965	0	17430	600	0

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.

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 16.

All (600) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic	Clash
1100111-1	1100111-2	distance $(Å)$	overlap (Å)
2:G:27:GLN:HG2	2:G:28:SER:H	1.33	0.91
2:B:41:TRP:CE3	2:B:89:LEU:HD11	2.11	0.84
2:H:2:ILE:N	2:H:26:SER:HG	1.76	0.83
2:J:95:GLN:HG2	2:J:96:PRO:HD2	1.59	0.82
2:G:179:GLU:HG2	2:G:193:LEU:HD21	1.61	0.81
1:D:24:ALA:HA	1:D:86:THR:HG22	1.63	0.81
2:E:138:PRO:HD3	2:E:150:VAL:HG22	1.63	0.81
1:C:34:LEU:HB2	1:C:107:SER:HB2	1.63	0.81
1:F:56:ILE:HD11	1:F:78:ILE:HG12	1.63	0.80
1:D:34:LEU:HB3	1:D:107:SER:HB2	1.66	0.78
2:G:27:GLN:HG2	2:G:28:SER:N	1.99	0.77
1:D:108:ALA:HB2	1:D:122:PRO:HD2	1.66	0.77
2:B:132:SER:HB2	2:B:155:ASN:HB3	1.67	0.77
2:G:8:PRO:HB3	2:G:11:LEU:HD12	1.67	0.77
2:J:20:THR:HG22	2:J:90:THR:HG22	1.67	0.77



		Interatomic	Clash
Atom-1	Atom-2	distance (Å)	overlap (Å)
1:D:145:VAL:HG22	1:D:166:VAL:HG12	1.67	0.76
2:L:166:TRP:HE1	2:L:195:SER:HG	1.32	0.76
2:B:41:TRP:CD2	2:B:89:LEU:HD11	2.19	0.75
2:G:42:TYR:HE2	2:G:105:GLN:HG2	1.51	0.74
1:A:24:ALA:HA	1:A:86:THR:HG22	1.68	0.74
1:F:108:ALA:HB3	1:F:122:PRO:HG2	1.67	0.74
2:H:20:THR:HG22	2:H:90:THR:HG22	1.70	0.73
1:I:179:ASN:HB2	1:I:182:ALA:HB3	1.69	0.73
2:G:160:ARG:HB2	2:G:191:TYR:CE2	2.24	0.72
2:H:173:GLN:OE1	2:H:176:ASN:ND2	2.21	0.72
2:L:11:LEU:HD21	2:L:21:ILE:HG22	1.71	0.72
1:D:140:THR:HG22	1:D:171:PRO:HD3	1.71	0.72
2:E:228:ASN:O	2:E:229:ARG:HD2	1.90	0.72
1:A:177:SER:HB2	1:A:221:ASN:HB2	1.72	0.71
1:C:145:VAL:HG22	1:C:166:VAL:HG12	1.73	0.71
2:L:104:CYS:O	2:L:117:GLY:N	2.24	0.71
2:B:154:LEU:HD11	2:B:214:VAL:HG11	1.73	0.71
2:B:8:PRO:HB3	2:B:11:LEU:HD13	1.71	0.70
1:C:119:HIS:N	2:G:109:SER:OG	2.23	0.70
2:B:205:GLU:HA	2:B:229:ARG:NH2	2.06	0.70
1:C:75:ARG:NH2	1:C:98:ASP:OD2	2.25	0.69
1:A:145:VAL:HG22	1:A:166:VAL:HG12	1.74	0.69
1:C:176:VAL:HG22	1:C:222:VAL:HG22	1.74	0.69
2:E:166:TRP:NE1	2:E:195:SER:OG	2.26	0.69
1:A:146:PHE:HE2	2:B:139:SER:H	1.40	0.68
1:D:162:LEU:HD13	1:D:235:VAL:HG21	1.76	0.68
1:I:176:VAL:HG22	1:I:222:VAL:HG22	1.76	0.68
2:H:157:PHE:HZ	2:H:193:LEU:HD13	1.59	0.68
1:K:145:VAL:HG22	1:K:166:VAL:HG12	1.76	0.68
2:J:24:ARG:NH1	2:J:86:ASP:OD2	2.28	0.67
1:A:162:LEU:HD12	1:A:235:VAL:HG22	1.75	0.67
1:I:184:THR:O	1:I:187:VAL:HG12	1.95	0.67
1:K:176:VAL:HG22	1:K:222:VAL:HG12	1.77	0.66
2:H:153:LEU:HD21	2:H:155:ASN:HB2	1.75	0.66
2:G:45:LYS:NZ	2:G:97:GLU:O	2.27	0.66
2:G:42:TYR:CE2	2:G:105:GLN:HG2	2.29	0.66
2:B:104:CYS:O	2:B:117:GLY:N	2.27	0.66
2:H:107:TYR:HD1	2:H:114:ILE:HG12	1.60	0.66
2:B:169:ASP:HA	2:B:209:VAL:HG13	1.77	0.65
1:I:106:ARG:O	1:I:124:MET:HA	1.96	0.65
2:B:41:TRP:CZ3	2:B:104:CYS:HB2	2.31	0.65



		Interatomic	Clash
Atom-1	Atom-2	distance (\AA)	overlap (Å)
1:A:146:PHE:CE1	2:B:141:GLU:HB2	2.31	0.65
1:C:43:ARG:NH1	1:C:51:GLU:OE1	2.30	0.64
1:C:166:VAL:HG11	1:C:222:VAL:HG11	1.79	0.64
1:F:145:VAL:HG22	1:F:166:VAL:HG12	1.77	0.64
1:F:170:PHE:HB3	1:F:171:PRO:HD3	1.80	0.64
2:H:8:PRO:HD2	2:H:21:ILE:HG22	1.80	0.64
1:I:3:GLN:HG2	1:I:26:SER:HB3	1.78	0.64
1:K:166:VAL:HG23	1:K:202:LEU:HB3	1.78	0.64
1:A:146:PHE:CZ	2:B:142:GLN:HB2	2.33	0.63
1:C:52:TRP:HE1	1:C:55:SER:HG	1.46	0.63
2:G:104:CYS:O	2:G:117:GLY:N	2.31	0.63
2:G:138:PRO:HD3	2:G:150:VAL:HG22	1.80	0.63
2:B:12:SER:HB3	2:B:123:GLU:HB2	1.79	0.63
1:I:150:PRO:HB3	1:I:162:LEU:HB3	1.79	0.63
1:I:168:ASP:OD1	1:I:195:GLN:NE2	2.28	0.63
2:H:41:TRP:CE3	2:H:89:LEU:HD11	2.33	0.63
2:L:138:PRO:HD3	2:L:150:VAL:HG22	1.81	0.63
2:B:138:PRO:HD3	2:B:150:VAL:HG22	1.80	0.63
1:I:52:TRP:HE1	1:I:55:SER:HG	1.45	0.63
2:G:213:GLU:HA	2:G:224:THR:HG22	1.81	0.62
1:F:75:ARG:NH2	1:F:98:ASP:OD2	2.32	0.62
2:L:20:THR:HG22	2:L:90:THR:HA	1.80	0.62
1:C:106:ARG:NH2	1:C:125:ASP:OD2	2.31	0.62
2:J:21:ILE:HG21	2:J:120:THR:HG21	1.81	0.62
2:J:142:GLN:HE21	2:J:142:GLN:HA	1.65	0.62
1:I:224:HIS:CD2	1:I:226:PRO:HD2	2.35	0.62
1:D:15:PRO:HD2	1:D:137:SER:HB2	1.81	0.61
1:K:3:GLN:HA	1:K:126:TYR:CE2	2.34	0.61
1:K:52:TRP:CZ3	2:L:113:LEU:HB2	2.35	0.61
2:L:184:GLN:HG2	2:L:191:TYR:CE1	2.36	0.61
2:G:152:CYS:HB2	2:G:166:TRP:CZ3	2.36	0.61
1:F:171:PRO:HD2	1:F:224:HIS:CE1	2.35	0.61
2:L:166:TRP:NE1	2:L:195:SER:OG	2.29	0.61
1:A:159:THR:HG22	1:A:209:PRO:HA	1.81	0.60
1:F:146:PHE:CE2	2:H:142:GLN:HG3	2.36	0.60
2:H:104:CYS:O	2:H:117:GLY:N	2.33	0.60
2:H:108:VAL:HG21	2:H:113:LEU:HG	1.83	0.60
2:B:213:GLU:HA	2:B:224:THR:HG22	1.84	0.60
2:H:16:GLY:H	2:H:94:LEU:HB3	1.65	0.60
1:A:108:ALA:HB3	1:A:122:PRO:HG3	1.83	0.60
1:C:194:LEU:HA	1:C:200:TYR:HA	1.84	0.60



