Full wwPDB X-ray Structure Validation Report (i)

Feb 1, 2016 – 08:02 AM GMT

PDB ID	:	3D3V
Title	:	The complex between TCR A6 and human Class I MHC HLA-A2 with the modified HTLV-1 TAX (Y5(3,4-difluoroPhenylalanine)) peptide
Authors	:	Borbulevych, O.Y.; Clemens, J.R.; Baker, B.M.
Deposited on	:	2008-05-12
Resolution	:	2.80 Å(reported)

This is a Full wwPDB X-ray Structure Validation Report for a publicly released PDB entry.
We welcome your comments at validation@mail.wwpdb.org
A user guide is available at
http://wwpdb.org/validation/2016/XrayValidationReportHelp
with specific help available everywhere you see the (i) symbol.

The following versions of software and data (see references (1)) were used in the production of this report:

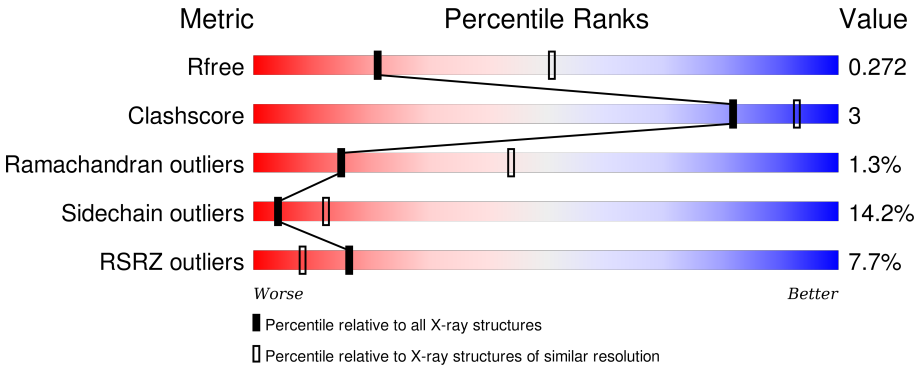
MolProbity	:	4.02b-467
Mogul	:	1.7 (RC4), CSD as536be (2015)
Xtriage (Phenix)	:	1.9-1692
EDS	:	rb-20026688
Percentile statistics	:	20151230.v01 (using entries in the PDB archive December 30th 2015)
Refmac	:	5.8.0135
CCP4	:	6.5.0
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	trunk26865

1 Overall quality at a glance (i)

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

The reported resolution of this entry is 2.80 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	91344	2393 (2.80-2.80)
Clashscore	102246	2827 (2.80-2.80)
Ramachandran outliers	100387	2782 (2.80-2.80)
Sidechain outliers	100360	2784 (2.80-2.80)
RSRZ outliers	91569	2404 (2.80-2.80)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments on the lower bar indicate the fraction of residues that contain outliers for >=3, 2, 1 and 0 types of geometric quality criteria. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions <=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	275	7%, 82%, 16%
2	B	100	4%, 87%, 10%
3	C	9	100%
4	D	200	15%, 74%, 21%, 5%
5	E	245	4%, 80%, 16%

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
6	GOL	A	276	-	-	-	X
6	GOL	B	101	-	-	-	X
6	GOL	E	247	-	-	-	X

2 Entry composition

There are 7 unique types of molecules in this entry. The entry contains 6732 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 HLA class I histocompatibility antigen, A-2 alpha chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	275	Total	C	N	O	S	0	3	0
			2265	1413	415	428	9			

- Molecule 2 is a protein called Beta-2-microglobulin.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	100	Total	C	N	O	S	0	0	0
			837	533	141	159	4			

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	0	MET	-	EXPRESSION TAG	UNP P61769

- Molecule 3 is a protein called Modified HTLV-1 TAX (Y5(3,4-difluoro)F) peptide.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	C	9	Total	C	F	N	O	0	1	0
			87	63	4	9	11			

