



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 5, 2026 – 08:09 PM UTC

PDB ID : 5C08 / pdb_00005c08
Title : 1E6 TCR in Complex with HLA-A0e carrying RQWGPDPAAV
Authors : Rizkallah, P.J.; Bulek, A.M.; Cole, D.K.; Sewell, A.K.
Deposited on : 2015-06-12
Resolution : 2.33 Å(reported)

This is a wwPDB X-ray Structure Validation Summary 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 ⓘ 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 ⓘ](#)) were used in the production of this report:

MolProbity : 4-5-2 with Phenix2.0
Mogul : 2022.3.0, CSD as543be (2022)
Xtriage (Phenix) : 2.0
EDS : 3.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4 : 9.0.010 (Gargrove)
Density-Fitness : 1.0.12
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

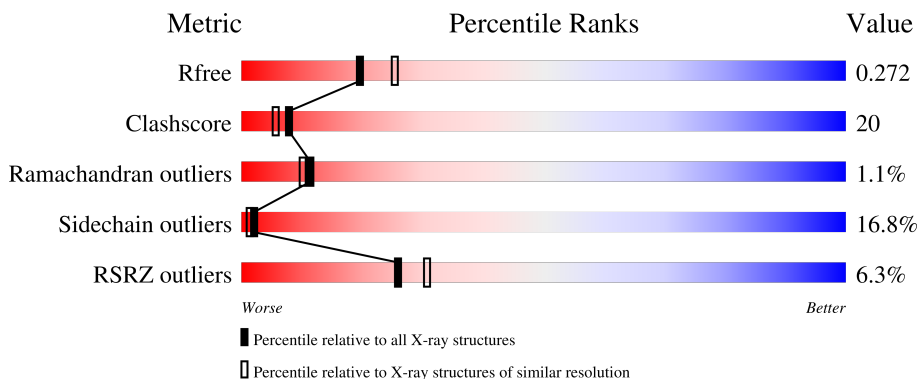
1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.33 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}	180053	3031 (2.36-2.32)
Clashscore	190562	3127 (2.36-2.32)
Ramachandran outliers	187476	3095 (2.36-2.32)
Sidechain outliers	187428	3095 (2.36-2.32)
RSRZ outliers	180081	3033 (2.36-2.32)

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 $\leq 5\%$. 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	276	<div style="display: flex; align-items: center;"> <div style="width: 5%; height: 10px; background-color: red; margin-right: 5px;"></div> <div style="width: 61%; height: 10px; background-color: green; margin-right: 5px;"></div> <div style="width: 30%; height: 10px; background-color: yellow; margin-right: 5px;"></div> <div style="width: 9%; height: 10px; background-color: orange; margin-right: 5px;"></div> <div style="width: 5%; height: 10px; background-color: red; margin-right: 5px;"></div> </div>
1	F	276	<div style="display: flex; align-items: center;"> <div style="width: 3%; height: 10px; background-color: red; margin-right: 5px;"></div> <div style="width: 57%; height: 10px; background-color: green; margin-right: 5px;"></div> <div style="width: 33%; height: 10px; background-color: yellow; margin-right: 5px;"></div> <div style="width: 8%; height: 10px; background-color: orange; margin-right: 5px;"></div> <div style="width: 5%; height: 10px; background-color: red; margin-right: 5px;"></div> </div>
2	B	100	<div style="display: flex; align-items: center;"> <div style="width: 3%; height: 10px; background-color: red; margin-right: 5px;"></div> <div style="width: 60%; height: 10px; background-color: green; margin-right: 5px;"></div> <div style="width: 33%; height: 10px; background-color: yellow; margin-right: 5px;"></div> <div style="width: 6%; height: 10px; background-color: orange; margin-right: 5px;"></div> <div style="width: 5%; height: 10px; background-color: red; margin-right: 5px;"></div> </div>
2	G	100	<div style="display: flex; align-items: center;"> <div style="width: 0%; height: 10px; background-color: red; margin-right: 5px;"></div> <div style="width: 65%; height: 10px; background-color: green; margin-right: 5px;"></div> <div style="width: 26%; height: 10px; background-color: yellow; margin-right: 5px;"></div> <div style="width: 9%; height: 10px; background-color: orange; margin-right: 5px;"></div> </div>
3	C	10	<div style="display: flex; align-items: center;"> <div style="width: 90%; height: 10px; background-color: green; margin-right: 5px;"></div> <div style="width: 10%; height: 10px; background-color: orange; margin-right: 5px;"></div> </div>

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Mol	Chain	Length	Quality of chain
3	H	10	
4	D	191	
4	I	191	
5	E	245	
5	J	245	

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	EDO	F	301	-	-	X	-
6	EDO	F	303	-	-	X	-
7	GOL	E	306	-	-	X	-

2 Entry composition i

There are 9 unique types of molecules in this entry. The entry contains 13627 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
			Total	C	N	O	S			
1	A	276	Total	C	N	O	S	0	0	0
			2254	1408	410	427	9			
1	F	276	Total	C	N	O	S	0	0	0
			2254	1408	410	427	9			

