

Full wwPDB X-ray Structure Validation Report (i)

May 13, 2020 – 12:33 pm BST

PDB ID : 1FV1	
Title : STRUCTURAL BASIS FOR THE BINDING	G OF AN IMMUNODOMINANT
PEPTIDE FROM MYELIN BASIC PROT	FEIN IN DIFFERENT REGIS-
TERS BY TWO HLA-DR2 ALLELES	
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Deposited on : 2000-09-18	
m Resolution : 1.90 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 following versions of software and data (see references (1)) were used in the production of this report:

$\operatorname{MolProbity}$:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.11
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)	:	2.11
Ideal geometry (proteins) Ideal geometry (DNA, RNA) Validation Pipeline (wwPDB-VP)	: : :	Engh & Huber (2001) Parkinson et al. (1996) 2.11

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure: X-RAY DIFFRACTION

The reported resolution of this entry is 1.90 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	$egin{array}{c} { m Whole \ archive} \ (\#{ m Entries}) \end{array}$	${f Similar\ resolution}\ (\#{ m Entries,\ resolution\ range}({ m \AA}))$
Clashscore	141614	6847 (1.90-1.90)
Ramachandran outliers	138981	6760 (1.90-1.90)
Sidechain outliers	138945	6760 (1.90-1.90)
RSRZ outliers	127900	6082(1.90-1.90)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments on the lower bar indicate the fraction of residues that contain outliers for >=3, 2, 1 and 0 types of geometric quality criteria 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	A	181	% 	25%	
1	П	181	%	2004	
	D	101	11%	29%	••
2	В	190	69%	29%	••
2	Е	190	72%	26%	•
3	С	20	<u>30%</u> 55%	40%	5%
			15%		
3	F	20	50% 35%	5%	10%



2 Entry composition (i)

There are 6 unique types of molecules in this entry. The entry contains 6795 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the ZeroOcc column contains the number of atoms modelled with zero occupancy, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

• Molecule 1 is a protein called MAJOR HISTOCOMPATIBILITY COMPLEX ALPHA CHAIN.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	Δ	170	Total	С	Ν	Ο	\mathbf{S}	0	2	0
	A	179	1466	949	235	277	5	0		0
1	П	178	Total	С	Ν	Ο	S	0	2	0
		170	1463	949	235	274	5	0	0	0

• Molecule 2 is a protein called MAJOR HISTOCOMPATIBILITY COMPLEX BETA CHAIN.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	В	190	Total	С	Ν	Ο	S	0	1	0
	D		1522	956	270	291	5	0		
	F	190	Total	С	Ν	Ο	\mathbf{S}	0	1	0
			1526	956	271	294	5			U

• Molecule 3 is a protein called MYELIN BASIC PROTEIN.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf	Trace
3	С	20	Total C N O 153 101 27 25	0	0	0
3	F	18	Total C N O 144 97 25 22	0	0	0

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





Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	А	1	$\begin{array}{ccc} \text{Total} & \text{O} & \text{S} \\ 5 & 4 & 1 \end{array}$	0	0
4	В	1	$\begin{array}{ccc} \text{Total} & \text{O} & \text{S} \\ 5 & 4 & 1 \end{array}$	0	0
4	D	1	$\begin{array}{ccc} \text{Total} & \text{O} & \text{S} \\ 5 & 4 & 1 \end{array}$	0	0

• Molecule 5 is GLYCEROL (three-letter code: GOL) (formula: $C_3H_8O_3$).



	onan	nesiques	Att	oms		ZeroOcc	AltConf
5	В	1	Total 6	С 3	0 3	0	0

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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	D	1	Total 6	${ m C} { m 3}$	O 3	0	0

• Molecule 6 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
6	А	152	Total O 152 152	0	0
6	В	86	Total O 86 86	0	0
6	С	8	Total O 8 8	0	0
6	D	148	Total O 148 148	0	0
6	Е	89	Total O 89 89	0	0
6	F	11	Total O 11 11	0	0



