



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 8, 2026 – 12:24 PM UTC

PDB ID : 8RYP / pdb_00008ryp
Title : Structure of S8 TCR in complex with HLA-A*03:01 bound to ELFSYLIEK peptide
Authors : Karuppiah, V.
Deposited on : 2024-02-09
Resolution : 1.81 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 ⓘ 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

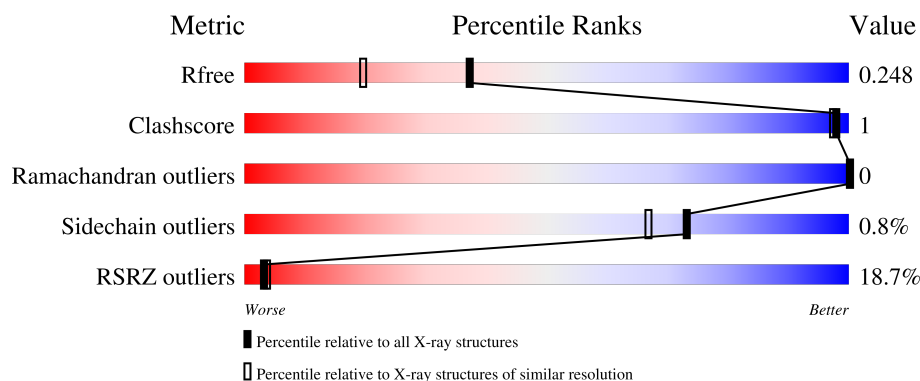
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.81 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	1112 (1.82-1.82)
Clashscore	190562	1148 (1.82-1.82)
Ramachandran outliers	187476	1140 (1.82-1.82)
Sidechain outliers	187428	1140 (1.82-1.82)
RSRZ outliers	180081	1112 (1.82-1.82)

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	8% 100%
2	B	100	3% 96% .
3	C	9	78% 22%
4	D	200	28% 93% 5%
5	E	244	29% 93% .

2 Entry composition

There are 7 unique types of molecules in this entry. The entry contains 6870 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 alpha chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	276	Total	C	N	O	S	0	1	0
			2252	1401	408	434	9			

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	276	PRO	-	expression tag	UNP P04439

- 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	-	initiating methionine	UNP P61769

- Molecule 3 is a protein called ELFSYLIEK peptide.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
3	C	9	Total	C	N	O	0	0	0
			81	55	10	16			

- Molecule 4 is a protein called TCR alpha.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
4	D	190	Total	C	N	O	S	0	1	0
			1461	903	254	296	8			

- Molecule 5 is a protein called TCR beta.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
5	E	237	Total 1881	C 1189	N 326	O 361	S 5	0	1	0

- Molecule 6 is 1,2-ETHANEDIOL (CCD ID: EDO) (formula: $C_2H_6O_2$).



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

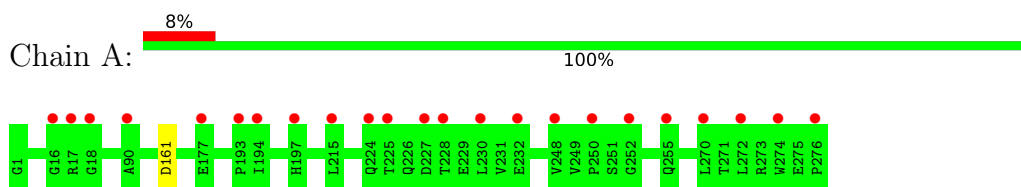
- Molecule 7 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	A	159	Total 159	O 159	0	0
7	B	107	Total 107	O 107	0	0
7	C	5	Total 5	O 5	0	0
7	D	39	Total 39	O 39	0	0
7	E	44	Total 44	O 44	0	0

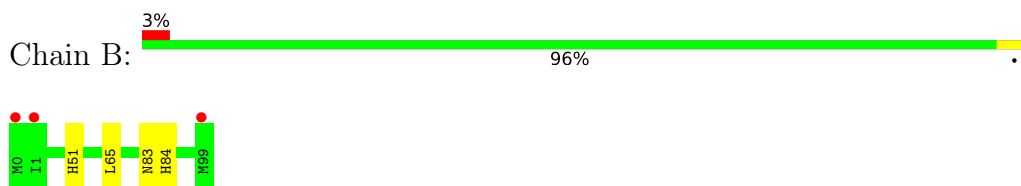
3 Residue-property plots [i](#)