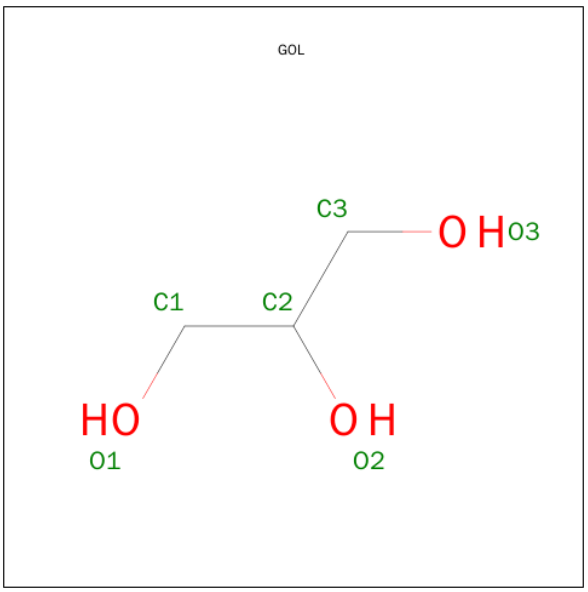
- Molecule 4 is a protein called A6 TCR alpha chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
4	D	200	Total	C	N	O	S	0	0	0
			1552	965	255	325	7			

- Molecule 5 is a protein called A6 TCR beta chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
5	E	245	Total	C	N	O	S	0	0	0
			1928	1209	339	372	8			

- Molecule 6 is GLYCEROL (three-letter code: GOL) (formula: $C_3H_8O_3$).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
6	A	1	Total C O 6 3 3	0	0
6	A	1	Total C O 6 3 3	0	0
6	B	1	Total C O 6 3 3	0	0
6	B	1	Total C O 6 3 3	0	0
6	E	1	Total C O 6 3 3	0	0
6	E	1	Total C O 6 3 3	0	0

- Molecule 7 is water.

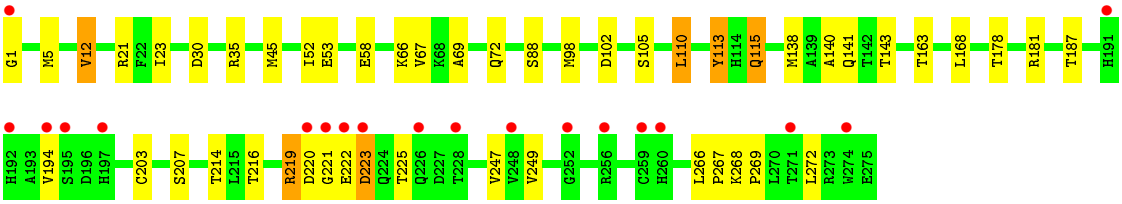
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
7	A	13	Total O 13 13	0	0
7	B	6	Total O 6 6	0	0
7	D	2	Total O 2 2	0	0
7	E	6	Total O 6 6	0	0

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 errors displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red dot above a residue indicates a poor fit to the electron density (RSRZ > 2). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

- Molecule 1: HLA class I histocompatibility antigen, A-2 alpha chain

Chain A:

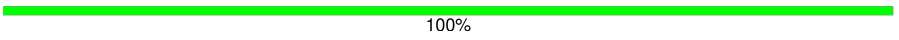


- Molecule 2: Beta-2-microglobulin

Chain B:

- Molecule 3: Modified HTLV-1 TAX (Y5(3,4-difluoro)F) peptide

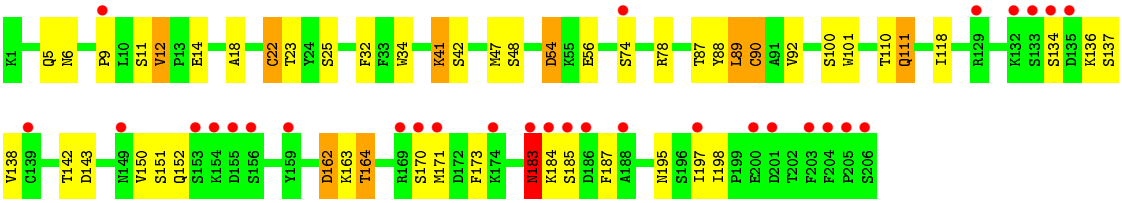
Chain C:



There are no outlier residues recorded for this chain.