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

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

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	0	MET	-	initiating methionine	UNP P61769
G	0	MET	-	initiating methionine	UNP P61769

- Molecule 3 is a protein called Marker peptide.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
			Total	C	N	O			
3	C	10	Total	C	N	O	0	0	0
			78	49	15	14			
3	H	10	Total	C	N	O	0	0	0
			78	49	15	14			

- Molecule 4 is a protein called 1E6 TCR Alpha Chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
4	D	189	Total	C	N	O	S	0	0	0
			1488	927	248	303	10			

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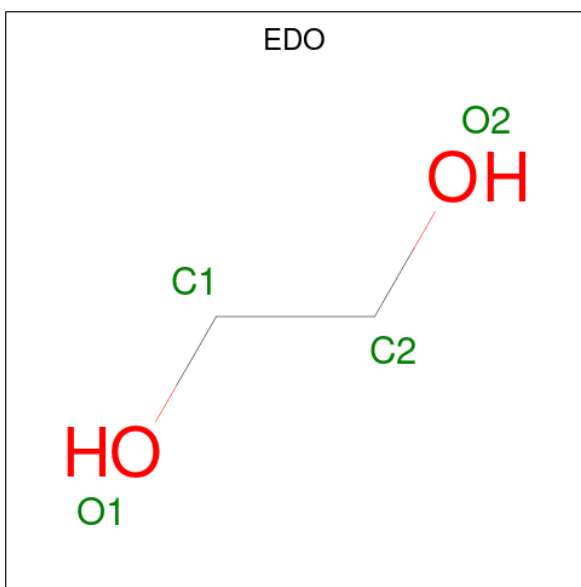
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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
4	I	191	1501	936	250	305	10	0	0	0

- Molecule 5 is a protein called 1E6 TCR Beta Chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
5	E	244	1961	1242	339	370	10	0	0	0
5	J	245	1966	1245	340	371	10	0	0	0

- Molecule 6 is 1,2-ETHANEDIOL (CCD ID: EDO) (formula: C₂H₆O₂).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
			Total	C	O		
6	A	1	4	2	2	0	0
6	A	1	4	2	2	0	0
6	B	1	4	2	2	0	0
6	B	1	4	2	2	0	0
6	B	1	4	2	2	0	0
6	C	1	4	2	2	0	0

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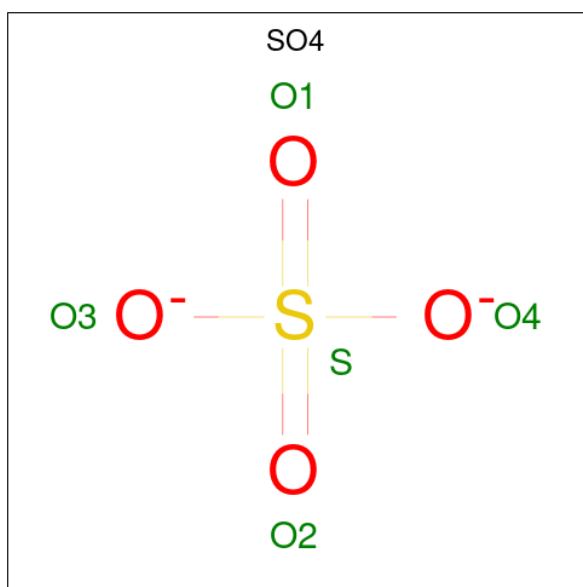
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
6	D	1	Total C O 4 2 2	0	0
6	E	1	Total C O 4 2 2	0	0
6	E	1	Total C O 4 2 2	0	0
6	E	1	Total C O 4 2 2	0	0
6	E	1	Total C O 4 2 2	0	0
6	E	1	Total C O 4 2 2	0	0
6	F	1	Total C O 4 2 2	0	0
6	F	1	Total C O 4 2 2	0	0
6	F	1	Total C O 4 2 2	0	0
6	F	1	Total C O 4 2 2	0	0
6	G	1	Total C O 4 2 2	0	0
6	I	1	Total C O 4 2 2	0	0
6	I	1	Total C O 4 2 2	0	0
6	I	1	Total C O 4 2 2	0	0
6	I	1	Total C O 4 2 2	0	0
6	I	1	Total C O 4 2 2	0	0
6	J	1	Total C O 4 2 2	0	0
6	J	1	Total C O 4 2 2	0	0
6	J	1	Total C O 4 2 2	0	0

- Molecule 7 is GLYCEROL (CCD ID: GOL) (formula: $C_3H_8O_3$).



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

- Molecule 8 is SULFATE ION (CCD ID: SO4) (formula: O₄S).