		Interatomic	Clash	
Atom-1	Atom-2	distance (Å)	overlap (Å)	
1:A:146:PHE:HE1	2:B:141:GLU:HB2	1.66	0.60	
1:I:145:VAL:HG22	1:I:166:VAL:HG12	1.84	0.59	
1:F:166:VAL:HG23	1:F:202:LEU:HB3	1.84	0.59	
1:C:180:SER:HA	1:C:221:ASN:HD21	1.68	0.59	
1:A:110:SER:OG	1:A:113:GLY:N	2.31	0.59	
2:E:154:LEU:HB2	2:E:193:LEU:HB3	1.84	0.59	
2:E:31:SER:HB2	2:E:106:GLN:NE2	2.18	0.59	
2:G:169:ASP:HA	2:G:209:VAL:HG13	1.85	0.58	
1:K:177:SER:HB2	1:K:221:ASN:HD21	1.67	0.58	
2:E:166:TRP:HE1	2:E:195:SER:HG	1.41	0.58	
2:J:39:VAL:HG21	2:J:87:PHE:CD1	2.38	0.58	
1:D:12:LEU:HD11	1:D:171:PRO:HG3	1.85	0.58	
2:G:228:ASN:O	2:G:229:ARG:HG3	2.04	0.57	
2:B:6:GLN:NE2	2:B:119:GLY:H	2.02	0.57	
2:B:159:PRO:HD2	2:B:216:HIS:NE2	2.19	0.57	
1:K:33:TYR:HB3	1:K:106:ARG:HG3	1.86	0.57	
2:G:15:VAL:HG11	2:G:96:PRO:HG3	1.85	0.57	
1:C:119:HIS:H	2:G:109:SER:HG	1.51	0.57	
1:K:91:MET:HE2	1:K:94:LEU:HD11	1.85	0.57	
1:C:77:THR:HB	1:C:90:GLN:HB3	1.86	0.57	
1:I:114:TYR:HE1	2:J:112:TRP:CD1	2.21	0.57	
1:K:3:GLN:HA	1:K:126:TYR:HE2	1.70	0.57	
1:C:13:VAL:O	1:C:135:VAL:HA	2.04	0.56	
2:B:7:SER:HB3	2:B:8:PRO:HD3	1.86	0.56	
1:A:146:PHE:HE2	2:B:139:SER:N	2.03	0.56	
2:B:32:ALA:O	2:B:106:GLN:HG3	2.05	0.56	
1:I:194:LEU:HA	1:I:200:TYR:HA	1.87	0.56	
2:E:149:SER:HA	2:E:197:LEU:O	2.05	0.56	
1:A:224:HIS:HD2	1:A:226:PRO:HD2	1.70	0.56	
1:C:120:PHE:HA	2:G:32:ALA:HB2	1.88	0.56	
2:L:169:ASP:HB2	2:L:207:HIS:NE2	2.21	0.56	
2:H:16:GLY:HA2	2:H:94:LEU:H	1.71	0.56	
2:H:41:TRP:CD2	2:H:89:LEU:HD11	2.40	0.56	
2:G:27:GLN:HE21	2:G:108:VAL:HG23	1.70	0.56	
1:A:95:ARG:NH1	1:A:97:GLU:OE2	2.39	0.56	
1:D:106:ARG:NH2	1:D:125:ASP:OD2	2.39	0.56	
2:H:138:PRO:HD3	2:H:150:VAL:HG22	1.87	0.56	
2:J:138:PRO:HB3	2:J:149:SER:H	1.69	0.56	
1:C:195:GLN:HA	2:G:178:GLN:HE22	1.71	0.56	
2:H:21:ILE:HG21	2:H:120:THR:HG21	1.87	0.56	
2:G:27:GLN:CG	2:G:28:SER:H	2.15	0.56	



		Interatomic	Clash
Atom-1	Atom-2	distance (Å)	overlap (Å)
1:A:12:LEU:HD11	1:A:171:PRO:HB3	1.88	0.55
1:A:34:LEU:HB2	1:A:107:SER:HB2	1.88	0.55
1:A:176:VAL:HG22	1:A:222:VAL:HG22	1.87	0.55
2:G:19:VAL:HG23	2:G:91:ILE:HG12	1.88	0.55
2:H:181:VAL:HG12	2:H:193:LEU:HD11	1.87	0.55
1:I:132:LEU:HD21	1:I:134:THR:HG23	1.89	0.55
1:F:119:HIS:HD2	2:H:32:ALA:HB3	1.70	0.55
2:G:166:TRP:CD1	2:G:197:LEU:HD22	2.41	0.55
1:I:190:PHE:O	1:I:202:LEU:HD11	2.06	0.55
1:D:2:VAL:HA	1:D:26:SER:O	2.07	0.55
2:H:75:ARG:NH2	2:H:95:GLN:H	2.05	0.55
2:L:25:ALA:N	2:L:85:THR:O	2.40	0.55
1:K:219:ILE:HD11	1:K:232:ASP:HB3	1.88	0.55
1:I:24:ALA:HA	1:I:86:THR:HG22	1.89	0.55
1:I:150:PRO:HG2	1:I:237:PRO:HG3	1.88	0.55
2:L:41:TRP:CZ3	2:L:104:CYS:HB2	2.41	0.55
1:D:176:VAL:HG22	1:D:222:VAL:HG22	1.88	0.54
2:L:25:ALA:HB1	2:L:29:VAL:HG22	1.89	0.54
1:F:41:TRP:HD1	1:F:78:ILE:HD11	1.72	0.54
1:A:148:LEU:HD13	2:B:136:PHE:CE1	2.42	0.54
1:D:190:PHE:O	1:D:202:LEU:HD11	2.06	0.54
2:B:100:ALA:O	2:B:122:VAL:HG22	2.07	0.54
2:H:152:CYS:HB2	2:H:166:TRP:CH2	2.43	0.54
1:I:125:ASP:OD1	1:I:126:TYR:N	2.41	0.54
1:I:119:HIS:HD1	2:J:32:ALA:HB3	1.71	0.54
1:C:50:LEU:HD13	2:G:103:TYR:CE2	2.43	0.54
2:G:123:GLU:OE1	2:G:191:TYR:OH	2.21	0.54
2:L:124:ILE:N	2:L:184:GLN:OE1	2.33	0.54
1:D:221:ASN:HB3	1:D:232:ASP:OD1	2.07	0.54
2:B:169:ASP:HA	2:B:209:VAL:CG1	2.38	0.53
2:B:205:GLU:HA	2:B:229:ARG:HH22	1.70	0.53
2:E:190:THR:HG22	2:E:191:TYR:H	1.74	0.53
1:F:2:VAL:HB	1:F:126:TYR:CZ	2.43	0.53
2:G:4:MET:HB3	2:G:117:GLY:HA2	1.91	0.53
2:G:39:VAL:HG21	2:G:87:PHE:CG	2.44	0.53
2:G:12:SER:HB2	2:G:123:GLU:HG3	1.90	0.53
1:D:129:GLN:HA	2:E:49:ALA:HB2	1.91	0.53
2:E:31:SER:HB2	2:E:106:GLN:HE22	1.74	0.53
2:G:75:ARG:NH1	2:G:98:ASP:OD2	2.42	0.53
1:C:166:VAL:HG23	1:C:202:LEU:HB3	1.90	0.52
2:G:21:ILE:HG21	2:G:120:THR:HG21	1.91	0.52



