



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 09:20 PM UTC

PDB ID : 2FYY / pdb_00002fyy
Title : The role of T cell receptor alpha genes in directing human MHC restriction
Authors : Miles, J.J.; Borg, N.A.
Deposited on : 2006-02-08
Resolution : 1.50 Å(reported)

This is a Full wwPDB X-ray Structure Validation Report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ 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
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

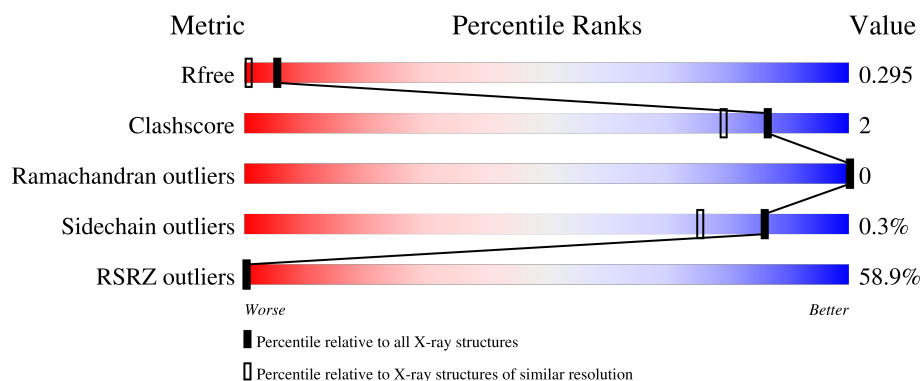
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.50 Å.

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



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	180053	4037 (1.50-1.50)
Clashscore	190562	4235 (1.50-1.50)
Ramachandran outliers	187476	4153 (1.50-1.50)
Sidechain outliers	187428	4150 (1.50-1.50)
RSRZ outliers	180081	4039 (1.50-1.50)

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	57% 95% 5%
2	B	99	66% 97% .
3	C	11	18% 64% 36%

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 3433 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, B-35 alpha chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	276	Total	C	N	O	S	0	0	0
			2254	1405	411	431	7			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	99	Total	C	N	O	S	0	0	0
			829	528	140	158	3			

- Molecule 3 is a protein called 11-mer peptide from Epstein-Barr nuclear antigen 1.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
3	C	7	Total	C	N	O	0	0	0
			55	35	9	11			

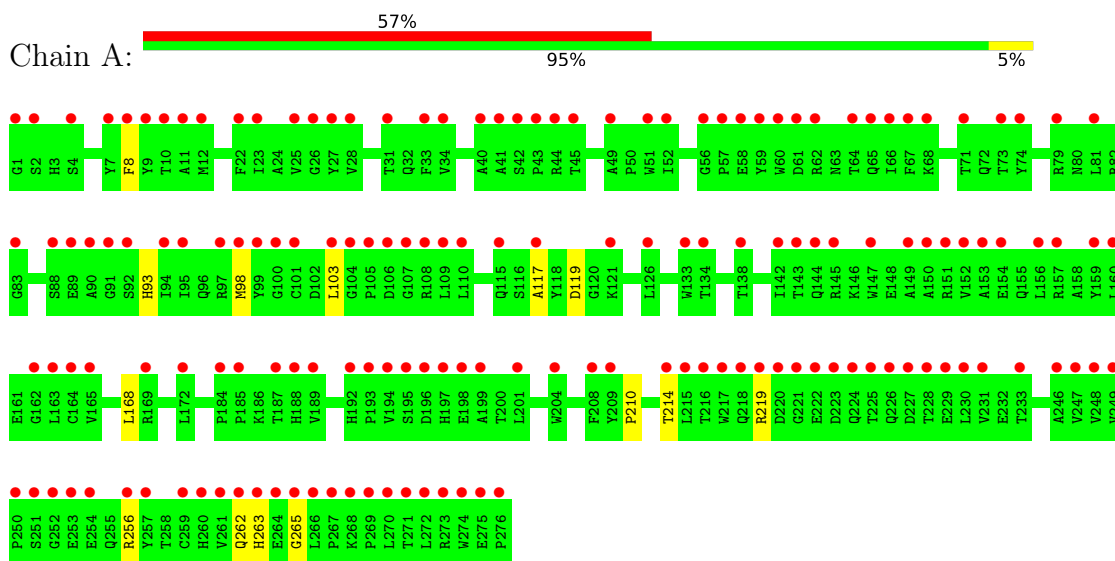
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	225	Total	O	0	0
			225	225		
4	B	65	Total	O	0	0
			65	65		
4	C	5	Total	O	0	0
			5	5		