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

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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
8	D	1	Total 5	O 4	S 1	0	0
8	E	1	Total 5	O 4	S 1	0	0
8	E	1	Total 5	O 4	S 1	0	0
8	F	1	Total 5	O 4	S 1	0	0
8	J	1	Total 5	O 4	S 1	0	0
8	J	1	Total 5	O 4	S 1	0	0

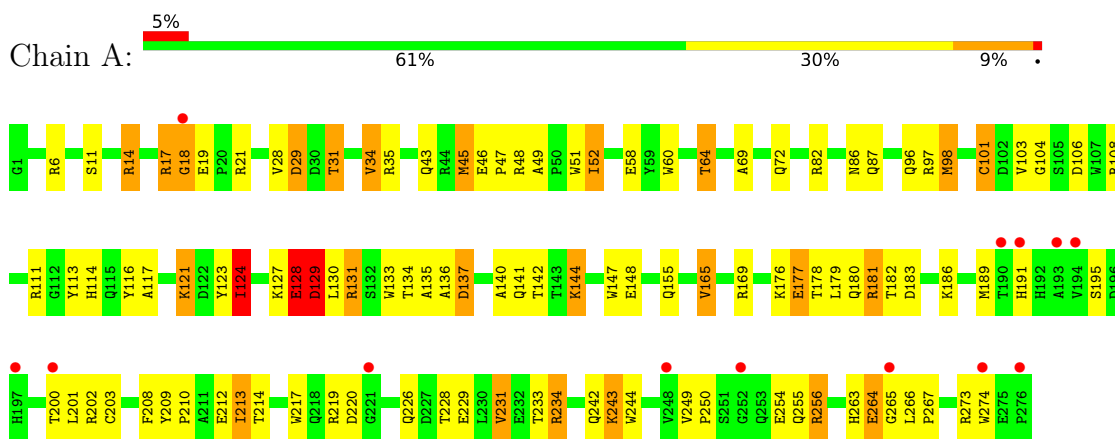
- Molecule 9 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
9	A	35	Total 35	O 35	0	0
9	B	18	Total 18	O 18	0	0
9	C	6	Total 6	O 6	0	0
9	D	21	Total 21	O 21	0	0
9	E	32	Total 32	O 32	0	0
9	F	33	Total 33	O 33	0	0
9	G	15	Total 15	O 15	0	0
9	H	5	Total 5	O 5	0	0
9	I	16	Total 16	O 16	0	0
9	J	39	Total 39	O 39	0	0

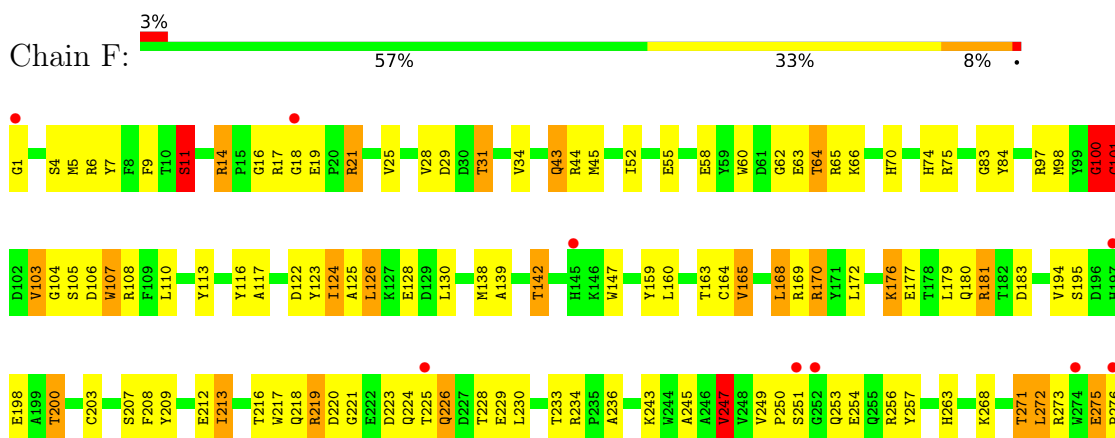
3 Residue-property plots

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

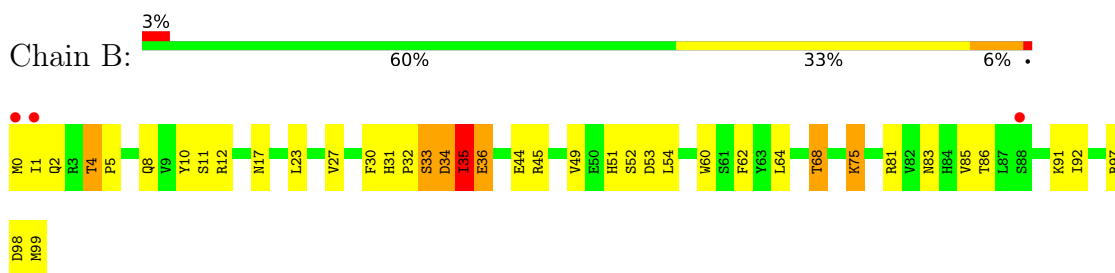
- Molecule 1: HLA class I histocompatibility antigen, A-2 alpha chain