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

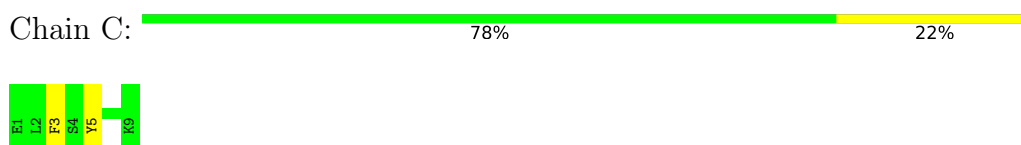
- Molecule 1: HLA class I histocompatibility antigen, A alpha chain



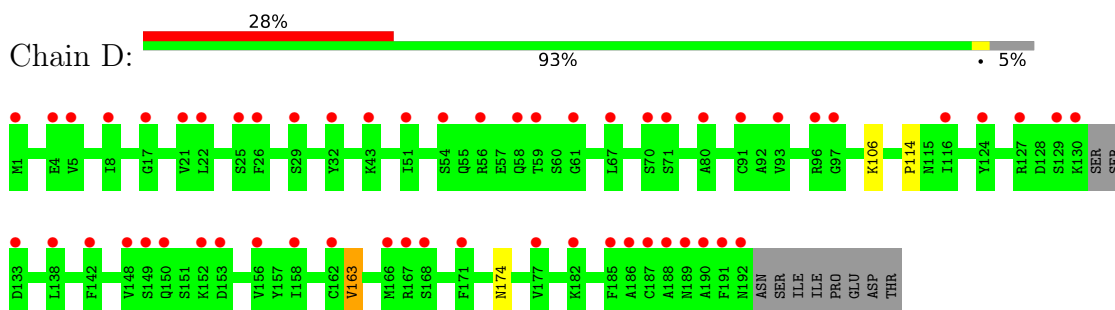
- Molecule 2: Beta-2-microglobulin



- Molecule 3: ELFSYLIEK peptide

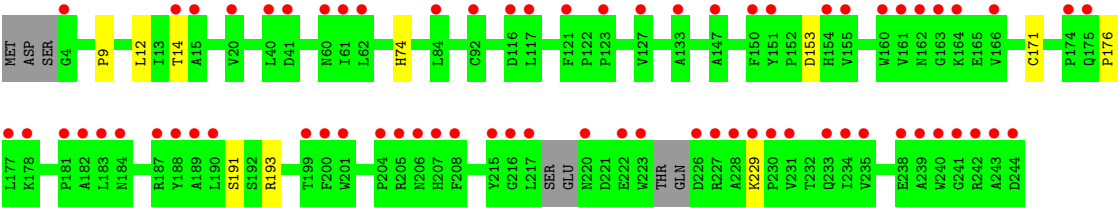


- Molecule 4: TCR alpha



- Molecule 5: TCR beta





4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	208.12Å 45.71Å 121.68Å 90.00° 94.93° 90.00°	Depositor
Resolution (Å)	121.23 – 1.81 121.23 – 1.81	Depositor EDS
% Data completeness (in resolution range)	99.9 (121.23-1.81) 99.9 (121.23-1.81)	Depositor EDS
R_{merge}	0.06	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.58 (at 1.81Å)	Xtriage
Refinement program	REFMAC 5.8.0267	Depositor
R, R_{free}	0.221 , 0.241 0.228 , 0.248	Depositor DCC
R_{free} test set	5073 reflections (4.84%)	wwPDB-VP
Wilson B-factor (Å ²)	34.9	Xtriage
Anisotropy	0.483	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.30 , 40.7	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.34$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	6870	wwPDB-VP
Average B, all atoms (Å ²)	56.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.86% 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: 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	0.97	0/2316	1.29	0/3144
2	B	0.96	0/860	1.14	0/1162
3	C	0.93	0/82	1.28	0/107
4	D	1.03	0/1486	1.27	0/2007
5	E	1.00	0/1934	1.22	0/2631
All	All	0.99	0/6678	1.25	0/9051

There are no bond length outliers.

There are no bond angle outliers.

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	2252	0	2106	1	0
2	B	837	0	803	2	0
3	C	81	0	83	1	0
4	D	1461	0	1430	2	0
5	E	1881	0	1777	3	0
6	B	4	0	6	0	0
7	A	159	0	0	0	0
7	B	107	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
7	C	5	0	0	0	0
7	D	39	0	0	0	0
7	E	44	0	0	0	0
All	All	6870	0	6205	9	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 1.