3 Residue-property plots (i)

These plots are drawn for all protein, RNA and DNA 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: MAJOR HISTOCOMPATIBILITY COMPLEX ALPHA CHAIN





4 Data and refinement statistics (i)

Property	Value	Source	
Space group	P 1 21 1	Depositor	
Cell constants	63.19Å 114.89Å 63.17 Å	Deperitor	
$\mathrm{a,b,c,\alpha,\beta,\gamma}$	90.00° 90.90° 90.00°	Depositor	
$\mathbf{P}_{\text{assolution}}(\hat{\mathbf{A}})$	100.00 - 1.90	Depositor	
Resolution (A)	31.59 - 1.90	EDS	
% Data completeness	(Not available) $(100.00-1.90)$	Depositor	
(in resolution range)	90.6 (31.59 - 1.90)	EDS	
R_{merge}	0.08	Depositor	
R_{sym}	(Not available)	Depositor	
$< I/\sigma(I) > 1$	$2.31 (at 1.91 \text{\AA})$	Xtriage	
Refinement program	CNS	Depositor	
D D .	0.233 , 0.267	Depositor	
Π, Π_{free}	0.228 , (Not available)	DCC	
R_{free} test set	No test flags present.	wwPDB-VP	
Wilson B-factor $(Å^2)$	20.7	Xtriage	
Anisotropy	0.263	Xtriage	
Bulk solvent $k_{sol}(e/Å^3), B_{sol}(Å^2)$	0.33 , 34.4	EDS	
L-test for $twinning^2$	$< L > = 0.49, < L^2 > = 0.33$	Xtriage	
	0.035 for -l,k,h		
Estimated twinning fraction	$0.044 { m for} -{ m h}, -{ m k}, { m l}$	Xtriage	
	0.467 for l,-k,h		
F_o, F_c correlation	0.95	EDS	
Total number of atoms	6795	wwPDB-VP	
Average B, all atoms $(Å^2)$	33.0	wwPDB-VP	

Xtriage's analysis on translational NCS is as follows: The largest off-origin peak in the Patterson function is 5.92% 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: GOL, $\mathrm{SO4}$

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

Mal Chain		Bond lengths		Bond angles		
	Chain	RMSZ	# Z > 5	RMSZ	# Z > 5	
1	А	0.45	0/1519	0.68	0/2073	
1	D	0.38	0/1520	0.67	0/2074	
2	В	0.34	0/1565	0.65	2/2131~(0.1%)	
2	Е	0.35	0/1569	0.63	0/2132	
3	С	0.36	0/160	0.66	0/219	
3	F	0.37	0/151	0.72	0/208	
All	All	0.38	0/6484	0.66	2/8837~(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	В	6	ARG	NE-CZ-NH1	5.98	123.29	120.30
2	В	6	ARG	NE-CZ-NH2	-5.87	117.37	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.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	1466	0	1379	45	0
1	D	1463	0	1393	51	0
2	В	1522	0	1393	58	0



Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	Е	1526	0	1400	50	0
3	С	153	0	150	10	0
3	F	144	0	149	8	0
4	А	5	0	0	0	0
4	В	5	0	0	0	0
4	D	5	0	0	1	0
5	В	6	0	8	2	0
5	D	6	0	8	1	0
6	А	152	0	0	4	0
6	В	86	0	0	0	0
6	С	8	0	0	0	0
6	D	148	0	0	4	0
6	Е	89	0	0	4	0
6	F	11	0	0	0	0
All	All	6795	0	5880	183	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 15.

All (183)	close	$\operatorname{contacts}$	within	the same	e asymmetric	unit	are	listed	below,	sorted	by	their	clash
magnitud	le.												