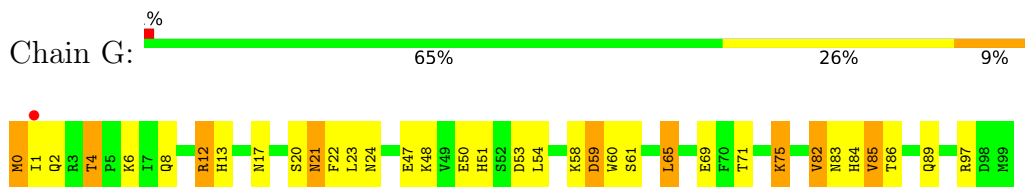
- Molecule 1: HLA class I histocompatibility antigen, A-2 alpha chain



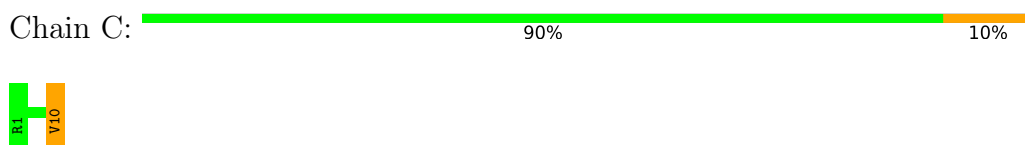
- Molecule 2: Beta-2-microglobulin



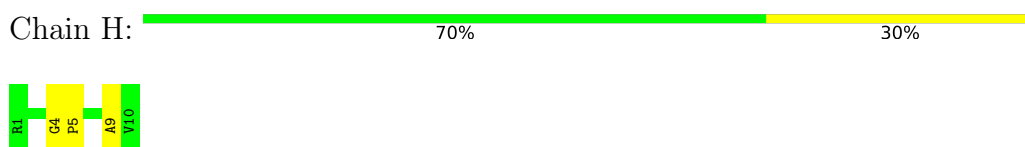
• Molecule 2: Beta-2-microglobulin



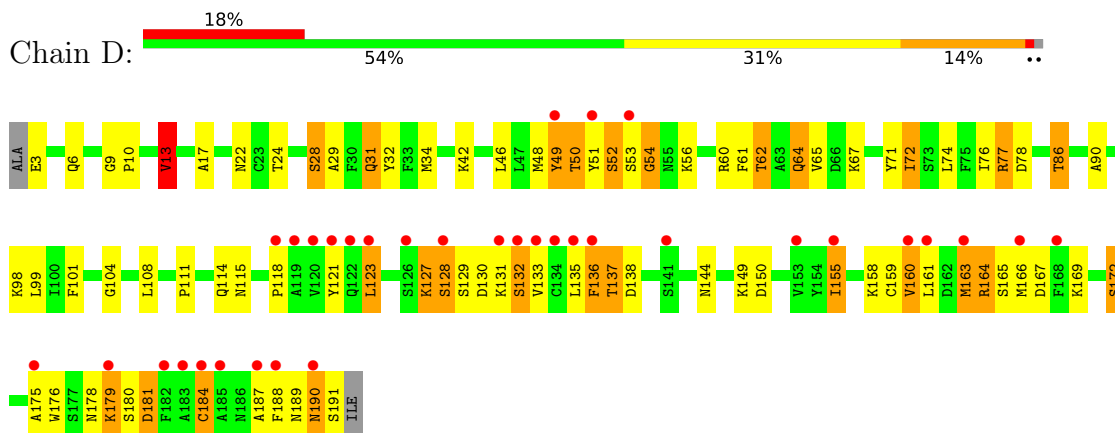
• Molecule 3: Marker peptide



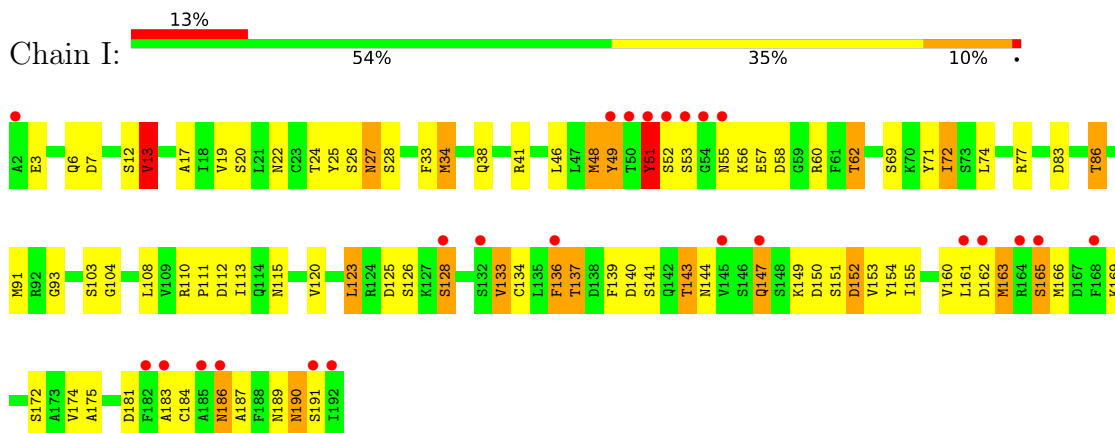
• Molecule 3: Marker peptide



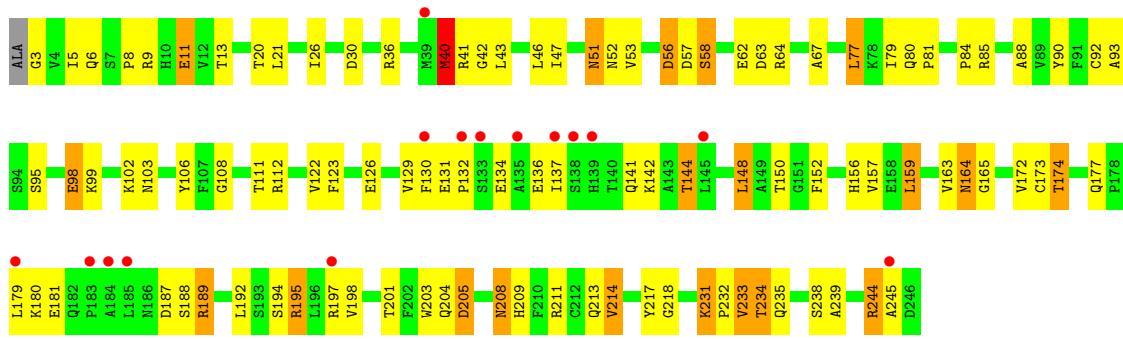
• Molecule 4: 1E6 TCR Alpha Chain



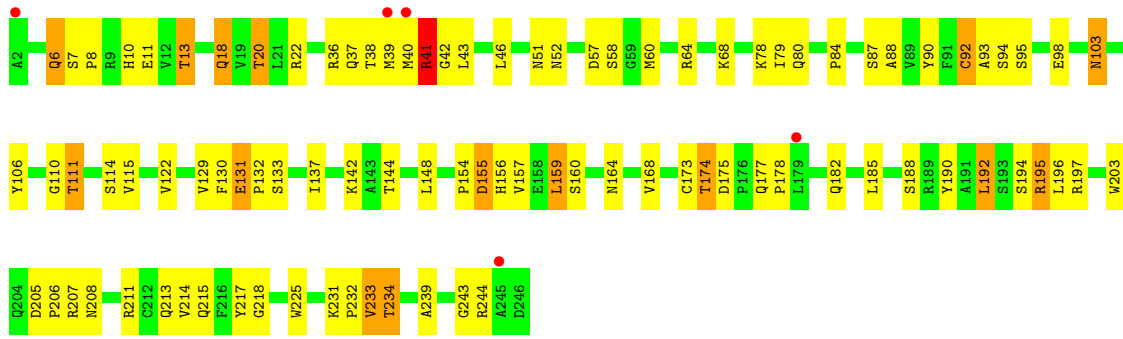
• Molecule 4: 1E6 TCR Alpha Chain



• Molecule 5: 1E6 TCR Beta Chain



• Molecule 5: 1E6 TCR Beta Chain



4 Data and refinement statistics

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α , β , γ	43.80Å 99.26Å 122.15Å 96.33° 98.07° 96.42°	Depositor
Resolution (Å)	48.91 – 2.33 48.91 – 2.33	Depositor EDS
% Data completeness (in resolution range)	97.4 (48.91-2.33) 97.4 (48.91-2.33)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.04	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.24 (at 2.34Å)	Xtrriage
Refinement program	REFMAC 5.8.0073	Depositor
R, R_{free}	0.206 , 0.272 0.206 , 0.272	Depositor DCC
R_{free} test set	4159 reflections (4.99%)	wwPDB-VP
Wilson B-factor (Å ²)	41.5	Xtrriage
Anisotropy	0.332	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 49.9	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	13627	wwPDB-VP