All (9) 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)
3:C:3:PHE:CZ	3:C:5:TYR:HB3	2.46	0.51
2:B:51:HIS:HA	2:B:65:LEU:O	2.16	0.46
1:A:161:ASP:C	1:A:161:ASP:OD1	2.61	0.43
5:E:153:ASP:HB2	5:E:176:PRO:HG2	1.99	0.43
2:B:83:ASN:HD22	2:B:84:HIS:H	1.65	0.43
5:E:9:PRO:HG2	5:E:12:LEU:HG	2.01	0.43
4:D:163:VAL:HG22	4:D:174:ASN:OD1	2.20	0.42
4:D:114:PRO:HG2	4:D:163:VAL:HG11	2.01	0.42
5:E:191:SER:OG	5:E:193:ARG:NH1	2.53	0.42

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	275/276 (100%)	270 (98%)	5 (2%)	0	100	100
2	B	98/100 (98%)	98 (100%)	0	0	100	100
3	C	7/9 (78%)	7 (100%)	0	0	100	100
4	D	187/200 (94%)	183 (98%)	4 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
5	E	232/244 (95%)	225 (97%)	7 (3%)	0	100	100
All	All	799/829 (96%)	783 (98%)	16 (2%)	0	100	100

There are no Ramachandran outliers to report.

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	234/233 (100%)	234 (100%)	0	100	100
2	B	95/95 (100%)	95 (100%)	0	100	100
3	C	9/9 (100%)	9 (100%)	0	100	100
4	D	167/176 (95%)	165 (99%)	2 (1%)	63	54
5	E	204/211 (97%)	200 (98%)	4 (2%)	48	35
All	All	709/724 (98%)	703 (99%)	6 (1%)	73	67

All (6) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
4	D	106	LYS
4	D	163	VAL
5	E	14	THR
5	E	74	HIS
5	E	171	CYS
5	E	229	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (16) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	43	GLN
1	A	62	GLN
1	A	151	HIS

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Mol	Chain	Res	Type
1	A	224	GLN
1	A	262	GLN
2	B	13	HIS
2	B	83	ASN
4	D	39	GLN
4	D	58	GLN
5	E	38	GLN
5	E	100	HIS
5	E	101	ASN
5	E	103	GLN
5	E	154	HIS
5	E	167	HIS
5	E	202	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 oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

1 ligand is 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	EDO	B	101	-	3,3,3	0.10	0	2,2,2	0.05	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	B	101	-	-	0/1/1/1	-

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 [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

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, 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%)	0.56	23 (8%)	17 20	20, 43, 88, 101	1 (0%)
2	B	100/100 (100%)	0.27	3 (3%)	52 59	27, 36, 56, 61	0
3	C	9/9 (100%)	-0.16	0	100 100	32, 33, 34, 39	0
4	D	190/200 (95%)	1.66	56 (29%)	1 1	27, 66, 96, 112	1 (0%)
5	E	237/244 (97%)	1.63	70 (29%)	1 1	36, 67, 108, 150	1 (0%)
All	All	812/829 (97%)	1.09	152 (18%)	3 4	20, 53, 96, 150	3 (0%)

All (152) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
5	E	223	TRP	6.4
5	E	121	PHE	5.9
4	D	152	LYS	5.4
5	E	183	LEU	4.7
1	A	248	VAL	4.1
5	E	242	ARG	4.1
5	E	204	PRO	4.1
5	E	217	LEU	4.1
5	E	241	GLY	3.9
5	E	181	PRO	3.9
5	E	239	ALA	3.9
5	E	243	ALA	3.9
5	E	228	ALA	3.9
5	E	60	ASN	3.8
1	A	194	ILE	3.8
5	E	240	TRP	3.7
4	D	188	ALA	3.5
5	E	62	LEU	3.4
4	D	1	MET	3.4
1	A	225	THR	3.4