Atom 1	Atom 2	Interatomic	Clash	
Atom-1	Atom-2	$distance ({ m \AA})$	overlap (Å)	
2:B:107:GLN:HE22	2:B:114:LEU:HB3	1.24	0.98	
1:D:14:LEU:HD11	2:E:6:ARG:HG3	1.46	0.97	
2:E:13:TYR:OH	3:F:97:THR:HG22	1.74	0.86	
2:B:13:TYR:OH	3:C:97:THR:HG22	1.79	0.82	
1:A:36:MET:CE	1:A:63:ILE:HG13	2.13	0.79	
1:D:93[B]:THR:HG22	1:D:95:SER:H	1.48	0.76	
2:B:104:ALA:HB3	2:B:107:GLN:HE21	1.52	0.74	
2:B:94[A]:ARG:HG3	2:B:94[A]:ARG:HH11	1.52	0.74	
2:B:104:ALA:HB3	2:B:107:GLN:NE2	2.02	0.74	
2:E:115:LEU:HD21	2:E:188:TRP:CE3	2.24	0.72	
2:E:98:LYS:HE3	2:E:100:THR:HG23	1.70	0.72	
1:D:140:ARG:HH12	5:D:183:GOL:H11	1.53	0.72	
1:A:36:MET:HE2	1:A:63:ILE:HG13	1.70	0.72	
1:A:181:ASP:HA	2:B:105:ARG:HH22	1.54	0.72	
2:E:116:VAL:HG22	2:E:160:MET:HG3	1.73	0.70	
2:B:170:VAL:HG23	2:B:170:VAL:O	1.92	0.70	
1:D:17:ASP:OD1	2:E:6:ARG:HD2	1.92	0.69	
1:D:164:ARG:HH12	1:D:166:GLU:CD	1.95	0.68	
1:D:167:HIS:HD2	1:D:169:GLY:H	1.39	0.68	



Atom-1	Atom-2	Interatomic	Clash	
7100HI 1	7100111 2	distance (Å)	overlap (Å)	
1:D:16:PRO:HD2	2:E:6:ARG:HD3	1.76	0.68	
1:D:167:HIS:CD2	1:D:169:GLY:H	2.12	0.68	
1:A:167:HIS:HD2	1:A:169:GLY:H	1.43	0.67	
1:A:181:ASP:HA	2:B:105:ARG:NH2	2.09	0.67	
2:B:105:ARG:HB3	2:B:105:ARG:NH2	2.09	0.66	
2:B:35:GLU:OE1	2:E:52:GLU:HG3	1.95	0.66	
1:A:110:ASP:OD1	1:A:146:ARG:HG2	1.96	0.66	
1:A:41:THR:HG21	1:A:54:PHE:O	1.96	0.65	
1:D:62:ASN:ND2	3:F:97:THR:HG23	2.12	0.64	
1:D:101:GLU:HG2	6:D:270:HOH:O	1.96	0.64	
2:B:134:ASN:ND2	2:B:170:VAL:HG22	2.12	0.64	
1:A:167:HIS:CD2	1:A:169:GLY:H	2.15	0.64	
1:A:73:MET:CE	2:B:53:LEU:HG	2.29	0.63	
2:E:98:LYS:HE3	2:E:100:THR:CG2	2.28	0.63	
1:D:36:MET:CE	1:D:63:ILE:HG13	2.29	0.62	
1:D:123:ARG:HG3	1:D:161:TYR:CE2	2.35	0.61	
1:A:47:GLU:HG3	6:A:280:HOH:O	1.99	0.61	
1:A:36:MET:HE1	1:A:63:ILE:HG13	1.81	0.60	
1:D:50:ARG:HD2	6:D:298:HOH:O	2.00	0.60	
1:D:181:ASP:C	2:E:105:ARG:HH22	2.05	0.59	
2:E:55:ARG:HB3	2:E:56:PRO:HD3	1.84	0.58	
2:B:55:ARG:O	2:B:59:GLU:HG3	2.04	0.58	
2:B:94[A]:ARG:NH1	2:B:94[A]:ARG:HG3	2.18	0.58	
2:B:2:ASP:CG	2:B:6:ARG:HH22	2.06	0.58	
2:B:131:TRP:O	2:B:137:GLU:HA	2.03	0.58	
1:D:136:VAL:O	1:D:138:LEU:HD22	2.04	0.57	
1:A:111:LYS:HG2	1:A:140:ARG:CZ	2.34	0.57	
1:A:77:SER:O	1:A:80:THR:HG22	2.05	0.57	
1:D:14:LEU:HD11	2:E:6:ARG:CG	2.30	0.57	
1:D:181:ASP:C	2:E:105:ARG:NH2	2.58	0.57	
2:B:107:GLN:NE2	2:B:114:LEU:HB3	2.08	0.57	
2:E:131:TRP:O	2:E:137:GLU:HA	2.05	0.56	
1:D:4:GLU:HG2	1:D:5:HIS:CD2	2.40	0.56	
1:D:36:MET:HE2	1:D:63:ILE:HG21	1.88	0.55	
1:A:90:THR:HG23	6:A:211:HOH:O	2.06	0.55	
1:D:73:MET:HE1	2:E:53:LEU:HB3	1.88	0.55	
2:B:55:ARG:HB3	2:B:56:PRO:HD3	1.89	0.55	
1:D:138:LEU:N	1:D:138:LEU:HD22	2.22	0.55	
1:A:132:VAL:HG12	1:A:151:LEU:HD13	1.89	0.55	
2:E:114:LEU:HD11	2:E:160:MET:HB3	1.88	0.54	
2:E:27:LEU:HD12	2:E:41:ASP:HA	1.89	0.54	