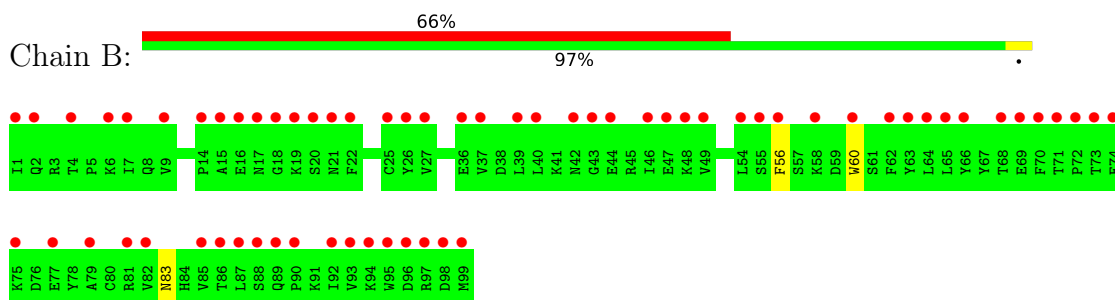
3 Residue-property plots [i](#)

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.

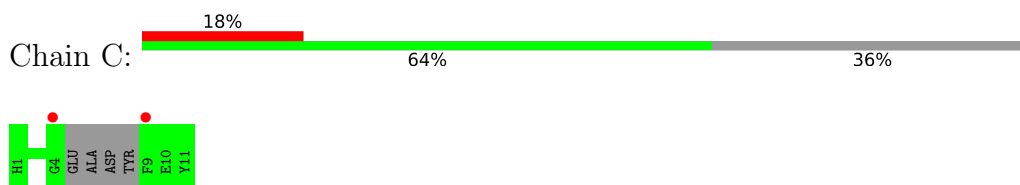
- Molecule 1: HLA class I histocompatibility antigen, B-35 alpha chain



- Molecule 2: Beta-2-microglobulin



- Molecule 3: 11-mer peptide from Epstein-Barr nuclear antigen 1



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	51.05Å 81.78Å 110.31Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	65.65 – 1.50 65.65 – 1.50	Depositor EDS
% Data completeness (in resolution range)	87.3 (65.65-1.50) 87.2 (65.65-1.50)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	6.12 (at 1.50Å)	Xtriage
Refinement program	REFMAC 5.2.0005	Depositor
R, R_{free}	0.225 , 0.236 0.279 , 0.295	Depositor DCC
R_{free} test set	1620 reflections (2.17%)	wwPDB-VP
Wilson B-factor (Å ²)	16.3	Xtriage
Anisotropy	0.590	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.39 , 35.4	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.92	EDS
Total number of atoms	3433	wwPDB-VP
Average B, all atoms (Å ²)	24.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.37% 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](#)

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	0.38	0/2317	0.67	0/3150
2	B	0.37	0/852	0.62	0/1152
3	C	0.44	0/56	0.54	0/73
All	All	0.38	0/3225	0.66	0/4375

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	2254	0	2117	13	0
2	B	829	0	794	3	0
3	C	55	0	44	0	0
4	A	225	0	0	1	0
4	B	65	0	0	0	0
4	C	5	0	0	0	0
All	All	3433	0	2955	13	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 2.

All (13) 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)
1:A:98:MET:HE3	2:B:56:PHE:HE2	1.55	0.71
1:A:98:MET:HE3	2:B:56:PHE:CE2	2.26	0.71
1:A:263:HIS:CD2	1:A:265:GLY:H	2.14	0.66
1:A:93:HIS:HD2	1:A:119:ASP:OD2	1.86	0.59
1:A:263:HIS:HD2	1:A:265:GLY:H	1.50	0.57
1:A:8:PHE:HE2	1:A:98:MET:HE2	1.74	0.53
1:A:210:PRO:O	1:A:263:HIS:HE1	1.96	0.48
1:A:214:THR:HB	1:A:262:GLN:HB2	1.99	0.45
1:A:8:PHE:CE2	1:A:98:MET:HE2	2.53	0.42
1:A:93:HIS:HE1	4:A:357:HOH:O	2.03	0.42
1:A:103:LEU:HG	1:A:168:LEU:HD23	2.02	0.42
1:A:117:ALA:HB2	2:B:60:TRP:CE2	2.55	0.41
1:A:219:ARG:HH21	1:A:256:ARG:HH22	1.69	0.41

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%)	271 (99%)	3 (1%)	0	100	100
2	B	97/99 (98%)	95 (98%)	2 (2%)	0	100	100
3	C	3/11 (27%)	3 (100%)	0	0	100	100
All	All	374/386 (97%)	369 (99%)	5 (1%)	0	100	100

There are no Ramachandran outliers to report.