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Mol	Chain	Res	Type	RSRZ
5	E	177	LEU	3.4
4	D	130	LYS	3.3
5	E	206	ASN	3.3
2	B	1	ILE	3.3
1	A	276	PRO	3.3
4	D	185	PHE	3.3
5	E	208	PHE	3.3
5	E	227	ARG	3.3
4	D	26	PHE	3.2
1	A	17	ARG	3.2
4	D	127	ARG	3.2
5	E	226	ASP	3.2
1	A	16	GLY	3.2
4	D	56	ARG	3.1
5	E	163	GLY	3.1
5	E	199	THR	3.1
5	E	40	LEU	3.1
4	D	192	ASN	3.1
5	E	61	ILE	3.0
5	E	201	TRP	3.0
4	D	21	VAL	3.0
5	E	188	TYR	3.0
4	D	186	ALA	3.0
4	D	32	TYR	3.0
5	E	92	CYS	3.0
5	E	84	LEU	2.9
4	D	162	CYS	2.9
5	E	147	ALA	2.9
4	D	191	PHE	2.9
5	E	229	LYS	2.9
5	E	220	ASN	2.8
4	D	71	SER	2.8
5	E	184	ASN	2.8
4	D	5	VAL	2.8
4	D	190	ALA	2.8
1	A	270	LEU	2.7
4	D	67	LEU	2.7
5	E	230	PRO	2.7
4	D	177	VAL	2.7
5	E	127	VAL	2.7
1	A	18	GLY	2.7
4	D	96	ARG	2.7

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Mol	Chain	Res	Type	RSRZ
4	D	25	SER	2.7
4	D	158	ILE	2.7
5	E	164	LYS	2.7
5	E	189	ALA	2.6
5	E	160	TRP	2.6
4	D	4	GLU	2.6
4	D	168	SER	2.6
4	D	187	CYS	2.6
4	D	149	SER	2.6
5	E	234	ILE	2.6
1	A	255	GLN	2.6
5	E	155	VAL	2.6
5	E	182	ALA	2.6
4	D	182	LYS	2.6
5	E	200	PHE	2.6
1	A	274	TRP	2.6
4	D	58	GLN	2.6
5	E	116	ASP	2.6
5	E	15	ALA	2.6
5	E	123	PRO	2.5
5	E	175	GLN	2.5
4	D	29	SER	2.5
1	A	197	HIS	2.5
5	E	187	ARG	2.5
4	D	124	TYR	2.5
5	E	151	TYR	2.5
5	E	117	LEU	2.5
5	E	231	VAL	2.5
1	A	272	LEU	2.5
4	D	116	ILE	2.5
4	D	150	GLN	2.5
5	E	161	VAL	2.5
5	E	154	HIS	2.4
4	D	8	ILE	2.4
5	E	4	GLY	2.4
5	E	238	GLU	2.4
2	B	0	MET	2.4
4	D	22	LEU	2.4
4	D	153	ASP	2.4
5	E	41	ASP	2.4
5	E	244	ASP	2.4
5	E	235	VAL	2.4

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Mol	Chain	Res	Type	RSRZ
1	A	228	THR	2.4
4	D	54	SER	2.4
5	E	174	PRO	2.3
4	D	148	VAL	2.3
4	D	156	VAL	2.3
4	D	171	PHE	2.3
5	E	150	PHE	2.3
5	E	20	VAL	2.3
1	A	215	LEU	2.3
4	D	138	LEU	2.3
5	E	215	TYR	2.3
4	D	51	ILE	2.3
1	A	227	ASP	2.3
5	E	14	THR	2.3
5	E	207	HIS	2.2
4	D	43	LYS	2.2
4	D	59	THR	2.2
5	E	133	ALA	2.2
4	D	166	MET	2.2
5	E	166	VAL	2.2
1	A	193	PRO	2.2
5	E	162	ASN	2.2
4	D	70	SER	2.2
5	E	216	GLY	2.2
4	D	142	PHE	2.1
4	D	189	ASN	2.1
4	D	133	ASP	2.1
4	D	61	GLY	2.1
4	D	97	GLY	2.1
5	E	190	LEU	2.1
1	A	232	GLU	2.1
4	D	80	ALA	2.1
4	D	93	VAL	2.1
4	D	167	ARG	2.1
2	B	99	MET	2.1
1	A	90	ALA	2.1
4	D	129	SER	2.1
1	A	177	GLU	2.1
4	D	17	GLY	2.1
1	A	250	PRO	2.1
4	D	91	CYS	2.1
5	E	205	ARG	2.1

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Mol	Chain	Res	Type	RSRZ
5	E	178	LYS	2.0
1	A	252	GLY	2.0
5	E	233	GLN	2.0
1	A	230	LEU	2.0
5	E	222	GLU	2.0
1	A	224	GLN	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 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($\text{\AA}^2$)	Q<0.9
6	EDO	B	101	4/4	0.83	0.17	38,40,42,45	0

6.5 Other polymers [i](#)

There are no such residues in this entry.