Atom 1	Atom 2	Interatomic	Clash	
Atom-1	Atom-2	distance (Å)	overlap (Å)	
1:D:17:ASP:OD1	2:E:6:ARG:CD	2.56	0.54	
2:E:75:VAL:HG13	6:E:216:HOH:O	2.07	0.54	
3:C:103:PRO:O	3:C:104:SER:HB3	2.08	0.54	
2:E:36:GLU:HG2	2:E:50:VAL:HG11	1.89	0.54	
1:A:73:MET:HE1	2:B:53:LEU:HG	1.91	0.53	
2:E:132:PHE:CE2	2:E:137:GLU:HB2	2.44	0.53	
1:A:162:ASP:OD1	1:A:177:HIS:ND1	2.42	0.53	
1:A:3:GLU:HA	2:B:18:PHE:CE2	2.44	0.53	
1:D:46:GLU:HG2	6:D:298:HOH:O	2.07	0.53	
2:B:94[A]:ARG:HD3	5:B:192:GOL:H11	1.90	0.53	
1:A:73:MET:HE3	2:B:53:LEU:HG	1.90	0.53	
1:D:108:PHE:CE1	1:D:146:ARG:HG3	2.43	0.53	
1:A:118:ASN:HB3	1:A:166:GLU:HB2	1.89	0.53	
2:B:149:GLN:HG2	2:B:155:PHE:CE2	2.44	0.52	
2:B:27:LEU:HD12	2:B:41:ASP:HA	1.92	0.52	
2:B:108:THR:O	2:B:109:LEU:CB	2.58	0.51	
1:D:70:LEU:HD13	2:E:9:GLN:HB2	1.91	0.51	
2:E:60:TYR:CE2	3:F:101:PRO:HG2	2.45	0.51	
1:A:9:GLN:HB3	2:B:13:TYR:HB2	1.93	0.51	
2:E:27:LEU:HD11	2:E:39:ARG:HD3	1.92	0.51	
1:A:164:ARG:HH12	1:A:166:GLU:CD	2.13	0.51	
2:B:26:PHE:HB3	2:B:42:SER:HB3	1.92	0.50	
1:A:3:GLU:HA	2:B:18:PHE:CD2	2.46	0.50	
1:D:93[B]:THR:CG2	1:D:95:SER:O	2.59	0.50	
2:B:161:LEU:HD13	2:B:163:THR:CG2	2.42	0.50	
2:E:142:VAL:HG22	2:E:161:LEU:HD13	1.94	0.50	
1:D:36:MET:HE1	1:D:63:ILE:HG13	1.94	0.50	
2:B:13:TYR:HH	3:C:97:THR:HG22	1.75	0.50	
1:D:180:PHE:CE1	2:E:105:ARG:NH2	2.80	0.50	
1:A:181:ASP:CA	2:B:105:ARG:NH2	2.75	0.50	
1:D:111:LYS:HG2	1:D:140:ARG:CZ	2.42	0.49	
2:B:177:HIS:CG	2:B:178:PRO:HD2	2.47	0.49	
6:A:288:HOH:O	3:C:103:PRO:HG3	2.13	0.49	
1:D:129:THR:O	1:D:132:VAL:HG22	2.13	0.49	
1:A:97:VAL:HG12	1:A:98:GLU:N	2.28	0.48	
1:A:62:ASN:ND2	3:C:97:THR:HG23	2.28	0.48	
2:E:10:GLN:HB2	2:E:31:ILE:HB	1.94	0.48	
2:E:117:CYS:HB2	2:E:131:TRP:CZ2	2.48	0.48	
2:E:177:HIS:CD2	2:E:178:PRO:HD2	2.49	0.48	
1:A:81:PRO:HB3	2:B:5:PRO:HB3	1.95	0.48	
2:B:113:ASN:N	2:B:163:THR:O	2.46	0.48	