		Interatomic	Clash
Atom-1	Atom-2	distance (Å)	overlap (Å)
2:B:16:GLY:HA2	2:B:93:SER:HA	1.92	0.52
1:F:146:PHE:CD2	2:H:142:GLN:HG3	2.44	0.52
1:I:13:VAL:HG11	1:I:94:LEU:HD23	1.91	0.52
2:L:96:PRO:HA	2:L:99:PHE:HD2	1.73	0.52
1:C:21:LEU:HD12	1:C:89:LEU:HD23	1.91	0.52
1:K:6:GLU:HG2	1:K:104:CYS:HB3	1.92	0.52
2:G:159:PRO:HD2	2:G:216:HIS:CE1	2.45	0.52
1:A:118:TYR:HD2	2:B:112:TRP:HD1	1.58	0.52
2:B:214:VAL:HG23	2:B:219:LEU:HD21	1.90	0.52
1:F:52:TRP:CG	2:H:114:ILE:HB	2.45	0.52
1:F:106:ARG:HD3	1:F:126:TYR:HB2	1.92	0.52
2:L:154:LEU:HD13	2:L:193:LEU:HD23	1.91	0.52
1:A:224:HIS:CD2	1:A:226:PRO:HD2	2.44	0.52
2:H:157:PHE:CZ	2:H:193:LEU:HD13	2.44	0.52
1:I:219:ILE:HG13	1:I:234:LYS:HA	1.92	0.52
2:J:148:ALA:O	2:J:198:THR:HA	2.10	0.52
1:K:171:PRO:HG2	1:K:224:HIS:NE2	2.25	0.52
1:C:31:GLY:O	1:C:59:SER:HB2	2.10	0.52
1:I:69:ASP:OD1	1:I:69:ASP:N	2.43	0.51
1:F:2:VAL:HG13	1:F:28:PHE:HD2	1.75	0.51
1:F:184:THR:O	1:F:187:VAL:HG12	2.10	0.51
1:K:171:PRO:HG2	1:K:224:HIS:HE2	1.76	0.51
1:A:100:ALA:HB3	1:A:102:TYR:HE1	1.75	0.51
1:D:194:LEU:HD12	1:D:200:TYR:CZ	2.45	0.51
1:I:95:ARG:NH1	1:I:97:GLU:OE2	2.44	0.51
2:G:152:CYS:HB2	2:G:166:TRP:HZ3	1.76	0.51
1:I:91:MET:HE3	1:I:94:LEU:HD11	1.92	0.51
2:J:159:PRO:HD2	2:J:216:HIS:CE1	2.46	0.51
1:K:15:PRO:HD2	1:K:137:SER:HB2	1.92	0.51
1:K:40:HIS:CG	1:K:124:MET:HE2	2.45	0.51
2:E:99:PHE:HA	2:E:122:VAL:HG23	1.93	0.51
2:B:136:PHE:CE2	2:B:153:LEU:HD12	2.46	0.51
1:A:108:ALA:CB	1:A:122:PRO:HG3	2.40	0.51
2:B:136:PHE:CE1	2:B:151:VAL:HG13	2.46	0.51
2:E:153:LEU:HD21	2:E:155:ASN:HB2	1.92	0.51
1:F:94:LEU:HG	1:F:135:VAL:HG21	1.93	0.51
2:H:23:CYS:HB2	2:H:41:TRP:CH2	2.46	0.51
1:K:52:TRP:CG	2:L:114:ILE:HG12	2.46	0.50
1:A:189:THR:HG23	1:A:202:LEU:HD21	1.94	0.50
1:K:115:TRP:HA	2:L:112:TRP:HZ2	1.76	0.50
1:C:178:TRP:CD1	1:C:187:VAL:HG23	2.47	0.50



	to as pagem	Interatomic	Clash
Atom-1	Atom-2	distance (Å)	overlap (Å)
1:F:71:VAL:HG21	1:F:76:PHE:CE2	2.46	0.50
2:J:178:GLN:O	2:J:195:SER:HA	2.10	0.50
2:G:132:SER:HB2	2:G:155:ASN:HB3	1.93	0.50
2:E:193:LEU:HD23	2:E:194:SER:N	2.26	0.50
2:H:166:TRP:CD2	2:H:197:LEU:HD23	2.46	0.50
1:I:15:PRO:HD2	1:I:137:SER:HB2	1.92	0.50
2:B:43:GLN:HG3	2:B:102:TYR:CE2	2.47	0.50
2:B:219:LEU:HD22	2:B:223:VAL:HB	1.93	0.50
1:A:20:ARG:HD2	1:A:90:GLN:HB2	1.92	0.50
2:E:5:THR:HB	2:E:24:ARG:HB2	1.93	0.50
2:J:158:TYR:HB3	2:J:159:PRO:HD3	1.94	0.50
2:G:39:VAL:H	2:G:56:SER:HB3	1.75	0.50
1:A:143:PRO:HD3	1:A:224:HIS:ND1	2.27	0.50
1:D:35:ARG:HD2	1:D:104:CYS:SG	2.52	0.50
1:I:52:TRP:NE1	1:I:55:SER:OG	2.40	0.50
1:K:159:THR:HA	1:K:209:PRO:HA	1.94	0.50
1:D:2:VAL:HG21	1:D:106:ARG:NH1	2.26	0.50
2:E:154:LEU:HB3	2:E:157:PHE:CE2	2.46	0.49
2:L:204:TYR:HE1	2:L:210:TYR:HE2	1.58	0.49
1:C:43:ARG:HD3	1:C:102:TYR:CZ	2.46	0.49
1:C:95:ARG:O	1:C:135:VAL:HG21	2.10	0.49
1:F:54:ALA:HB3	1:F:78:ILE:HD12	1.93	0.49
2:J:53:LEU:HD12	2:J:76:PHE:CD2	2.48	0.49
1:C:183:LEU:HD13	1:C:206:VAL:HG21	1.94	0.49
2:G:126:ARG:HG2	2:G:158:TYR:CD1	2.47	0.49
1:A:106:ARG:O	1:A:124:MET:HA	2.13	0.49
1:A:140:THR:HB	1:I:227:SER:HA	1.94	0.49
1:F:176:VAL:HG22	1:F:222:VAL:HG22	1.94	0.49
1:I:67:TYR:CE1	1:I:78:ILE:HG22	2.47	0.49
1:I:71:VAL:HG21	1:I:76:PHE:CD2	2.47	0.49
2:J:7:SER:HB2	2:J:8:PRO:HD3	1.94	0.49
2:G:216:HIS:H	2:G:219:LEU:HD11	1.76	0.49
1:D:118:TYR:CD2	2:E:112:TRP:HD1	2.31	0.49
1:F:106:ARG:O	1:F:124:MET:HA	2.12	0.49
2:H:30:SER:HB3	2:H:106:GLN:HE22	1.77	0.49
2:H:180:SER:HB3	2:H:194:SER:OG	2.12	0.49
1:K:62:TYR:HH	1:K:115:TRP:HZ2	1.58	0.49
1:F:41:TRP:HD1	1:F:78:ILE:CD1	2.26	0.49
2:J:176:ASN:O	2:J:197:LEU:HA	2.13	0.49
1:K:118:TYR:HB3	2:L:109:SER:HA	1.94	0.49
1:C:170:PHE:HE2	1:D:228:ASN:HD22	1.60	0.49