Average B, all atoms (Å ²)	55.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.33% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

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.

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, SO4, EDO

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	0.96	1/2320 (0.0%)	1.17	7/3149 (0.2%)
1	F	0.95	1/2320 (0.0%)	1.19	7/3149 (0.2%)
2	B	0.93	0/860	1.10	2/1162 (0.2%)
2	G	0.92	0/860	1.21	6/1162 (0.5%)
3	C	1.33	0/81	1.36	1/110 (0.9%)
3	H	1.01	0/81	1.10	0/110
4	D	0.94	0/1520	1.25	10/2055 (0.5%)
4	I	0.98	1/1533 (0.1%)	1.17	7/2073 (0.3%)
5	E	0.94	0/2016	1.23	14/2741 (0.5%)
5	J	1.01	3/2021 (0.1%)	1.24	14/2748 (0.5%)
All	All	0.96	6/13612 (0.0%)	1.20	68/18459 (0.4%)

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
1	A	0	2
1	F	0	1
All	All	0	3

The worst 5 of 6 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	F	101	CYS	CA-C	-5.95	1.45	1.52
5	J	58	SER	C-O	-5.73	1.17	1.24
5	J	6	GLN	CA-C	-5.29	1.46	1.52
1	A	43	GLN	CA-C	5.25	1.60	1.53
5	J	94	SER	CB-OG	-5.21	1.31	1.42

The worst 5 of 68 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	F	101	CYS	CB-CA-C	-9.92	95.76	110.24
4	D	28	SER	CA-C-N	-8.41	113.66	126.86
4	D	28	SER	C-N-CA	-8.41	113.66	126.86
5	E	57	ASP	N-CA-CB	-8.24	99.50	110.88
4	D	28	SER	N-CA-C	-8.08	99.86	110.53

There are no chirality outliers.