Atom 1	Atom 2	Interatomic	Clash	
Atom-1	Atom-2	${ m distance}~({ m \AA})$	overlap (Å)	
2:B:60:TYR:CE2	3:C:101:PRO:HG2	2.49	0.48	
2:B:13:TYR:CE2	3:C:95:ILE:HG21	2.49	0.48	
2:E:177:HIS:CG	2:E:178:PRO:HD2	2.48	0.48	
1:A:157:THR:HG22	1:A:180:PHE:CD1	2.48	0.48	
1:D:162:ASP:OD1	1:D:177:HIS:ND1	2.46	0.48	
1:A:92:LEU:HD23	1:A:92:LEU:N	2.29	0.47	
1:D:9:GLN:HB3	2:E:13:TYR:HB2	1.96	0.47	
2:B:176:GLU:HG2	2:B:183:PRO:HB3	1.95	0.47	
1:A:21:GLU:OE2	1:A:137:PHE:O	2.32	0.47	
1:D:108:PHE:HE1	1:D:146:ARG:HG3	1.78	0.47	
2:E:119:VAL:HG21	2:E:129:VAL:HG21	1.97	0.47	
2:B:105:ARG:HB3	2:B:105:ARG:CZ	2.44	0.47	
1:D:93[B]:THR:HG21	1:D:95:SER:O	2.14	0.47	
2:E:13:TYR:HH	3:F:97:THR:HG22	1.76	0.47	
1:A:97:VAL:CG1	1:A:98:GLU:N	2.78	0.47	
2:B:133:ARG:O	2:B:134:ASN:HB2	2.14	0.46	
2:E:141:GLY:O	2:E:161:LEU:HD12	2.16	0.46	
1:A:98:GLU:CG	1:A:101[B]:GLU:CD	2.84	0.46	
1:A:96:PRO:HD3	2:B:120:ASN:ND2	2.30	0.46	
2:B:81:HIS:CD2	3:C:93:LYS:HG2	2.50	0.46	
3:C:87:PRO:O	3:C:88:VAL:HB	2.15	0.46	
3:C:86:ASN:N	3:C:87:PRO:HD3	2.31	0.46	
2:B:117:CYS:HB2	2:B:131:TRP:CZ2	2.51	0.45	
1:D:89:VAL:HG12	1:D:176:LYS:HG3	1.98	0.45	
1:A:89:VAL:HG12	1:A:176:LYS:HG3	1.98	0.45	
2:B:27:LEU:HD11	2:B:39:ARG:HD3	1.99	0.45	
1:D:92:LEU:N	1:D:92:LEU:HD12	2.32	0.45	
3:F:87:PRO:O	3:F:88:VAL:HB	2.17	0.45	
1:D:157:THR:HG22	1:D:180:PHE:CD1	2.52	0.44	
1:D:26:PHE:HB2	1:D:31:ILE:HD11	2.00	0.44	
1:A:29:ASP:HB3	2:B:153:TRP:CE2	2.53	0.44	
2:B:2:ASP:OD2	2:B:6:ARG:NH2	2.48	0.44	
1:A:87:PRO:HB2	1:A:109:ILE:HG23	2.00	0.44	
2:E:37:ASP:C	2:E:50:VAL:HG12	2.37	0.44	
1:D:36:MET:HE2	1:D:63:ILE:HG13	1.99	0.43	
1:A:8:ILE:HG12	2:B:14:GLU:HG2	1.99	0.43	
1:D:113:THR:OG1	1:D:114:PRO:HA	2.18	0.43	
2:E:113:ASN:HD22	2:E:114:LEU:N	2.17	0.43	
1:D:92:LEU:HD13	1:D:106:ILE:HB	2.00	0.43	
1:D:167:HIS:HB3	1:D:170:LEU:HD22	2.01	0.43	
2:B:94[B]:ARG:HD3	5:B:192:GOL:H11	1.98	0.43	