	to as pagem	Interatomic	Clash
Atom-1	Atom-2	distance (Å)	overlap (Å)
1:K:125:ASP:OD1	1:K:126:TYR:N	2.46	0.49
1:D:6:GLU:OE2	1:D:128:GLY:HA3	2.13	0.49
2:E:7:SER:HB3	2:E:8:PRO:HD3	1.93	0.49
2:B:160:ARG:HD2	2:B:191:TYR:CE2	2.48	0.49
2:L:204:TYR:CE1	2:L:210:TYR:HE2	2.31	0.49
2:G:23:CYS:O	2:G:86:ASP:HA	2.13	0.49
1:A:106:ARG:NH2	1:A:125:ASP:OD2	2.44	0.49
1:D:110:SER:HB2	1:D:113:GLY:H	1.78	0.49
1:A:127:TRP:CZ3	2:B:50:PRO:HG2	2.48	0.48
2:E:131:PRO:HB3	2:E:157:PHE:CD2	2.48	0.48
1:K:43:ARG:HD3	1:K:102:TYR:CZ	2.49	0.48
1:D:106:ARG:O	1:D:124:MET:HA	2.13	0.48
3:C:301:EPE:H22	1:I:120:PHE:CG	2.48	0.48
1:D:195:GLN:HB2	1:D:199:LEU:O	2.14	0.48
2:E:226:SER:OG	2:E:227:PHE:N	2.46	0.48
2:B:136:PHE:HE1	2:B:151:VAL:HG13	1.78	0.48
1:D:60:TYR:HH	1:F:110:SER:HG	1.61	0.48
1:A:34:LEU:CB	1:A:107:SER:HB2	2.44	0.48
1:I:34:LEU:HB2	1:I:107:SER:HB3	1.96	0.48
2:B:126:ARG:H	2:B:158:TYR:HE2	1.61	0.48
1:I:150:PRO:HD2	1:I:237:PRO:HA	1.95	0.48
2:L:154:LEU:HB2	2:L:193:LEU:HB3	1.95	0.48
2:B:23:CYS:O	2:B:86:ASP:HA	2.13	0.48
2:B:53:LEU:HD11	2:B:76:PHE:HD2	1.79	0.48
1:I:112:TYR:HB2	1:K:112:TYR:CB	2.44	0.48
1:C:2:VAL:HG12	1:C:27:GLY:HA3	1.96	0.48
1:C:69:ASP:OD1	1:C:69:ASP:N	2.42	0.47
1:C:106:ARG:O	1:C:124:MET:HA	2.14	0.47
2:E:96:PRO:HA	2:E:99:PHE:HD2	1.79	0.47
1:F:136:SER:HB3	1:F:170:PHE:CZ	2.48	0.47
2:J:142:GLN:HE21	2:J:142:GLN:CA	2.26	0.47
1:K:177:SER:HB2	1:K:221:ASN:ND2	2.28	0.47
1:A:136:SER:HB2	1:A:170:PHE:CZ	2.49	0.47
1:K:41:TRP:NE1	1:K:89:LEU:HB2	2.29	0.47
2:B:99:PHE:HD1	2:B:122:VAL:HG23	1.78	0.47
1:D:71:VAL:HG21	1:D:76:PHE:CD2	2.49	0.47
2:H:124:ILE:HB	2:H:184:GLN:HE22	1.79	0.47
1:A:100:ALA:HB3	1:A:102:TYR:CE1	2.50	0.47
1:A:112:TYR:CE1	1:A:116:HIS:HD2	2.33	0.47
1:A:175:THR:OG1	1:A:223:ASN:OD1	2.32	0.47
1:D:208:VAL:HG11	1:D:218:TYR:CZ	2.50	0.47



		Interatomic	Clash	
Atom-1	Atom-2	distance $(Å)$	overlap (Å)	
2:E:44:GLN:HB2	2:E:50:PRO:HG3	1.96	0.47	
1:C:110:SER:OG	1:C:113:GLY:N	2.40	0.47	
2:B:137:PRO:HG3	2:B:227:PHE:CD1	2.50	0.47	
2:L:108:VAL:HB	2:L:113:LEU:HD23	1.95	0.47	
2:B:133:VAL:HG21	2:B:214:VAL:HG21	1.96	0.47	
2:B:168:VAL:HG11	2:B:173:GLN:NE2	2.30	0.47	
2:B:214:VAL:HG22	2:B:223:VAL:O	2.14	0.47	
1:D:166:VAL:HG23	1:D:202:LEU:HB3	1.96	0.47	
2:E:98:ASP:O	2:E:102:TYR:OH	2.21	0.47	
2:E:108:VAL:HB	2:E:113:LEU:HG	1.96	0.47	
1:F:50:LEU:HD23	2:H:103:TYR:CZ	2.50	0.47	
1:F:194:LEU:HB3	1:F:200:TYR:CE2	2.50	0.47	
2:H:108:VAL:CG2	2:H:113:LEU:HG	2.44	0.47	
1:I:119:HIS:CE1	2:J:32:ALA:H	2.33	0.47	
2:J:95:GLN:HG2	2:J:96:PRO:CD	2.38	0.47	
1:K:94:LEU:HD12	1:K:135:VAL:HG21	1.97	0.47	
2:L:134:PHE:HD2	2:L:153:LEU:HD23	1.78	0.47	
2:G:166:TRP:NE1	2:G:197:LEU:HD22	2.30	0.47	
2:E:15:VAL:HG13	2:E:96:PRO:HD3	1.95	0.47	
2:J:125:LYS:HA	2:J:158:TYR:CE2	2.50	0.47	
1:C:184:THR:O	1:C:187:VAL:HG12	2.15	0.47	
1:C:224:HIS:CD2	1:C:226:PRO:HD2	2.50	0.47	
1:A:192:ALA:HB2	1:A:202:LEU:HD12	1.96	0.47	
2:E:16:GLY:N	2:E:94:LEU:O	2.30	0.47	
1:I:163:GLY:HA3	1:I:205:VAL:HG12	1.97	0.47	
2:G:149:SER:HA	2:G:197:LEU:O	2.15	0.46	
1:D:3:GLN:HG2	1:D:26:SER:HB3	1.97	0.46	
1:C:41:TRP:CG	1:C:89:LEU:HD22	2.50	0.46	
1:A:14:GLN:HB3	1:A:137:SER:HA	1.96	0.46	
2:B:131:PRO:HG3	2:B:157:PHE:HB3	1.96	0.46	
1:C:41:TRP:CD1	1:C:89:LEU:HB2	2.50	0.46	
2:G:27:GLN:HG3	2:G:29:VAL:HG12	1.97	0.46	
1:A:71:VAL:HG21	1:A:76:PHE:CE2	2.50	0.46	
1:D:67:TYR:CE1	1:D:78:ILE:HG22	2.50	0.46	
2:E:150:VAL:HG12	2:E:166:TRP:CH2	2.51	0.46	
2:E:225:LYS:HB3	2:E:225:LYS:HE3	1.65	0.46	
2:B:8:PRO:HG2	2:B:21:ILE:HA	1.97	0.46	
1:I:84:LYS:O	1:I:86:THR:HG23	2.16	0.46	
1:K:33:TYR:HD1	1:K:108:ALA:HA	1.81	0.46	
2:L:184:GLN:HG2	2:L:191:TYR:HE1	1.76	0.46	
2:B:184:GLN:HB3	2:B:191:TYR:CE2	2.50	0.46	