All (3) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	131	ARG	Peptide
1	A	136	ALA	Peptide
1	F	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	2254	0	2103	85	0
1	F	2254	0	2103	104	0
2	B	837	0	803	40	0
2	G	837	0	803	29	0
3	C	78	0	73	0	0
3	H	78	0	73	2	0
4	D	1488	0	1405	82	0
4	I	1501	0	1421	71	0
5	E	1961	0	1875	80	0
5	J	1966	0	1880	61	0
6	A	8	0	12	3	0
6	B	12	0	18	9	0
6	C	4	0	6	0	0
6	D	4	0	6	0	0
6	E	20	0	30	4	0
6	F	16	0	24	9	0
6	G	4	0	6	2	0
6	I	20	0	30	8	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
6	J	12	0	18	2	0
7	A	6	0	8	3	0
7	D	6	0	8	3	0
7	E	6	0	8	4	0
8	D	10	0	0	0	0
8	E	10	0	0	1	0
8	F	5	0	0	0	0
8	J	10	0	0	0	0
9	A	35	0	0	0	0
9	B	18	0	0	0	0
9	C	6	0	0	0	0
9	D	21	0	0	0	0
9	E	32	0	0	0	0
9	F	33	0	0	4	0
9	G	15	0	0	1	0
9	H	5	0	0	0	0
9	I	16	0	0	1	0
9	J	39	0	0	3	0
All	All	13627	0	12713	518	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 20.

The worst 5 of 518 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:40:MET:HE2	5:E:41:ARG:NH2	1.49	1.25
5:E:40:MET:CE	5:E:41:ARG:HH21	1.56	1.17
5:E:218:GLY:H	5:E:234:THR:HG22	1.04	1.16
2:G:75:LYS:HE3	2:G:75:LYS:H	1.12	1.10
4:I:60:ARG:HD3	6:I:203:EDO:H21	1.14	1.06

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	A	274/276 (99%)	267 (97%)	4 (2%)	3 (1%)	11	10
1	F	274/276 (99%)	265 (97%)	9 (3%)	0	100	100
2	B	98/100 (98%)	94 (96%)	4 (4%)	0	100	100
2	G	98/100 (98%)	91 (93%)	7 (7%)	0	100	100
3	C	8/10 (80%)	8 (100%)	0	0	100	100
3	H	8/10 (80%)	7 (88%)	1 (12%)	0	100	100
4	D	187/191 (98%)	168 (90%)	12 (6%)	7 (4%)	2	1
4	I	189/191 (99%)	172 (91%)	11 (6%)	6 (3%)	3	1
5	E	242/245 (99%)	225 (93%)	15 (6%)	2 (1%)	16	16
5	J	243/245 (99%)	236 (97%)	7 (3%)	0	100	100
All	All	1621/1644 (99%)	1533 (95%)	70 (4%)	18 (1%)	11	10

5 of 18 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
4	D	128	SER
4	D	167	ASP
4	D	181	ASP
4	I	51	TYR
4	I	152	ASP

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	Percentiles	
1	A	232/232 (100%)	188 (81%)	44 (19%)	1	1
1	F	232/232 (100%)	189 (82%)	43 (18%)	1	1
2	B	95/95 (100%)	81 (85%)	14 (15%)	3	2
2	G	95/95 (100%)	77 (81%)	18 (19%)	1	1

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
3	C	7/7 (100%)	6 (86%)	1 (14%)	3	2
3	H	7/7 (100%)	7 (100%)	0	100	100
4	D	170/171 (99%)	138 (81%)	32 (19%)	1	1
4	I	171/171 (100%)	141 (82%)	30 (18%)	2	1
5	E	215/215 (100%)	184 (86%)	31 (14%)	3	2
5	J	215/215 (100%)	186 (86%)	29 (14%)	4	3
All	All	1439/1440 (100%)	1197 (83%)	242 (17%)	2	1

5 of 242 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
5	E	201	THR
5	J	43	LEU
1	F	170	ARG
5	J	40	MET
5	J	192	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 58 such sidechains are listed below:

Mol	Chain	Res	Type
5	E	209	HIS
5	J	208	ASN
1	F	180	GLN
5	J	169	HIS
4	I	190	ASN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry