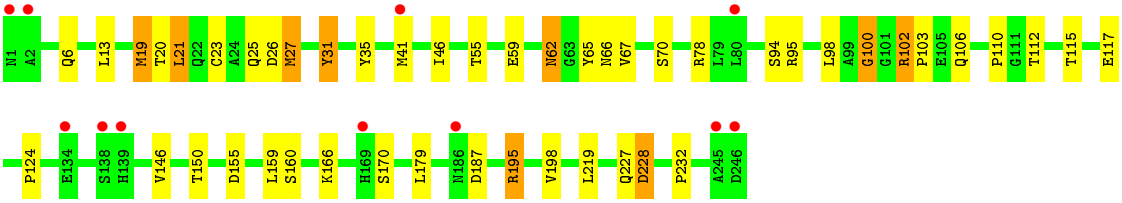
- Molecule 4: A6 TCR alpha chain

Chain D:



- Molecule 5: A6 TCR beta chain

Chain E:


N1
A2
Q6
L13
M19
T20
L21
Q22
C23
A24
Q25
D26
M27
Y31
Y35
M41
I46
T55
E59
N62
G63
Y65
N66
V67
S70
R78
L79
L80
S94
R95
L98
A99
G100
G101
R102
P103
E105
Q106
P110
G111
T112
T115
E117
P124
E134
S138
H139
V146
T150
D155
L159
S160
K166
H169
S170
L179
N186
D187
R195
V198
L219
Q227
D228
P232
A245
D246

4 Data and refinement statistics (i)

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α, β, γ	224.45Å 48.54Å 93.79Å 90.00° 90.61° 90.00°	Depositor
Resolution (Å)	20.00 – 2.80 19.18 – 2.80	Depositor EDS
% Data completeness (in resolution range)	98.6 (20.00-2.80) 98.6 (19.18-2.80)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	1.57 (at 2.79Å)	Xtriage
Refinement program	REFMAC 5.2.0019	Depositor
R, R_{free}	0.220 , 0.278 0.218 , 0.272	Depositor DCC
R_{free} test set	1277 reflections (5.39%)	DCC
Wilson B-factor (Å^2)	75.0	Xtriage
Anisotropy	0.231	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.30 , 60.3	EDS
Estimated twinning fraction	0.017 for -h,-k,l	Xtriage
L-test for twinning[2]	$< \|L\| > = 0.49$, $< L^2 > = 0.32$	Xtriage
Outliers	1 of 24962 reflections (0.004%)	Xtriage
F_o,F_c correlation	0.94	EDS
Total number of atoms	6732	wwPDB-VP
Average B, all atoms (Å^2)	63.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.98% of the height of the origin peak. No significant pseudotranslation is detected.*

[1] Intensities estimated from amplitudes.

[2] Theoretical values of $< |L| >$, $< L^2 >$ for acentric reflections are 0.5, 0.375 respectively for untwinned datasets, and 0.333, 0.2 for perfectly twinned datasets.

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: GOL, F2F

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#$\|Z\|>5$	RMSZ	#$\|Z\|>5$
1	A	0.82	3/2342 (0.1%)	0.81	0/3176
2	B	0.71	0/860	0.84	0/1162
3	C	0.95	0/66	0.92	0/86
4	D	0.66	3/1585 (0.2%)	0.79	1/2150 (0.0%)
5	E	0.92	7/1981 (0.4%)	0.90	3/2699 (0.1%)
All	All	0.80	13/6834 (0.2%)	0.84	4/9273 (0.0%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
5	E	0	1