	A 4 a m 2	Interatomic	Clash
Atom-1	Atom-2	distance (\AA)	overlap (Å)
2:H:83:SER:HB3	2:H:86:ASP:HB2	1.98	0.46
1:I:114:TYR:HE1	2:J:112:TRP:CG	2.33	0.46
2:J:169:ASP:CG	2:J:207:HIS:HB3	2.36	0.46
1:K:163:GLY:HA3	1:K:205:VAL:HG12	1.97	0.46
2:H:181:VAL:HG12	2:H:193:LEU:CD1	2.45	0.46
1:A:9:GLY:HA2	1:A:133:VAL:HG22	1.98	0.46
1:A:29:ASP:OD2	1:D:33:TYR:OH	2.20	0.46
2:B:185:ASP:OD1	2:B:186:SER:N	2.49	0.46
1:K:13:VAL:O	1:K:135:VAL:HA	2.15	0.46
1:D:91:MET:HE2	1:D:94:LEU:HD21	1.96	0.46
2:G:155:ASN:O	2:G:157:PHE:HD1	1.98	0.46
1:A:118:TYR:O	1:A:121:SER:HB2	2.15	0.46
2:E:71:VAL:N	2:E:72:PRO:HD2	2.31	0.45
2:E:162:ALA:HB2	2:E:216:HIS:HD2	1.81	0.45
2:L:6:GLN:O	2:L:118:GLN:NE2	2.49	0.45
1:A:31:GLY:O	1:A:59:SER:OG	2.33	0.45
1:F:3:GLN:HB2	1:F:26:SER:HB3	1.99	0.45
1:I:146:PHE:CE2	2:J:142:GLN:NE2	2.84	0.45
2:J:143:LEU:HD21	2:J:204:TYR:CD2	2.51	0.45
1:C:67:TYR:CE2	1:C:78:ILE:HG22	2.51	0.45
2:G:181:VAL:HA	2:G:192:SER:O	2.16	0.45
1:A:228:ASN:HD22	1:I:170:PHE:HE2	1.64	0.45
2:B:133:VAL:C	2:B:134:PHE:HD1	2.19	0.45
2:B:136:PHE:HA	2:B:137:PRO:HD3	1.85	0.45
2:L:140:ASP:OD1	2:L:140:ASP:N	2.48	0.45
1:C:2:VAL:HG23	1:C:126:TYR:CD2	2.52	0.45
1:A:118:TYR:CD2	2:B:112:TRP:HD1	2.34	0.45
1:D:13:VAL:HG11	1:D:94:LEU:HD23	1.97	0.45
2:H:75:ARG:NH2	2:H:98:ASP:OD2	2.49	0.45
2:J:11:LEU:O	2:J:122:VAL:HA	2.16	0.45
2:J:104:CYS:O	2:J:116:PHE:HA	2.16	0.45
2:J:139:SER:O	2:J:142:GLN:HB3	2.17	0.45
2:G:4:MET:HG2	2:G:24:ARG:O	2.17	0.45
2:B:161:GLU:O	2:B:216:HIS:HD2	2.00	0.45
1:D:116:HIS:CE1	3:D:302:EPE:H82	2.51	0.45
2:H:107:TYR:CD1	2:H:114:ILE:HG12	2.48	0.45
1:C:115:TRP:CE2	3:C:301:EPE:H51	2.52	0.45
2:G:126:ARG:HG3	2:G:127:THR:O	2.16	0.45
2:G:167:TYR:CE2	2:G:172:LEU:HB3	2.51	0.45
2:G:193:LEU:HD23	2:G:194:SER:N	2.32	0.45
1:K:108:ALA:HB3	1:K:122:PRO:HG2	1.98	0.45



	A L O	Interatomic	Clash
Atom-1	Atom-2	distance (\AA)	overlap (Å)
1:K:147:PRO:O	2:L:139:SER:OG	2.34	0.45
1:C:6:GLU:OE2	1:C:130:GLY:N	2.49	0.45
2:E:158:TYR:CD1	2:E:159:PRO:HA	2.52	0.45
2:J:100:ALA:O	2:J:122:VAL:HG22	2.17	0.45
2:L:105:GLN:HB2	2:L:116:PHE:CE1	2.51	0.45
1:D:107:SER:HB3	1:D:108:ALA:H	1.58	0.45
2:J:125:LYS:HA	2:J:158:TYR:HE2	1.81	0.45
1:C:178:TRP:CZ3	1:C:220:CYS:HB3	2.52	0.45
2:G:152:CYS:HB2	2:G:166:TRP:CH2	2.51	0.45
1:A:67:TYR:CE1	1:A:78:ILE:HG22	2.52	0.45
1:A:194:LEU:H	1:A:194:LEU:HD23	1.81	0.45
2:B:43:GLN:O	2:B:50:PRO:HA	2.17	0.45
2:B:173:GLN:OE1	2:B:176:ASN:ND2	2.50	0.45
2:L:167:TYR:CE1	2:L:172:LEU:HD13	2.52	0.45
2:B:21:ILE:HG21	2:B:120:THR:HG21	1.98	0.44
1:D:150:PRO:HG3	1:D:162:LEU:HB3	1.98	0.44
1:D:222:VAL:O	1:D:230:LYS:HA	2.16	0.44
2:J:101:THR:HA	2:J:121:LYS:HA	1.99	0.44
2:L:11:LEU:HD21	2:L:21:ILE:CG2	2.45	0.44
2:G:75:ARG:H	2:G:75:ARG:HG2	1.50	0.44
2:L:89:LEU:HD13	2:L:91:ILE:HG13	1.98	0.44
2:H:105:GLN:HB2	2:H:116:PHE:CE1	2.53	0.44
2:J:67:LEU:HD12	2:J:71:VAL:HG12	1.99	0.44
1:C:94:LEU:HD12	1:C:94:LEU:HA	1.80	0.44
1:D:230:LYS:HB3	1:D:230:LYS:HE2	1.83	0.44
1:F:57:TYR:CE1	1:F:109:ALA:HB1	2.53	0.44
2:J:23:CYS:N	2:J:87:PHE:O	2.36	0.44
2:L:11:LEU:O	2:L:122:VAL:HA	2.18	0.44
2:L:44:GLN:NE2	2:L:48:LYS:O	2.51	0.44
2:G:173:GLN:OE1	2:G:176:ASN:ND2	2.49	0.44
1:F:23:CYS:O	1:F:86:THR:HA	2.17	0.44
1:K:75:ARG:NH2	1:K:95:ARG:HG3	2.32	0.44
1:K:190:PHE:O	1:K:202:LEU:HD11	2.17	0.44
2:L:158:TYR:O	2:L:216:HIS:HE1	2.00	0.44
1:A:67:TYR:HE1	1:A:78:ILE:HG22	1.83	0.44
1:A:91:MET:CE	1:A:94:LEU:HD11	2.48	0.44
1:A:97:GLU:OE1	1:A:97:GLU:N	2.43	0.44
1:K:6:GLU:CG	1:K:104:CYS:HB3	2.48	0.44
2:L:108:VAL:HG12	2:L:111:GLY:H	1.83	0.44
1:D:105:ALA:HB1	1:D:124:MET:HB3	2.00	0.44
1:C:112:TYR:CD1	1:C:116:HIS:HD2	2.36	0.44



