



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 10, 2026 – 12:01 AM UTC

PDB ID : 2JFU / pdb_00002jfu
Title : Crystal structure of Enterococcus faecium glutamate racemase in complex with phosphate
Authors : Lundqvist, T.
Deposited on : 2007-02-04
Resolution : 1.80 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

<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

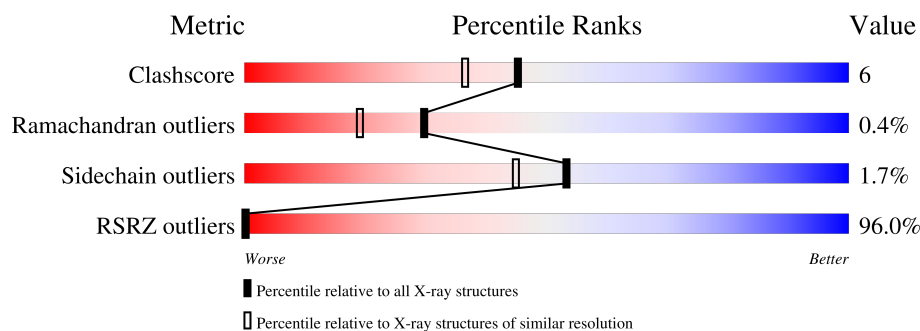
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.80 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))
Clashscore	190562	8479 (1.80-1.80)
Ramachandran outliers	187476	8391 (1.80-1.80)
Sidechain outliers	187428	8390 (1.80-1.80)
RSRZ outliers	180081	7663 (1.80-1.80)

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 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	291	90% 78% 15% 7%

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
2	PO4	A	1274	-	-	-	X

2 Entry composition [i](#)

There are 3 unique types of molecules in this entry. The entry contains 2328 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 GLUTAMATE RACEMASE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	272	Total	C	N	O	S	0	0	1
			2069	1321	343	395	10			

- Molecule 2 is PHOSPHATE ION (CCD ID: PO4) (formula: O₄P).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	A	1	Total	O	P	0	0
			5	4	1		
2	A	1	Total	O	P	0	0
			5	4	1		

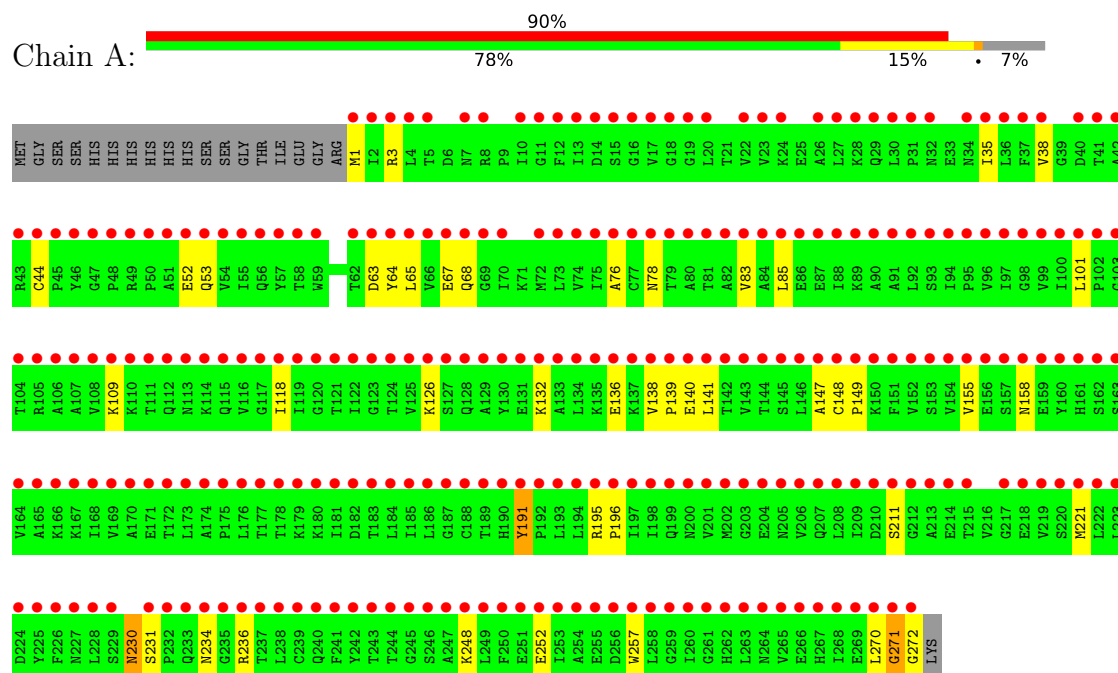
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	249	Total	O	0	0
			249	249		

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: GLUTAMATE RACEMASE



4 Data and refinement statistics

Property	Value	Source
Space group	P 31 2 1	Depositor
Cell constants a, b, c, α , β , γ	85.96Å 85.96Å 92.30Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	34.00 – 1.80 34.00 – 1.80	Depositor EDS
% Data completeness (in resolution range)	(Not available) (34.00-1.80) 99.4 (34.00-1.80)	Depositor EDS
R_{merge}	0.08	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	5.11 (at 1.80Å)	Xtriage
Refinement program	CNX 2000.2	Depositor
R, R_{free}	0.193 , 0.209 0.544 , (Not available)	Depositor DCC
R_{free} test set	No test flags present.	wwPDB-VP
Wilson B-factor (Å ²)	19.1	Xtriage
Anisotropy	0.313	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.39 , 140.1	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	0.028 for -h,-k,l	Xtriage
F_o, F_c correlation	0.50	EDS
Total number of atoms	2328	wwPDB-VP
Average B, all atoms (Å ²)	22.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.68% 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