All (13) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	E	65	TYR	CG-CD2	14.36	1.57	1.39
1	A	222	GLU	CD-OE1	12.87	1.39	1.25
1	A	222	GLU	CG-CD	12.74	1.71	1.51
5	E	117	GLU	CD-OE2	10.10	1.36	1.25
5	E	117	GLU	CD-OE1	10.09	1.36	1.25
5	E	65	TYR	CE2-CZ	7.10	1.47	1.38
4	D	163	LYS	CE-NZ	6.50	1.65	1.49
1	A	222	GLU	CD-OE2	6.26	1.32	1.25
5	E	117	GLU	CG-CD	5.63	1.60	1.51
4	D	22	CYS	CB-SG	-5.63	1.72	1.81
5	E	23	CYS	CB-SG	-5.41	1.73	1.81
5	E	62	ASN	N-CA	5.17	1.56	1.46
4	D	90	CYS	CB-SG	-5.15	1.73	1.81

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
5	E	65	TYR	CZ-CE2-CD2	-6.70	113.77	119.80
5	E	62	ASN	CB-CG-ND2	-5.93	102.46	116.70
5	E	35	TYR	CB-CA-C	-5.76	98.88	110.40
4	D	89	LEU	CA-CB-CG	5.61	128.20	115.30

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
5	E	100	GLY	Peptide

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	2265	0	2114	14	0
2	B	837	0	803	5	0
3	C	87	0	82	0	0
4	D	1552	0	1461	13	0
5	E	1928	0	1832	13	0
6	A	12	0	16	0	0
6	B	12	0	16	0	0
6	E	12	0	16	0	0
7	A	13	0	0	0	0
7	B	6	0	0	0	0
7	D	2	0	0	0	0
7	E	6	0	0	0	0
All	All	6732	0	6340	42	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 3.

All (42) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:E:228:ASP:N	5:E:228:ASP:OD2	2.29	0.63
2:B:98:ASP:OD1	2:B:98:ASP:N	2.33	0.62
4:D:142:THR:OG1	4:D:143:ASP:N	2.31	0.61
4:D:164:THR:OG1	5:E:195:ARG:NH2	2.34	0.59
1:A:21:ARG:HE	1:A:23:ILE:HD11	1.68	0.59
5:E:95:ARG:HG3	5:E:106:GLN:HB2	1.85	0.57
1:A:102:ASP:OD1	1:A:113:TYR:OH	2.19	0.57
4:D:183:ASN:N	4:D:183:ASN:OD1	2.35	0.57
5:E:155:ASP:N	5:E:155:ASP:OD1	2.37	0.56
4:D:54:ASP:N	4:D:54:ASP:OD2	2.40	0.55
4:D:171:MET:HB3	4:D:173:PHE:HB2	1.88	0.54
4:D:9:PRO:HB3	4:D:111:GLN:HG2	1.93	0.51
5:E:6:GLN:HG2	5:E:110:PRO:HD2	1.94	0.49
1:A:12:VAL:HG13	1:A:21:ARG:HB3	1.95	0.49
1:A:140:ALA:O	1:A:143:THR:HB	2.13	0.49
5:E:124:PRO:HD3	5:E:232:PRO:HB3	1.96	0.48
5:E:21:LEU:HD22	5:E:112:THR:HG21	1.97	0.47
1:A:115:GLN:H	1:A:115:GLN:HG2	1.59	0.47
1:A:5:MET:HB2	1:A:168:LEU:HD13	1.98	0.46
2:B:64:LEU:HA	2:B:64:LEU:HD12	1.73	0.46
2:B:96:ASP:HB3	2:B:99:MET:HB2	1.97	0.46
4:D:5:GLN:NE2	4:D:88:TYR:O	2.49	0.45
1:A:69:ALA:HB1	5:E:98:LEU:HD11	1.98	0.44
5:E:31:TYR:HB3	5:E:95:ARG:HB3	1.99	0.44
5:E:219:LEU:HD22	5:E:232:PRO:HD2	1.98	0.44
1:A:219:ARG:O	1:A:221:GLY:N	2.48	0.44
2:B:39:LEU:HA	2:B:39:LEU:HD23	1.75	0.43
2:B:17:ASN:HD21	2:B:74:GLU:HG3	1.84	0.43
1:A:266:LEU:HA	1:A:267:PRO:HD3	1.79	0.43
4:D:162:ASP:N	4:D:162:ASP:OD1	2.51	0.43
1:A:110:LEU:HA	1:A:110:LEU:HD12	1.74	0.42
4:D:32:PHE:HD1	4:D:92:VAL:HG22	1.84	0.42
1:A:266:LEU:HA	1:A:266:LEU:HD23	1.84	0.42
4:D:12:VAL:HG21	4:D:18:ALA:HB2	2.01	0.42
4:D:138:VAL:HG11	5:E:146:VAL:HG21	2.02	0.41
1:A:268:LYS:HA	1:A:269:PRO:HD3	1.91	0.41
5:E:13:LEU:HD11	5:E:19:MET:HB3	2.02	0.41
1:A:1:GLY:HA2	1:A:105:SER:HB3	2.01	0.41
4:D:41:LYS:HB2	4:D:42:SER:H	1.68	0.41
1:A:223:ASP:N	1:A:223:ASP:OD1	2.38	0.41
5:E:27:MET:H	5:E:27:MET:HG2	1.51	0.41
4:D:34:TRP:HB2	4:D:47:MET:HB2	2.03	0.40