	to as pagem	Interatomic	Clash	
Atom-1	Atom-2	distance (Å)	overlap (Å)	
1:C:150:PRO:HD3	1:C:162:LEU:HB3	2.00	0.43	
1:C:71:VAL:HG21	1:C:76:PHE:CE2	2.54	0.43	
1:F:105:ALA:HB1	1:F:124:MET:HB3	1.99	0.43	
2:L:111:GLY:HA3	2:L:113:LEU:HD22	2.01	0.43	
1:C:150:PRO:HB3	1:C:161:ALA:O	2.18	0.43	
2:J:162:ALA:HA	2:J:215:THR:O	2.18	0.43	
1:K:106:ARG:O	1:K:124:MET:HA	2.18	0.43	
1:D:84:LYS:O	1:D:86:THR:HG23	2.19	0.43	
2:E:180:SER:HB3	2:E:194:SER:HB3	2.01	0.43	
2:H:108:VAL:HG22	2:H:113:LEU:O	2.19	0.43	
1:K:177:SER:CB	1:K:221:ASN:HD21	2.31	0.43	
1:F:171:PRO:HD2	1:F:224:HIS:HE1	1.83	0.43	
2:H:167:TYR:HA	2:H:171:ALA:O	2.19	0.43	
1:C:163:GLY:HA3	1:C:204:SER:O	2.19	0.43	
2:J:123:GLU:OE1	2:J:184:GLN:NE2	2.51	0.43	
2:J:204:TYR:HH	2:J:227:PHE:HE2	1.66	0.43	
1:K:90:GLN:HG3	1:K:92:ASN:OD1	2.18	0.43	
1:C:71:VAL:HG21	1:C:76:PHE:CD2	2.54	0.43	
1:C:123:GLY:HA3	2:G:52:LEU:HD11	2.01	0.43	
3:C:301:EPE:H72	1:I:117:TRP:CE2	2.54	0.43	
1:A:52:TRP:HB2	2:B:116:PHE:HE1	1.83	0.43	
2:B:159:PRO:HD2	2:B:216:HIS:CE1	2.54	0.43	
2:B:168:VAL:HG11	2:B:173:GLN:HE21	1.84	0.43	
1:D:112:TYR:CD2	1:D:116:HIS:HD2	2.37	0.43	
2:E:133:VAL:HG23	2:E:225:LYS:HG3	2.00	0.43	
1:I:2:VAL:HG23	1:I:26:SER:O	2.18	0.43	
2:G:184:GLN:HG3	2:G:191:TYR:CE1	2.53	0.43	
2:B:149:SER:HA	2:B:197:LEU:O	2.19	0.43	
1:F:194:LEU:HA	1:F:200:TYR:HA	2.01	0.43	
2:H:41:TRP:CZ3	2:H:104:CYS:HB2	2.53	0.43	
1:I:31:GLY:O	1:I:59:SER:OG	2.35	0.43	
1:I:94:LEU:HA	1:I:94:LEU:HD12	1.68	0.43	
1:K:52:TRP:CD1	2:L:114:ILE:HG12	2.53	0.43	
1:C:52:TRP:CE3	1:C:68:ALA:HB2	2.53	0.43	
1:K:91:MET:HB3	1:K:94:LEU:HD21	2.01	0.43	
1:K:183:LEU:HD11	1:K:218:TYR:CD1	2.54	0.43	
2:L:213:GLU:HA	2:L:224:THR:HG22	2.00	0.43	
1:C:52:TRP:CH2	2:G:113:LEU:HA	2.53	0.43	
1:A:119:HIS:CD2	2:B:109:SER:HB3	2.54	0.43	
1:D:52:TRP:CG	2:E:114:ILE:HB	2.54	0.43	
1:F:76:PHE:CE2	1:F:91:MET:HG2	2.53	0.43	



	to ao pagoin	Interatomic	Clash	
Atom-1	Atom-2	distance (Å)	overlap (Å)	
1:F:121:SER:HB2	2:H:107:TYR:CD2	2.53	0.43	
2:H:75:ARG:HH22	2:H:98:ASP:CG	2.22	0.43	
2:H:126:ARG:HG2	2:H:127:THR:N	2.34	0.43	
1:I:52:TRP:CG	2:J:114:ILE:HB	2.54	0.43	
1:K:138:ALA:HB3	1:K:170:PHE:CE1	2.54	0.43	
1:K:190:PHE:CE2	2:L:194:SER:HB2	2.53	0.43	
2:L:27:GLN:HB2	2:L:28:SER:H	1.70	0.43	
1:K:178:TRP:HB3	1:K:183:LEU:HD12	2.01	0.42	
1:K:224:HIS:CD2	1:K:226:PRO:HD2	2.53	0.42	
2:G:7:SER:HB2	2:G:8:PRO:HD3	2.01	0.42	
2:B:181:VAL:HA	2:B:192:SER:O	2.20	0.42	
2:H:54:ILE:HD11	2:H:76:PHE:HB3	2.01	0.42	
2:E:104:CYS:O	2:E:117:GLY:N	2.52	0.42	
1:F:80:ALA:HA	1:F:87:ALA:HA	2.02	0.42	
2:H:16:GLY:N	2:H:94:LEU:HB3	2.32	0.42	
1:I:163:GLY:HA2	1:I:178:TRP:CH2	2.54	0.42	
2:L:118:GLN:H	2:L:118:GLN:HG2	1.63	0.42	
1:A:118:TYR:HE2	2:B:112:TRP:HB3	1.83	0.42	
1:A:146:PHE:CE2	2:B:139:SER:HB3	2.54	0.42	
2:E:19:VAL:HG22	2:E:91:ILE:HB	2.01	0.42	
2:E:96:PRO:HA	2:E:99:PHE:CD2	2.55	0.42	
2:E:126:ARG:HD2	2:E:189:SER:OG	2.19	0.42	
1:F:166:VAL:HG11	1:F:222:VAL:HG11	2.00	0.42	
1:I:13:VAL:O	1:I:135:VAL:HA	2.19	0.42	
2:J:166:TRP:HD1	2:J:168:VAL:HG23	1.84	0.42	
1:C:141:LYS:HG2	1:C:142:GLY:O	2.20	0.42	
1:C:146:PHE:CE2	2:G:142:GLN:HG3	2.55	0.42	
1:A:125:ASP:OD1	1:A:126:TYR:N	2.52	0.42	
2:E:20:THR:HG22	2:E:90:THR:HG22	2.02	0.42	
2:E:167:TYR:CE1	2:E:172:LEU:HD12	2.54	0.42	
1:K:167:LYS:HG3	1:K:168:ASP:OD1	2.20	0.42	
2:L:100:ALA:O	2:L:122:VAL:HG22	2.19	0.42	
2:L:164:VAL:O	2:L:164:VAL:HG13	2.19	0.42	
2:B:155:ASN:CG	2:B:156:ASN:H	2.22	0.42	
1:D:13:VAL:O	1:D:135:VAL:HA	2.19	0.42	
2:H:18:ARG:HA	2:H:91:ILE:O	2.19	0.42	
2:H:154:LEU:O	2:H:192:SER:HA	2.19	0.42	
1:I:238:LYS:HD2	1:I:239:SER:N	2.34	0.42	
2:L:143:LEU:HD21	2:L:204:TYR:HE2	1.85	0.42	
1:C:190:PHE:CE2	2:G:194:SER:HB2	2.55	0.42	
2:G:89:LEU:O	2:G:89:LEU:HD23	2.20	0.42	



		Interatomic	Clash	
Atom-1	Atom-2	distance (Å)	overlap (Å)	
1:A:167:LYS:HB2	1:A:167:LYS:HE3	1.81	0.42	
1:F:13:VAL:O	1:F:135:VAL:HA	2.20	0.42	
1:K:76:PHE:N	1:K:76:PHE:CD1	2.88	0.42	
1:C:112:TYR:CE1	1:C:116:HIS:HD2	2.38	0.42	
1:A:146:PHE:CZ	2:B:139:SER:HB3	2.54	0.42	
1:D:112:TYR:HB2	1:F:112:TYR:CG	2.55	0.42	
2:E:152:CYS:HB2	2:E:195:SER:HB3	2.02	0.42	
1:F:171:PRO:HB2	1:F:226:PRO:HG2	2.01	0.42	
2:H:138:PRO:HB3	2:H:149:SER:H	1.85	0.42	
2:H:158:TYR:HB2	2:H:190:THR:HG22	2.00	0.42	
1:K:171:PRO:HG3	1:K:226:PRO:HB2	2.01	0.42	
1:A:13:VAL:O	1:A:135:VAL:HA	2.18	0.42	
2:B:137:PRO:HG3	2:B:227:PHE:CG	2.54	0.42	
1:F:18:SER:HB3	1:F:92:ASN:OD1	2.19	0.42	
2:G:99:PHE:CE2	2:G:124:ILE:HA	2.55	0.42	
2:G:125:LYS:HA	2:G:158:TYR:OH	2.20	0.42	
1:D:166:VAL:CG2	1:D:202:LEU:HB3	2.50	0.41	
2:E:95:GLN:HB2	2:E:97:GLU:HG2	2.02	0.41	
2:B:95:GLN:HB3	2:B:96:PRO:HD2	2.02	0.41	
2:E:101:THR:HA	2:E:121:LYS:HA	2.03	0.41	
2:J:108:VAL:HB	2:J:113:LEU:HB2	2.03	0.41	
1:C:12:LEU:HD13	1:D:228:ASN:HB2	2.02	0.41	
1:C:136:SER:HB3	1:C:170:PHE:CZ	2.56	0.41	
3:C:301:EPE:H81	3:C:301:EPE:H52	1.82	0.41	
1:A:120:PHE:HD2	2:B:57:ALA:HB2	1.84	0.41	
1:D:91:MET:HE3	1:D:94:LEU:HD11	2.02	0.41	
1:D:213:LEU:HD23	1:D:213:LEU:H	1.85	0.41	
1:D:40:HIS:CE1	1:D:107:SER:OG	2.73	0.41	
2:H:152:CYS:HB2	2:H:166:TRP:CZ2	2.56	0.41	
1:I:33:TYR:HA	1:I:108:ALA:O	2.21	0.41	
1:K:218:TYR:O	1:K:235:VAL:HG22	2.20	0.41	
1:C:15:PRO:HD2	1:C:137:SER:HB3	2.02	0.41	
1:C:34:LEU:H	1:C:34:LEU:HD12	1.85	0.41	
1:F:219:ILE:HG13	1:F:233:LYS:C	2.40	0.41	
2:J:204:TYR:OH	2:J:227:PHE:HE2	2.03	0.41	
1:K:75:ARG:HH21	1:K:95:ARG:HG3	1.85	0.41	
1:C:183:LEU:HD23	1:C:183:LEU:HA	1.93	0.41	
2:B:141:GLU:H	2:B:141:GLU:HG3	1.68	0.41	
1:K:163:GLY:HA2	1:K:178:TRP:CZ2	2.56	0.41	
2:L:83:SER:HB3	2:L:86:ASP:O	2.20	0.41	
1:A:176:VAL:HA	1:A:221:ASN:O	2.21	0.41	