35 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
8	SO4	F	305	-	4,4,4	0.55	0	6,6,6	0.24	0
6	EDO	E	302	-	3,3,3	0.42	0	2,2,2	0.50	0
6	EDO	E	303	-	3,3,3	0.41	0	2,2,2	0.54	0
6	EDO	D	201	-	3,3,3	0.39	0	2,2,2	1.02	0
6	EDO	I	202	-	3,3,3	0.61	0	2,2,2	0.27	0
6	EDO	B	303	-	3,3,3	0.36	0	2,2,2	0.57	0
6	EDO	A	302	-	3,3,3	0.49	0	2,2,2	0.42	0
6	EDO	C	101	-	3,3,3	0.50	0	2,2,2	0.39	0
6	EDO	E	304	-	3,3,3	0.60	0	2,2,2	0.74	0
7	GOL	D	202	-	5,5,5	0.44	0	5,5,5	0.61	0
6	EDO	F	303	-	3,3,3	0.68	0	2,2,2	0.69	0
8	SO4	J	304	-	4,4,4	0.58	0	6,6,6	0.31	0
8	SO4	E	307	-	4,4,4	0.56	0	6,6,6	0.37	0
6	EDO	A	301	-	3,3,3	0.54	0	2,2,2	0.65	0
8	SO4	E	308	-	4,4,4	0.47	0	6,6,6	0.42	0
6	EDO	J	303	-	3,3,3	0.68	0	2,2,2	0.57	0
6	EDO	I	203	-	3,3,3	0.70	0	2,2,2	0.33	0
7	GOL	E	306	-	5,5,5	0.49	0	5,5,5	0.71	0
6	EDO	I	201	-	3,3,3	0.40	0	2,2,2	0.75	0
6	EDO	B	301	-	3,3,3	0.32	0	2,2,2	0.46	0
6	EDO	E	301	-	3,3,3	0.57	0	2,2,2	0.28	0
6	EDO	F	302	-	3,3,3	0.48	0	2,2,2	0.65	0
6	EDO	I	205	-	3,3,3	0.70	0	2,2,2	0.43	0
6	EDO	I	204	-	3,3,3	0.56	0	2,2,2	0.27	0
8	SO4	D	203	-	4,4,4	0.52	0	6,6,6	0.12	0
6	EDO	E	305	-	3,3,3	0.68	0	2,2,2	0.04	0
7	GOL	A	303	-	5,5,5	0.80	0	5,5,5	1.41	0
8	SO4	J	305	-	4,4,4	0.65	0	6,6,6	0.27	0
6	EDO	F	304	-	3,3,3	0.64	0	2,2,2	0.19	0
6	EDO	J	302	-	3,3,3	0.51	0	2,2,2	0.66	0
8	SO4	D	204	-	4,4,4	0.60	0	6,6,6	0.58	0
6	EDO	B	302	-	3,3,3	0.60	0	2,2,2	0.20	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
6	EDO	J	301	-	3,3,3	0.45	0	2,2,2	0.35	0
6	EDO	F	301	-	3,3,3	0.70	0	2,2,2	0.46	0
6	EDO	G	101	-	3,3,3	0.50	0	2,2,2	0.32	0

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
6	EDO	E	302	-	-	1/1/1/1	-
6	EDO	E	303	-	-	1/1/1/1	-
6	EDO	D	201	-	-	0/1/1/1	-
6	EDO	I	202	-	-	0/1/1/1	-
6	EDO	B	303	-	-	0/1/1/1	-
6	EDO	A	302	-	-	0/1/1/1	-
6	EDO	C	101	-	-	0/1/1/1	-
6	EDO	E	304	-	-	1/1/1/1	-
7	GOL	D	202	-	-	1/4/4/4	-
6	EDO	F	303	-	-	1/1/1/1	-
6	EDO	A	301	-	-	1/1/1/1	-
6	EDO	J	303	-	-	1/1/1/1	-
6	EDO	I	203	-	-	0/1/1/1	-
7	GOL	E	306	-	-	2/4/4/4	-
6	EDO	I	201	-	-	0/1/1/1	-
6	EDO	B	301	-	-	1/1/1/1	-
6	EDO	E	301	-	-	1/1/1/1	-
6	EDO	F	302	-	-	1/1/1/1	-
6	EDO	I	205	-	-	1/1/1/1	-
6	EDO	I	204	-	-	1/1/1/1	-
6	EDO	E	305	-	-	1/1/1/1	-
7	GOL	A	303	-	-	0/4/4/4	-
6	EDO	F	304	-	-	1/1/1/1	-
6	EDO	J	302	-	-	0/1/1/1	-
6	EDO	B	302	-	-	1/1/1/1	-
6	EDO	J	301	-	-	1/1/1/1	-
6	EDO	F	301	-	-	1/1/1/1	-
6	EDO	G	101	-	-	1/1/1/1	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

5 of 20 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
7	E	306	GOL	C1-C2-C3-O3
6	B	301	EDO	O1-C1-C2-O2
7	E	306	GOL	O2-C2-C3-O3
6	E	304	EDO	O1-C1-C2-O2
6	F	302	EDO	O1-C1-C2-O2

There are no ring outliers.