Atom 1	Atom 2	Interatomic	Clash
Atom-1	Atom-2	distance (Å)	overlap (Å)
2:E:13:TYR:CE2	3:F:95:ILE:HG21	2.54	0.43
2:B:10:GLN:HB2	2:B:31:ILE:HB	2.00	0.43
1:D:123:ARG:HD2	4:D:182:SO4:O4	2.18	0.43
2:B:97:PRO:HB3	2:B:119:VAL:HG12	2.01	0.43
2:E:96:GLU:HA	2:E:97:PRO:HD3	1.87	0.43
1:A:122:LEU:HB2	1:A:162:ASP:HB2	2.01	0.42
2:B:60:TYR:O	2:B:64:GLN:HG2	2.18	0.42
1:A:16:PRO:HD2	2:B:6:ARG:HD3	2.01	0.42
1:A:123:ARG:NH2	6:A:214:HOH:O	2.53	0.42
1:D:109:ILE:HD12	1:D:109:ILE:N	2.35	0.42
1:D:90:THR:HG23	6:D:213:HOH:O	2.17	0.42
1:A:77:SER:O	1:A:80:THR:CG2	2.68	0.42
2:B:47:TYR:O	2:B:48:ARG:HG2	2.19	0.42
1:D:143:HIS:HD2	2:E:12:LYS:NZ	2.17	0.42
1:D:118:ASN:HB3	1:D:166:GLU:HB2	2.01	0.42
2:B:94[A]:ARG:NH1	2:B:94[A]:ARG:CG	2.83	0.42
3:F:103:PRO:O	3:F:104:SER:HB3	2.19	0.42
2:E:36:GLU:O	2:E:50:VAL:HG13	2.19	0.42
1:A:109:ILE:HD12	1:A:109:ILE:N	2.34	0.42
2:B:107:GLN:HE22	2:B:114:LEU:CB	2.12	0.42
1:D:99:LEU:HA	1:D:155:PRO:HB2	2.01	0.42
1:D:12:PHE:C	1:D:12:PHE:CD1	2.93	0.42
1:D:120:THR:HB	1:D:164:ARG:HB3	2.02	0.42
2:E:189:ARG:CB	6:E:267:HOH:O	2.67	0.42
2:E:29:ARG:HG2	2:E:36:GLU:OE2	2.20	0.42
2:B:17:PHE:CZ	2:B:83:TYR:HB2	2.55	0.41
2:B:152:ASP:O	2:B:153:TRP:HB2	2.20	0.41
2:E:46:GLU:HB2	2:E:62:ASN:OD1	2.20	0.41
2:E:98:LYS:HE2	6:E:215:HOH:O	2.19	0.41
2:E:52:GLU:HG2	6:E:238:HOH:O	2.18	0.41
2:B:158:LEU:N	2:B:158:LEU:HD12	2.35	0.41
2:E:47:TYR:OH	2:E:71:ARG:NH1	2.54	0.41
2:E:97:PRO:HG3	2:E:122:PHE:HB3	2.03	0.41
2:E:119:VAL:HG11	2:E:127:ILE:CD1	2.51	0.41
1:D:88:GLU:OE2	1:D:111:LYS:HD2	2.21	0.41
1:A:59:ALA:O	1:A:63:ILE:HG12	2.22	0.40
2:B:4:ARG:HA	2:B:5:PRO:HD3	1.95	0.40
2:E:71:ARG:HA	2:E:71:ARG:HD3	1.88	0.40
1:A:12:PHE:CD1	1:A:12:PHE:C	2.94	0.40
2:E:81:HIS:CD2	3:F:93:LYS:HG2	2.56	0.40