		Interatomic	Clash	
Atom-1	Atom-2	distance (\AA)	overlap (Å)	
2:B:14:SER:OG	2:B:125:LYS:O	2.39	0.41	
2:B:53:LEU:HD23	2:B:89:LEU:CD2	2.51	0.41	
2:B:156:ASN:HA	2:B:191:TYR:O	2.20	0.41	
2:E:154:LEU:HD22	2:E:193:LEU:HD13	2.02	0.41	
1:F:62:TYR:HD2	1:F:114:TYR:CD2	2.39	0.41	
2:H:75:ARG:H	2:H:75:ARG:HG2	1.53	0.41	
1:I:112:TYR:HB2	1:K:112:TYR:HB2	2.02	0.41	
2:J:53:LEU:HA	2:J:71:VAL:HG21	2.02	0.41	
2:B:99:PHE:CZ	2:B:124:ILE:HG22	2.56	0.41	
1:D:94:LEU:HA	1:D:94:LEU:HD12	1.65	0.41	
1:F:194:LEU:HD23	1:F:194:LEU:H	1.86	0.41	
2:H:158:TYR:CD1	2:H:159:PRO:HA	2.55	0.41	
2:J:53:LEU:H	2:J:53:LEU:HD23	1.85	0.41	
2:J:212:CYS:O	2:J:224:THR:HA	2.21	0.41	
2:L:6:GLN:HA	2:L:23:CYS:HA	2.02	0.41	
1:A:46:PRO:HD3	1:A:99:THR:O	2.21	0.41	
1:I:143:PRO:HB3	1:I:169:TYR:HB3	2.02	0.41	
2:L:41:TRP:HB2	2:L:53:LEU:HD12	2.03	0.41	
1:C:124:MET:HB2	2:G:42:TYR:OH	2.21	0.40	
2:G:40:ALA:HB3	2:G:105:GLN:HG3	2.02	0.40	
2:G:108:VAL:HG12	2:G:113:LEU:O	2.21	0.40	
2:E:131:PRO:HB3	2:E:157:PHE:HD2	1.86	0.40	
2:E:185:ASP:OD1	2:E:186:SER:N	2.54	0.40	
2:E:199:LEU:H	2:E:199:LEU:HD23	1.86	0.40	
1:I:105:ALA:HB1	1:I:124:MET:HB3	2.03	0.40	
2:J:142:GLN:CA	2:J:142:GLN:NE2	2.84	0.40	
1:K:146:PHE:CE2	2:L:142:GLN:HG3	2.56	0.40	
1:C:125:ASP:OD1	1:C:126:TYR:N	2.51	0.40	
1:A:162:LEU:HD11	1:A:218:TYR:HD2	1.85	0.40	
2:E:39:VAL:HG12	2:E:57:ALA:HB2	2.03	0.40	
2:J:154:LEU:HD21	2:J:214:VAL:HG13	2.02	0.40	
1:K:43:ARG:HG3	1:K:44:GLN:N	2.35	0.40	
1:D:149:ALA:HA	1:D:150:PRO:HD3	1.92	0.40	
2:E:102:TYR:HE1	2:E:122:VAL:HG22	1.85	0.40	
2:E:125:LYS:HA	2:E:158:TYR:OH	2.21	0.40	
2:E:150:VAL:HG12	2:E:166:TRP:HH2	1.86	0.40	
1:F:2:VAL:HB	1:F:126:TYR:CE1	2.56	0.40	
2:H:150:VAL:HB	2:H:197:LEU:HG	2.03	0.40	
2:G:166:TRP:CD1	2:G:197:LEU:HD13	2.57	0.40	
1:D:2:VAL:HG21	1:D:106:ARG:HH11	1.85	0.40	
1:D:159:THR:O	1:D:159:THR:OG1	2.36	0.40	



Atom 1	Atom 2	Interatomic	Clash
Atom-1	Atom-2	distance (Å)	overlap (Å)
2:E:22:THR:HG22	2:E:88:THR:HG23	2.02	0.40
2:E:197:LEU:HG	2:E:199:LEU:HD22	2.04	0.40
2:H:212:CYS:O	2:H:224:THR:HA	2.21	0.40
1:I:9:GLY:HA2	1:I:133:VAL:HG22	2.04	0.40
2:J:140:ASP:N	2:J:140:ASP:OD1	2.54	0.40
1:K:171:PRO:CG	1:K:226:PRO:HB2	2.52	0.40
2:L:162:ALA:HB2	2:L:216:HIS:HD2	1.85	0.40
2:G:12:SER:HB2	2:G:123:GLU:CG	2.51	0.40
2:E:45:LYS:HG3	2:E:100:ALA:HB2	2.03	0.40
1:F:6:GLU:OE2	1:F:128:GLY:HA3	2.22	0.40
1:F:42:VAL:O	1:F:103:TYR:HB2	2.21	0.40

There are no symmetry-related clashes.

5.3 Torsion angles (i)

5.3.1 Protein backbone (i)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percent	tiles
1	А	222/237~(94%)	204 (92%)	16 (7%)	2(1%)	17 5	56
1	С	222/237~(94%)	202 (91%)	20 (9%)	0	100 1	100
1	D	220/237~(93%)	204 (93%)	15 (7%)	1 (0%)	29 6	68
1	F	221/237~(93%)	206 (93%)	15 (7%)	0	100 1	100
1	Ι	220/237~(93%)	203~(92%)	14 (6%)	3~(1%)	11 4	46
1	Κ	220/237~(93%)	204 (93%)	16 (7%)	0	100 1	100
2	В	196/216~(91%)	172 (88%)	23 (12%)	1 (0%)	29 6	68
2	Е	205/216~(95%)	186 (91%)	19 (9%)	0	100 1	100
2	G	206/216~(95%)	181 (88%)	24 (12%)	1 (0%)	29 6	68
2	Н	$20\overline{3/216}~(94\%)$	187 (92%)	16 (8%)	0	100 1	100
2	J	205/216~(95%)	187 (91%)	18 (9%)	0	100 1	100