19 monomers are involved in 48 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
6	E	303	EDO	3	0
6	B	303	EDO	3	0
6	A	302	EDO	3	0
7	D	202	GOL	3	0
6	F	303	EDO	4	0
8	E	308	SO4	1	0
6	J	303	EDO	2	0
6	I	203	EDO	3	0
7	E	306	GOL	4	0
6	I	201	EDO	2	0
6	B	301	EDO	3	0
6	E	301	EDO	1	0
6	F	302	EDO	1	0
6	I	205	EDO	2	0
6	I	204	EDO	1	0
7	A	303	GOL	3	0
6	B	302	EDO	3	0
6	F	301	EDO	4	0
6	G	101	EDO	2	0

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Fit of model and data [i](#)

6.1 Protein, DNA and RNA chains [i](#)

In the following table, the column labelled ‘#RSRZ> 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95th 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	276/276 (100%)	0.11	13 (4%) 36 42	24, 48, 97, 125	0
1	F	276/276 (100%)	0.12	9 (3%) 49 55	24, 52, 88, 101	0
2	B	100/100 (100%)	-0.09	3 (3%) 52 59	31, 46, 65, 98	0
2	G	100/100 (100%)	-0.06	1 (1%) 79 82	32, 45, 66, 74	0
3	C	10/10 (100%)	-0.65	0 100 100	27, 29, 33, 45	0
3	H	10/10 (100%)	-0.79	0 100 100	29, 32, 33, 44	0
4	D	189/191 (98%)	0.72	34 (17%) 3 4	29, 55, 124, 140	0
4	I	191/191 (100%)	0.66	24 (12%) 8 9	28, 55, 119, 141	0
5	E	244/245 (99%)	0.31	15 (6%) 27 32	21, 52, 107, 128	0
5	J	245/245 (100%)	0.06	5 (2%) 65 70	22, 46, 85, 111	0
All	All	1641/1644 (99%)	0.23	104 (6%) 26 31	21, 49, 105, 141	0

The worst 5 of 104 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
4	I	168	PHE	5.1
4	I	192	ILE	4.9
5	E	185	LEU	4.8
4	I	145	VAL	4.6
4	D	168	PHE	4.5

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 oligosaccharides 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, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
8	SO4	J	305	5/5	0.61	0.14	75,79,97,97	0
8	SO4	J	304	5/5	0.75	0.10	77,80,82,87	0
6	EDO	F	301	4/4	0.78	0.19	55,56,57,60	0
6	EDO	F	304	4/4	0.81	0.17	62,63,72,75	0
8	SO4	E	307	5/5	0.81	0.22	62,70,80,84	0
8	SO4	F	305	5/5	0.82	0.09	96,97,104,113	0
6	EDO	E	301	4/4	0.83	0.16	59,67,69,71	0
6	EDO	B	302	4/4	0.83	0.17	58,62,63,69	0
8	SO4	E	308	5/5	0.83	0.11	74,83,92,94	0
8	SO4	D	203	5/5	0.84	0.08	84,85,91,92	0
6	EDO	I	202	4/4	0.85	0.14	53,54,60,61	0
7	GOL	D	202	6/6	0.85	0.12	49,68,70,73	0
6	EDO	A	302	4/4	0.87	0.19	46,58,64,68	0
6	EDO	I	203	4/4	0.87	0.13	39,48,50,51	0
6	EDO	E	303	4/4	0.87	0.12	61,61,64,67	0
6	EDO	F	302	4/4	0.88	0.13	39,45,45,51	0
6	EDO	F	303	4/4	0.88	0.16	43,48,51,55	0
7	GOL	A	303	6/6	0.89	0.15	38,55,56,65	0
8	SO4	D	204	5/5	0.90	0.10	72,73,82,88	0
6	EDO	E	302	4/4	0.90	0.17	50,54,55,65	0
6	EDO	J	301	4/4	0.91	0.13	65,76,76,79	0
6	EDO	E	304	4/4	0.92	0.10	35,41,44,45	0
6	EDO	E	305	4/4	0.92	0.16	48,55,56,62	0
6	EDO	I	205	4/4	0.92	0.12	34,36,39,64	0
6	EDO	C	101	4/4	0.92	0.10	37,40,42,45	0
6	EDO	J	303	4/4	0.92	0.10	35,40,41,46	0
6	EDO	G	101	4/4	0.92	0.10	52,52,54,57	0
6	EDO	I	201	4/4	0.92	0.09	40,46,47,50	0
6	EDO	D	201	4/4	0.93	0.10	41,43,47,48	0
6	EDO	A	301	4/4	0.93	0.10	49,53,65,65	0
6	EDO	I	204	4/4	0.93	0.09	43,44,45,48	0
6	EDO	B	303	4/4	0.94	0.09	48,49,53,58	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
6	EDO	J	302	4/4	0.94	0.10	34,39,45,49	0
6	EDO	B	301	4/4	0.94	0.09	43,48,51,55	0
7	GOL	E	306	6/6	0.97	0.08	39,42,43,52	0

6.5 Other polymers [i](#)

There are no such residues in this entry.