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	234/234 (100%)	234 (100%)	0	100	100
2	B	94/94 (100%)	93 (99%)	1 (1%)	65	41
3	C	5/9 (56%)	5 (100%)	0	100	100
All	All	333/337 (99%)	332 (100%)	1 (0%)	86	75

All (1) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	B	83	ASN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (8) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	70	ASN
1	A	80	ASN
1	A	93	HIS
1	A	197	HIS
1	A	224	GLN
1	A	263	HIS
2	B	13	HIS
2	B	83	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

There are no ligands in this entry.

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, 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%)	2.32	158 (57%) 0 0	19, 23, 31, 34	0
2	B	99/99 (100%)	2.44	65 (65%) 0 0	21, 24, 27, 29	0
3	C	7/11 (63%)	1.31	2 (28%) 1 1	16, 17, 22, 23	0
All	All	382/386 (98%)	2.33	225 (58%) 0 0	16, 24, 30, 34	0

All (225) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	194	VAL	7.0
1	A	266	LEU	6.8
1	A	267	PRO	6.8
2	B	1	ILE	6.6
1	A	252	GLY	6.1
2	B	75	LYS	6.0
2	B	92	ILE	6.0
1	A	276	PRO	5.8
1	A	105	PRO	5.7
1	A	197	HIS	5.6
1	A	271	THR	5.3
1	A	107	GLY	5.0
1	A	108	ARG	5.0
1	A	109	LEU	4.8
1	A	193	PRO	4.6
1	A	151	ARG	4.5
1	A	249	VAL	4.4
1	A	247	VAL	4.4
2	B	19	LYS	4.4
2	B	73	THR	4.4
1	A	104	GLY	4.3
1	A	57	PRO	4.2
1	A	225	THR	4.1

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Mol	Chain	Res	Type	RSRZ
1	A	198	GLU	4.1
1	A	219	ARG	4.1
1	A	110	LEU	4.0
1	A	196	ASP	4.0
2	B	77	GLU	4.0
1	A	256	ARG	3.9
1	A	275	GLU	3.9
1	A	248	VAL	3.9
1	A	230	LEU	3.9
2	B	20	SER	3.9
1	A	274	TRP	3.9
2	B	74	GLU	3.9
2	B	69	GLU	3.8
1	A	257	TYR	3.8
2	B	72	PRO	3.8
1	A	1	GLY	3.8
1	A	226	GLN	3.8
1	A	231	VAL	3.8
1	A	250	PRO	3.8
1	A	121	LYS	3.8
1	A	73	THR	3.8
1	A	149	ALA	3.8
2	B	93	VAL	3.7
2	B	71	THR	3.7
1	A	272	LEU	3.7
1	A	25	VAL	3.7
2	B	16	GLU	3.7
2	B	36	GLU	3.7
2	B	47	GLU	3.7
1	A	98	MET	3.7
1	A	106	ASP	3.6
1	A	216	THR	3.6
2	B	88	SER	3.6
2	B	43	GLY	3.6
2	B	95	TRP	3.6
1	A	58	GLU	3.5
1	A	100	GLY	3.5
1	A	222	GLU	3.5
2	B	14	PRO	3.5
1	A	251	SER	3.5
1	A	261	VAL	3.5
2	B	42	ASN	3.5

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Mol	Chain	Res	Type	RSRZ
2	B	18	GLY	3.4
1	A	270	LEU	3.4
1	A	195	SER	3.4
1	A	156	LEU	3.4
1	A	56	GLY	3.4
1	A	92	SER	3.4
2	B	60	TRP	3.4
3	C	9	PHE	3.3
2	B	89	GLN	3.3
2	B	63	TYR	3.3
1	A	12	MET	3.3
1	A	147	TRP	3.2
1	A	227	ASP	3.2
3	C	4	GLY	3.2
2	B	99	MET	3.2
1	A	90	ALA	3.2
2	B	17	ASN	3.2
1	A	265	GLY	3.2
1	A	65	GLN	3.2
1	A	199	ALA	3.2
1	A	187	THR	3.1
1	A	28	VAL	3.1
1	A	145	ARG	3.1
1	A	150	ALA	3.1
1	A	103	LEU	3.0
1	A	27	TYR	3.0
1	A	269	PRO	3.0
1	A	34	VAL	3.0
2	B	49	VAL	3.0
1	A	192	HIS	2.9
2	B	58	LYS	2.9
2	B	82	VAL	2.9
1	A	221	GLY	2.9
2	B	56	PHE	2.9
1	A	217	TRP	2.9
1	A	215	LEU	2.9
2	B	44	GLU	2.8
1	A	42	SER	2.8
1	A	157	ARG	2.8
1	A	268	LYS	2.8
1	A	142	ILE	2.8
1	A	91	GLY	2.8