There are no symmetry-related clashes.



5.3 Torsion angles (i)

5.3.1 Protein backbone (i)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
1	А	179/181~(99%)	176~(98%)	3(2%)	0	100 100
1	D	179/181~(99%)	177~(99%)	2(1%)	0	100 100
2	В	189/190~(100%)	174 (92%)	11 (6%)	4 (2%)	7 1
2	E	189/190~(100%)	169~(89%)	17 (9%)	3 (2%)	9 2
3	С	18/20~(90%)	16 (89%)	1 (6%)	1 (6%)	2 0
3	F	16/20~(80%)	15 (94%)	0	1 (6%)	1 0
All	All	770/782~(98%)	727 (94%)	34 (4%)	9 (1%)	13 4

All (9) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	В	135	SER
2	Е	134	ASN
2	Е	135	SER
2	В	111	HIS
3	С	88	VAL
3	F	88	VAL
2	В	109	LEU
2	Е	109	LEU
2	В	165	PRO

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	Percer	ntiles
1	А	162/166~(98%)	158~(98%)	4 (2%)	47	41
1	D	164/166~(99%)	159 (97%)	5(3%)	41	33
2	В	159/171~(93%)	154 (97%)	5(3%)	40	32
2	Ε	161/171~(94%)	154~(96%)	7 (4%)	29	19
3	С	18/20~(90%)	18~(100%)	0	100	100
3	F	18/20 (90%)	18 (100%)	0	100	100
All	All	682/714~(96%)	661 (97%)	21 (3%)	41	32

All (21) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	А	71	GLU
1	А	80	THR
1	А	92	LEU
1	А	177	HIS
2	В	6	ARG
2	В	66	ASP
2	В	98	LYS
2	В	113	ASN
2	В	161	LEU
1	D	71	GLU
1	D	92	LEU
1	D	170	LEU
1	D	174	LEU
1	D	177	HIS
2	Е	6	ARG
2	Е	66[A]	ASP
2	Е	66[B]	ASP
2	Е	98	LYS
2	Е	107	GLN
2	Е	113	ASN
2	Е	160	MET

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (14) such sidechains are listed below:

Mol	Chain	Res	Type
1	А	149	HIS
1	А	167	HIS
2	В	107	GLN
2	В	113	ASN



Mol	Chain	Res	Type
2	В	120	ASN
2	В	134	ASN
2	В	174	GLN
1	D	118	ASN
1	D	143	HIS
1	D	149	HIS
1	D	167	HIS
2	Е	92	GLN
2	Е	113	ASN
2	Е	174	GLN

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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 carbohydrates in this entry.

5.6 Ligand geometry (i)

5 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 True	Tune	Chain	Dog	Tink	I inle Bond lengths			Bond angles		
	туре	Chain	nes		Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z >2
5	GOL	В	192	-	5, 5, 5	1.01	0	$5,\!5,\!5$	0.92	0
4	SO4	В	191	-	4,4,4	0.26	0	6,6,6	0.05	0
4	SO4	А	182	-	4,4,4	0.28	0	6,6,6	0.06	0
4	SO4	D	182	-	4,4,4	0.26	0	$6,\!6,\!6$	0.09	0



Mal	Tune	Chain	Chain	Dog	Dec Link	Bond lengths			Bond angles		
	туре	Chain	nes		Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2	
5	GOL	D	183	-	5, 5, 5	1.00	0	$5,\!5,\!5$	0.93	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
5	GOL	В	192	-	-	4/4/4/4	-
5	GOL	D	183	-	-	2/4/4/4	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (6) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
5	В	192	GOL	O1-C1-C2-C3
5	В	192	GOL	C1-C2-C3-O3
5	В	192	GOL	O2-C2-C3-O3
5	D	183	GOL	C1-C2-C3-O3
5	D	183	GOL	O2-C2-C3-O3
5	В	192	GOL	O1-C1-C2-O2

There are no ring outliers.