Mol	Chain	Analysed	Favoured	Allowed	Outliers	Perce	ntiles	
2	L	196/216~(91%)	178~(91%)	18 (9%)	0	100	100	
All	All	2536/2718~(93%)	2314 (91%)	214 (8%)	8 (0%)	41	75	

All (8) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	А	9	GLY
1	D	9	GLY
1	Ι	182	ALA
2	В	99	PHE
2	G	99	PHE
1	А	183	LEU
1	Ι	237	PRO
1	Ι	9	GLY

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 sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Perce	ntiles
1	А	172/195~(88%)	169~(98%)	3~(2%)	60	82
1	С	177/195~(91%)	175 (99%)	2(1%)	73	88
1	D	175/195~(90%)	172 (98%)	3 (2%)	60	82
1	F	172/195~(88%)	170 (99%)	2(1%)	71	87
1	Ι	170/195~(87%)	167 (98%)	3 (2%)	59	81
1	K	170/195~(87%)	166 (98%)	4 (2%)	49	76
2	В	154/188~(82%)	150 (97%)	4 (3%)	46	74
2	Ε	164/188~(87%)	154 (94%)	10 (6%)	18	51
2	G	170/188~(90%)	163 (96%)	7 (4%)	30	63
2	Н	149/188~(79%)	148 (99%)	1 (1%)	84	93
2	J	151/188~(80%)	148 (98%)	3 (2%)	55	79
2	L	151/188 (80%)	148 (98%)	3(2%)	55	79



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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
All	All	1975/2298~(86%)	1930~(98%)	45 (2%)	50 77

All (45) residues with a non-rotameric side chain are listed below:

Mol	Chain	Res	Type
1	С	43	ARG
1	С	57	TYR
2	G	18	ARG
2	G	27	GLN
2	G	80	ARG
2	G	104	CYS
2	G	163	LYS
2	G	184	GLN
2	G	203	ASP
1	А	20	ARG
1	А	57	TYR
1	А	118	TYR
2	В	52	LEU
2	В	136	PHE
2	В	152	CYS
2	В	203	ASP
1	D	40	HIS
1	D	57	TYR
1	D	59	SER
2	Е	18	ARG
2	Е	23	CYS
2	Е	104	CYS
2	Е	118	GLN
2	Е	122	VAL
2	Е	123	GLU
2	Е	139	SER
2	Е	140	ASP
2	Е	142	GLN
2	Е	143	LEU
1	F	57	TYR
1	F	141	LYS
2	Н	75	ARG
1	Ι	107	SER
1	Ι	114	TYR
1	Ι	115	TRP
2	J	66	ASP
2	J	142	GLN



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Mol	Chain	\mathbf{Res}	Type
2	J	212	CYS
1	Κ	57	TYR
1	Κ	104	CYS
1	Κ	167	LYS
1	Κ	221	ASN
2	L	104	CYS
2	L	112	TRP
2	L	212	CYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (4) such sidechains are listed below:

Mol	Chain	Res	Type
2	G	178	GLN
2	G	184	GLN
2	Е	142	GLN
2	J	142	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)

4 ligands are modelled in this entry.

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	Turne	Chain	Dec	Tinle	Bo	ond leng	\mathbf{ths}	B	ond ang	les
INIOI	туре	Unam	nes		Counts	RMSZ	# Z >2	Counts	RMSZ	# Z > 2
4	SO4	K	301	-	4,4,4	0.17	0	6,6,6	0.09	0
3	EPE	D	302	-	$15,\!15,\!15$	0.89	1 (6%)	18,20,20	1.77	6 (33%)
4	SO4	D	301	-	4,4,4	0.16	0	6,6,6	0.11	0
3	EPE	С	301	-	$15,\!15,\!15$	0.92	1 (6%)	18,20,20	2.07	6 (33%)

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
3	EPE	D	302	-	-	5/9/19/19	0/1/1/1
3	EPE	С	301	-	-	3/9/19/19	0/1/1/1

All	(2)	bond	length	outliers	are	listed	below:
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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	$\mathrm{Ideal}(\mathrm{\AA})$
3	D	302	EPE	C10-S	3.05	1.81	1.77
3	С	301	EPE	C10-S	2.92	1.81	1.77

All (12) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	$\mathbf{Observed}(^{o})$	$Ideal(^{o})$
3	D	302	EPE	C5-N4-C3	4.43	118.81	108.83
3	С	301	EPE	C5-N4-C3	4.20	118.28	108.83
3	С	301	EPE	C7-N4-C5	3.89	121.19	111.23
3	С	301	EPE	C7-N4-C3	3.60	120.43	111.23
3	С	301	EPE	O1S-S-C10	3.16	110.72	106.92
3	D	302	EPE	C7-N4-C3	2.83	118.46	111.23
3	С	301	EPE	C6-N1-C2	2.68	114.86	108.83
3	D	302	EPE	O3S-S-C10	2.30	109.49	105.77
3	С	301	EPE	O2S-S-C10	2.28	109.66	106.92
3	D	302	EPE	C7-N4-C5	2.21	116.89	111.23
3	D	302	EPE	O1S-S-C10	2.12	109.47	106.92
3	D	302	EPE	O2S-S-C10	2.08	109.42	106.92

There are no chirality outliers.

All (8) torsion outliers are listed below:



Mol	Chain	Res	Type	Atoms
3	С	301	EPE	C8-C7-N4-C5
3	D	302	EPE	C9-C10-S-O1S
3	D	302	EPE	C9-C10-S-O3S
3	С	301	EPE	C10-C9-N1-C2
3	С	301	EPE	C10-C9-N1-C6
3	D	302	EPE	C9-C10-S-O2S
3	D	302	EPE	C10-C9-N1-C2
3	D	302	EPE	C10-C9-N1-C6

There are no ring outliers.

2 monomers are involved in 5 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	D	302	EPE	1	0
3	С	301	EPE	4	0

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	<rsrz></rsrz>	#RSRZ>2	$\mathbf{OWAB}(\mathbf{\AA}^2)$	Q<0.9
1	А	226/237~(95%)	-0.01	1 (0%) 92 90	70, 91, 140, 154	0
1	С	226/237~(95%)	-0.09	0 100 100	53, 69, 100, 121	0
1	D	224/237~(94%)	-0.08	0 100 100	53, 70, 108, 125	0
1	F	225/237~(94%)	-0.21	0 100 100	57, 83, 120, 129	0
1	Ι	224/237~(94%)	-0.08	2 (0%) 84 79	53, 90, 153, 172	0
1	Κ	224/237~(94%)	-0.20	0 100 100	67, 85, 133, 149	0
2	В	202/216~(93%)	-0.18	0 100 100	76, 113, 139, 153	0
2	Ε	209/216~(96%)	-0.16	1 (0%) 91 88	62, 103, 132, 136	0
2	G	210/216~(97%)	-0.19	0 100 100	62, 87, 116, 131	0
2	Н	207/216~(95%)	0.06	1 (0%) 91 88	69, 110, 143, 162	0
2	J	209/216~(96%)	-0.07	1 (0%) 91 88	67, 130, 181, 212	0
2	L	200/216~(92%)	0.12	0 100 100	82, 116, 145, 158	0
All	All	$258\overline{6}/2718~(95\%)$	-0.09	6 (0%) 95 93	53, 94, 145, 212	0

All (6) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	Ι	235	VAL	2.9
1	А	235	VAL	2.4
2	J	136	PHE	2.2
2	Н	136	PHE	2.1
1	Ι	183	LEU	2.0
2	Е	151	VAL	2.0

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

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



6.3 Carbohydrates (i)

There are no 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	$\mathbf{B} ext{-factors}(\mathrm{\AA}^2)$	Q < 0.9
3	EPE	С	301	15/15	0.79	0.36	$69,\!69,\!69,\!69$	0
3	EPE	D	302	15/15	0.90	0.27	79,79,79,79	0
4	SO4	D	301	5/5	0.97	0.26	$68,\!68,\!68,\!68$	0
4	SO4	K	301	5/5	0.97	0.28	66,66,66,66	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.