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
1	A	276/275 (100%)	252 (91%)	22 (8%)	2 (1%)	26 62
2	B	98/100 (98%)	94 (96%)	3 (3%)	1 (1%)	19 52
3	C	6/9 (67%)	5 (83%)	1 (17%)	0	100 100
4	D	198/200 (99%)	175 (88%)	20 (10%)	3 (2%)	13 40
5	E	243/245 (99%)	222 (91%)	16 (7%)	5 (2%)	9 29
All	All	821/829 (99%)	748 (91%)	62 (8%)	11 (1%)	15 44

All (11) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
4	D	6	ASN
5	E	27	MET
2	B	34	ASP
5	E	62	ASN
4	D	183	ASN
4	D	184	LYS
1	A	220	ASP
5	E	102	ARG
1	A	194	VAL
5	E	103	PRO
5	E	100	GLY

5.3.2 Protein sidechains

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
1	A	234/231 (101%)	202 (86%)	32 (14%)	4 13
2	B	95/95 (100%)	87 (92%)	8 (8%)	14 37
3	C	7/7 (100%)	7 (100%)	0	100 100
4	D	178/178 (100%)	143 (80%)	35 (20%)	1 5
5	E	209/209 (100%)	181 (87%)	28 (13%)	5 14
All	All	723/720 (100%)	620 (86%)	103 (14%)	4 12

All (103) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	12	VAL
1	A	30[A]	ASP
1	A	30[B]	ASP
1	A	35	ARG
1	A	45	MET
1	A	52	ILE
1	A	53	GLU
1	A	58	GLU
1	A	66	LYS
1	A	67	VAL
1	A	72	GLN
1	A	88	SER
1	A	98	MET
1	A	110	LEU
1	A	113	TYR
1	A	115	GLN
1	A	138	MET
1	A	141	GLN
1	A	163	THR
1	A	178	THR
1	A	181	ARG
1	A	187	THR
1	A	203	CYS
1	A	207	SER
1	A	214	THR
1	A	216	THR
1	A	219	ARG
1	A	223	ASP

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Mol	Chain	Res	Type
1	A	225	THR
1	A	247	VAL
1	A	249	VAL
1	A	272	LEU
2	B	4	THR
2	B	50	GLU
2	B	64	LEU
2	B	70	PHE
2	B	85	VAL
2	B	88	SER
2	B	98	ASP
2	B	99	MET
4	D	11	SER
4	D	12	VAL
4	D	14	GLU
4	D	22	CYS
4	D	23	THR
4	D	25	SER
4	D	41	LYS
4	D	48	SER
4	D	54	ASP
4	D	56	GLU
4	D	74	SER
4	D	78	ARG
4	D	87	THR
4	D	89	LEU
4	D	90	CYS
4	D	100	SER
4	D	101	TRP
4	D	110	THR
4	D	111	GLN
4	D	118	ILE
4	D	134	SER
4	D	136	LYS
4	D	137	SER
4	D	150	VAL
4	D	151	SER
4	D	152	GLN
4	D	162	ASP
4	D	164	THR
4	D	170	SER
4	D	183	ASN