3 monomers are involved in 4 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	В	192	GOL	2	0
4	D	182	SO4	1	0
5	D	183	GOL	1	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 $>$	# RSRZ > 2	$OWAB(Å^2)$	Q<0.9
1	А	$179/181 \ (98\%)$	-0.16	1 (0%) 89 90	16, 25, 44, 62	0
1	D	$178/181 \ (98\%)$	-0.19	1 (0%) 89 90	15, 25, 44, 56	0
2	В	190/190~(100%)	0.47	20 (10%) 6 7	18, 37, 73, 77	0
2	Е	190/190~(100%)	0.27	10 (5%) 26 29	18, 36, 74, 81	0
3	С	20/20~(100%)	1.27	6 (30%) 0 0	24, 37, 69, 69	0
3	F	18/20~(90%)	0.72	3 (16%) 1 1	23, 33, 60, 68	0
All	All	775/782 (99%)	0.15	41 (5%) 26 29	15, 31, 67, 81	0

All (41) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	В	165	PRO	7.4
3	F	87	PRO	7.1
3	С	104	SER	5.5
3	С	87	PRO	5.4
3	С	88	VAL	4.7
2	В	1	GLY	4.5
2	Е	110	GLN	4.3
2	Е	165	PRO	3.7
2	Е	109	LEU	3.7
2	В	168	GLY	3.7
2	Е	188	TRP	3.4
2	Е	108	THR	3.3
2	В	164	VAL	3.3
2	В	163	THR	3.3
2	Е	132	PHE	3.3
2	Е	190	ALA	3.2
2	Е	1	GLY	2.9
1	А	180	PHE	2.8
2	В	139	LYS	2.7



Mol	Mol Chain		Type	BSRZ	
2	B	171	TYR	2.7	
2	B	112	HIS	2.7	
2	B	134	ASN	2.6	
2	Е	106	THR	2.6	
2	В	135	SER	2.5	
3	F	104	SER	2.5	
2	В	190	ALA	2.5	
2	В	132	PHE	2.5	
2	В	109	LEU	2.4	
3	С	86	ASN	2.4	
2	В	143	VAL	2.4	
2	Е	134	ASN	2.3	
2	В	188	TRP	2.3	
2	В	170	VAL	2.3	
2	В	114	LEU	2.3	
1	D	100	ARG	2.3	
2	В	110	GLN	2.3	
3	C	105	GLN	2.2	
3	F	88	VAL	2.1	
2	В	166	ARG	2.1	
3	С	89	VAL	2.1	
2	B	133	ARG	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 carbohydrates in this entry.

6.4 Ligands (i)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. 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	\mathbf{Res}	Atoms	RSCC	RSR	$\mathbf{B} ext{-factors}(\mathrm{\AA}^2)$	Q<0.9
5	GOL	D	183	6/6	0.57	0.23	$69,\!70,\!70,\!70$	0



Mol	Type	Chain	Res	Atoms	RSCC	RSR	$\mathbf{B} ext{-factors}(\mathrm{\AA}^2)$	Q<0.9
4	SO4	В	191	5/5	0.87	0.15	$90,\!90,\!90,\!91$	0
4	SO4	D	182	5/5	0.87	0.20	72,72,72,73	0
5	GOL	В	192	6/6	0.87	0.18	$47,\!49,\!50,\!52$	0
4	SO4	А	182	5/5	0.92	0.15	$69,\!69,\!70,\!70$	0

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6.5 Other polymers (i)

There are no such residues in this entry.