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Mol	Chain	Res	Type	RSRZ
1	A	152	VAL	2.8
2	B	79	ALA	2.8
1	A	4	SER	2.8
2	B	70	PHE	2.8
2	B	54	LEU	2.8
1	A	260	HIS	2.8
2	B	48	LYS	2.8
2	B	90	PRO	2.8
1	A	11	ALA	2.7
1	A	49	ALA	2.7
1	A	10	THR	2.7
2	B	22	PHE	2.7
1	A	60	TRP	2.7
2	B	64	LEU	2.7
1	A	79	ARG	2.7
1	A	223	ASP	2.7
2	B	2	GLN	2.7
1	A	66	ILE	2.7
1	A	259	CYS	2.6
1	A	8	PHE	2.6
1	A	33	PHE	2.6
1	A	94	ILE	2.6
1	A	2	SER	2.6
1	A	97	ARG	2.6
1	A	88	SER	2.6
1	A	117	ALA	2.5
1	A	214	THR	2.5
1	A	169	ARG	2.5
2	B	81	ARG	2.5
1	A	64	THR	2.5
1	A	209	TYR	2.5
2	B	26	TYR	2.5
1	A	185	PRO	2.5
2	B	4	THR	2.5
2	B	97	ARG	2.5
1	A	95	ILE	2.5
2	B	46	ILE	2.5
1	A	26	GLY	2.5
1	A	264	GLU	2.5
1	A	204	TRP	2.5
2	B	39	LEU	2.5
2	B	40	LEU	2.5

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Mol	Chain	Res	Type	RSRZ
1	A	71	THR	2.4
1	A	228	THR	2.4
1	A	52	ILE	2.4
1	A	163	LEU	2.4
1	A	99	TYR	2.4
2	B	37	VAL	2.4
1	A	89	GLU	2.4
1	A	144	GLN	2.4
1	A	126	LEU	2.4
2	B	65	LEU	2.4
1	A	9	TYR	2.4
2	B	62	PHE	2.4
1	A	41	ALA	2.3
1	A	220	ASP	2.3
2	B	98	ASP	2.3
1	A	273	ARG	2.3
1	A	134	THR	2.3
1	A	253	GLU	2.3
1	A	61	ASP	2.3
1	A	101	CYS	2.3
1	A	51	TRP	2.3
2	B	96	ASP	2.3
2	B	94	LYS	2.3
2	B	86	THR	2.3
1	A	81	LEU	2.3
1	A	160	LEU	2.3
2	B	87	LEU	2.3
1	A	74	TYR	2.3
2	B	25	CYS	2.2
1	A	115	GLN	2.2
2	B	9	VAL	2.2
1	A	254	GLU	2.2
2	B	6	LYS	2.2
1	A	44	ARG	2.2
1	A	262	GLN	2.2
1	A	68	LYS	2.2
1	A	138	THR	2.2
1	A	143	THR	2.2
2	B	68	THR	2.2
1	A	208	PHE	2.2
2	B	55	SER	2.2
1	A	40	ALA	2.2

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Mol	Chain	Res	Type	RSRZ
1	A	153	ALA	2.2
1	A	154	GLU	2.2
1	A	23	ILE	2.1
1	A	162	GLY	2.1
1	A	31	THR	2.1
1	A	59	TYR	2.1
2	B	21	ASN	2.1
1	A	188	HIS	2.1
1	A	165	VAL	2.1
2	B	27	VAL	2.1
1	A	201	LEU	2.1
1	A	233	THR	2.1
1	A	62	ARG	2.1
1	A	67	PHE	2.1
1	A	189	VAL	2.1
1	A	43	PRO	2.1
1	A	246	ALA	2.1
2	B	15	ALA	2.1
1	A	159	TYR	2.1
2	B	7	ILE	2.1
1	A	263	HIS	2.1
1	A	218	GLN	2.1
1	A	224	GLN	2.1
1	A	133	TRP	2.1
1	A	184	PRO	2.1
1	A	22	PHE	2.0
2	B	85	VAL	2.0
1	A	164	CYS	2.0
1	A	7	TYR	2.0
2	B	66	TYR	2.0
1	A	83	GLY	2.0
1	A	45	THR	2.0
1	A	229	GLU	2.0
1	A	172	LEU	2.0

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

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](#)

There are no ligands in this entry.

6.5 Other polymers [i](#)

There are no such residues in this entry.