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Mol	Chain	Res	Type
4	D	185	SER
4	D	187	PHE
4	D	195	ASN
4	D	197	ILE
4	D	198	ILE
5	E	19	MET
5	E	20	THR
5	E	21	LEU
5	E	25	GLN
5	E	26	ASP
5	E	31	TYR
5	E	41	MET
5	E	46	ILE
5	E	55	THR
5	E	59	GLU
5	E	66	ASN
5	E	67	VAL
5	E	70	SER
5	E	78	ARG
5	E	94	SER
5	E	102	ARG
5	E	115	THR
5	E	150	THR
5	E	159	LEU
5	E	160	SER
5	E	166	LYS
5	E	170	SER
5	E	179	LEU
5	E	187	ASP
5	E	195	ARG
5	E	198	VAL
5	E	227	GLN
5	E	228	ASP

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (11) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	43	GLN
1	A	72	GLN
1	A	115	GLN
1	A	226	GLN
4	D	30	GLN

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Mol	Chain	Res	Type
4	D	37	GLN
4	D	111	GLN
4	D	152	GLN
4	D	176	ASN
5	E	28	ASN
5	E	57	GLN

5.3.3 RNA

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains

2 non-standard protein/DNA/RNA residues 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).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\| > 2$	Counts	RMSZ	$\#\|Z\| > 2$
3	F2F	C	5[A]	-	12,13,14	0.46	0	14,17,19	1.24	2 (14%)
3	F2F	C	5[B]	-	12,13,14	0.43	0	14,17,19	1.35	2 (14%)

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	F2F	C	5[A]	-	-	0/4/6/8	0/1/1/1
3	F2F	C	5[B]	-	-	0/4/6/8	0/1/1/1

There are no bond length outliers.

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
3	C	5[B]	F2F	CG-CB-CA	-3.51	106.29	114.21
3	C	5[B]	F2F	O-C-CA	-2.85	118.08	125.49
3	C	5[A]	F2F	O-C-CA	-2.85	118.08	125.49
3	C	5[A]	F2F	CG-CB-CA	-2.11	109.45	114.21

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.5 Carbohydrates (i)

There are no carbohydrates in this entry.

5.6 Ligand geometry (i)

6 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).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\| > 2$	Counts	RMSZ	$\#\|Z\| > 2$
6	GOL	A	276	-	5,5,5	0.43	0	5,5,5	0.18	0
6	GOL	A	277	-	5,5,5	0.30	0	5,5,5	0.34	0
6	GOL	B	100	-	5,5,5	0.28	0	5,5,5	0.46	0
6	GOL	B	101	-	5,5,5	0.40	0	5,5,5	0.07	0
6	GOL	E	247	-	5,5,5	0.49	0	5,5,5	0.66	0
6	GOL	E	248	-	5,5,5	0.29	0	5,5,5	0.28	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	GOL	A	276	-	-	0/4/4/4	0/0/0/0
6	GOL	A	277	-	-	0/4/4/4	0/0/0/0
6	GOL	B	100	-	-	0/4/4/4	0/0/0/0
6	GOL	B	101	-	-	0/4/4/4	0/0/0/0
6	GOL	E	247	-	-	0/4/4/4	0/0/0/0
6	GOL	E	248	-	-	0/4/4/4	0/0/0/0

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers

There are no such residues in this entry.

5.8 Polymer linkage issues

There are no chain breaks in this entry.

6 Fit of model and data

6.1 Protein, DNA and RNA chains

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	A	275/275 (100%)	0.27	19 (6%) 20 11	38, 63, 76, 85	0
2	B	100/100 (100%)	0.07	4 (4%) 42 30	53, 65, 73, 90	0
3	C	8/9 (88%)	-0.36	0 100 100	57, 61, 64, 65	0
4	D	200/200 (100%)	0.69	30 (15%) 3 2	53, 67, 77, 81	0
5	E	245/245 (100%)	0.10	11 (4%) 37 26	28, 61, 71, 77	0
All	All	828/829 (99%)	0.29	64 (7%) 16 8	28, 64, 75, 90	0

All (64) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
4	D	184	LYS	9.0
4	D	153	SER	8.8
4	D	133	SER	7.5
4	D	171	MET	7.0
4	D	205	PRO	6.4
5	E	1	ASN	6.3
4	D	183	ASN	5.0
1	A	1	GLY	5.0
4	D	154	LYS	4.9
1	A	260	HIS	4.8
4	D	206	SER	4.7
4	D	156	SER	4.5
1	A	221	GLY	4.4
4	D	186	ASP	4.3
4	D	185	SER	4.3
1	A	194	VAL	4.3
5	E	186	ASN	4.2
4	D	201	ASP	4.2
1	A	195	SER	4.0
1	A	223	ASP	4.0

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Mol	Chain	Res	Type	RSRZ
5	E	2	ALA	4.0
5	E	169	HIS	3.9
5	E	41	MET	3.8
5	E	245	ALA	3.7
1	A	191	HIS	3.6
4	D	159	TYR	3.5
1	A	197	HIS	3.5
1	A	222	GLU	3.3
4	D	135	ASP	3.3
1	A	226	GLN	3.3
4	D	203	PHE	3.3
5	E	246	ASP	3.1
4	D	204	PHE	3.1
5	E	139	HIS	3.1
1	A	252	GLY	3.1
4	D	134	SER	3.0
4	D	169	ARG	3.0
4	D	132	LYS	2.8
1	A	259	CYS	2.8
4	D	200	GLU	2.8
1	A	220	ASP	2.7
1	A	256	ARG	2.7
2	B	75	LYS	2.5
1	A	274	TRP	2.5
2	B	24	ASN	2.4
1	A	248	VAL	2.4
1	A	271	THR	2.4
4	D	149	ASN	2.4
4	D	170	SER	2.3
2	B	99	MET	2.3
1	A	192	HIS	2.3
4	D	129	ARG	2.2
4	D	188	ALA	2.2
5	E	134	GLU	2.2
4	D	74	SER	2.2
4	D	197	ILE	2.2
4	D	139	CYS	2.2
4	D	174	LYS	2.2
4	D	155	ASP	2.2
5	E	80	LEU	2.1
5	E	138	SER	2.1
2	B	25	CYS	2.1

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Mol	Chain	Res	Type	RSRZ
4	D	9	PRO	2.1
1	A	228	THR	2.0

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

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. The B-factors column lists the minimum, median, 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	LLDF	B-factors(Å^2)	Q<0.9
3	F2F	C	5[B]	13/14	0.96	0.15	-	64,66,66,66	9
3	F2F	C	5[A]	13/14	0.96	0.15	-	64,66,66,66	9

6.3 Carbohydrates (i)

There are no carbohydrates in this entry.

6.4 Ligands (i)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. The B-factors column lists the minimum, median, 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	LLDF	B-factors(Å^2)	Q<0.9
6	GOL	E	247	6/6	0.82	0.35	3.40	67,68,69,69	0
6	GOL	B	101	6/6	0.96	0.40	3.24	68,70,71,71	0
6	GOL	A	276	6/6	0.91	0.28	2.55	65,66,66,66	0
6	GOL	B	100	6/6	0.79	0.39	-	56,57,57,57	6
6	GOL	A	277	6/6	0.74	0.33	-	68,68,68,68	6
6	GOL	E	248	6/6	0.82	0.39	-	64,64,64,64	6

6.5 Other polymers (i)

There are no such residues in this entry.