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: PO4

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	0.36	1/2103 (0.0%)	0.90	8/2860 (0.3%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	271	GLY	C-N	-5.54	1.25	1.33

All (8) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	83	VAL	N-CA-C	8.42	119.05	111.81
1	A	148	CYS	CA-C-N	6.46	127.92	119.84
1	A	148	CYS	C-N-CA	6.46	127.92	119.84
1	A	230	ASN	N-CA-C	-6.37	101.35	110.59
1	A	76	ALA	N-CA-C	6.29	120.80	113.18
1	A	78	ASN	N-CA-C	6.03	117.53	111.07
1	A	191	TYR	N-CA-C	5.57	121.25	113.57
1	A	35	ILE	N-CA-C	5.25	116.29	108.46

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts

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	2069	0	2135	25	1
2	A	10	0	0	0	0
3	A	249	0	0	4	1
All	All	2328	0	2135	25	2

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 6.

All (25) 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:126:LYS:HA	1:A:126:LYS:HE2	1.65	0.79
1:A:132:LYS:O	1:A:136:GLU:HG3	1.96	0.66
1:A:158:ASN:HB3	3:A:2152:HOH:O	1.97	0.64
1:A:52:GLU:H	1:A:52:GLU:CD	2.15	0.54
1:A:230:ASN:HD21	1:A:234:ASN:HD22	1.53	0.54
1:A:139:PRO:HG2	1:A:140:GLU:OE2	2.10	0.52
1:A:44:CYS:HB3	3:A:2049:HOH:O	2.09	0.51
1:A:85:LEU:C	1:A:85:LEU:HD23	2.36	0.50
1:A:236:ARG:HD3	3:A:2208:HOH:O	2.11	0.49
1:A:248:LYS:HE2	1:A:252:GLU:OE2	2.13	0.48
1:A:63:ASP:O	1:A:67:GLU:HG3	2.14	0.47
1:A:155:VAL:HG12	1:A:257:TRP:CZ2	2.50	0.47
1:A:270:LEU:O	1:A:272:GLY:N	2.48	0.46
1:A:64:TYR:O	1:A:68:GLN:HG2	2.15	0.46
1:A:221:MET:C	1:A:221:MET:SD	2.98	0.46
1:A:191:TYR:CD1	1:A:191:TYR:N	2.84	0.43
1:A:1:MET:HE3	1:A:1:MET:HA	2.00	0.43
1:A:138:VAL:HB	1:A:141:LEU:HG	1.99	0.43
1:A:140:GLU:H	1:A:140:GLU:CD	2.27	0.43
1:A:147:ALA:C	1:A:149:PRO:HD3	2.43	0.42
1:A:109:LYS:HG3	3:A:2099:HOH:O	2.19	0.42
1:A:230:ASN:ND2	1:A:231:SER:H	2.18	0.42
1:A:101:LEU:HD23	1:A:101:LEU:HA	1.89	0.41
1:A:38:VAL:HG23	1:A:65:LEU:HD21	2.01	0.41
1:A:195:ARG:HB3	1:A:196:PRO:HD3	2.02	0.41

All (2) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:A:2100:HOH:O	3:A:2100:HOH:O[4_555]	1.60	0.60
1:A:221:MET:CE	1:A:221:MET:CE[4_555]	1.78	0.42

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	270/291 (93%)	266 (98%)	3 (1%)	1 (0%)	30 19

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	271	GLY

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	230/246 (94%)	226 (98%)	4 (2%)	53 45

All (4) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	3	ARG
1	A	53	GLN
1	A	118	ILE
1	A	211	SER

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (5) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	53	GLN
1	A	78	ASN
1	A	128	GLN
1	A	230	ASN
1	A	264	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 [i](#)

2 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	$\# Z > 2$
2	PO4	A	1273	-	4,4,4	1.54	1 (25%)	6,6,6	0.85	0
2	PO4	A	1274	-	4,4,4	1.48	1 (25%)	6,6,6	0.92	0

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	1273	PO4	P-O1	2.65	1.56	1.50
2	A	1274	PO4	P-O1	2.61	1.56	1.50

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	272/291 (93%)	4.38	261 (95%) 0 0	12, 19, 34, 50	0

All (261) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	260	ILE	12.6
1	A	1	MET	11.4
1	A	174	ALA	9.6
1	A	178	THR	8.6
1	A	112	GLN	8.6
1	A	206	VAL	8.3
1	A	175	PRO	8.3
1	A	109	LYS	8.1
1	A	2	ILE	8.0
1	A	100	ILE	7.9
1	A	181	ILE	7.4
1	A	127	SER	7.3
1	A	17	VAL	7.3
1	A	162	SER	7.3
1	A	205	ASN	7.3
1	A	253	ILE	7.1
1	A	163	SER	7.1
1	A	164	VAL	7.1
1	A	108	VAL	6.9
1	A	169	VAL	6.9
1	A	129	ALA	6.9
1	A	92	LEU	6.9
1	A	204	GLU	6.8
1	A	149	PRO	6.7
1	A	256	ASP	6.7
1	A	51	ALA	6.7
1	A	74	VAL	6.6

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Mol	Chain	Res	Type	RSRZ
1	A	222	LEU	6.6
1	A	161	HIS	6.5
1	A	249	LEU	6.5
1	A	170	ALA	6.5
1	A	200	ASN	6.4
1	A	238	LEU	6.4
1	A	99	VAL	6.3
1	A	203	GLY	6.3
1	A	194	LEU	6.3
1	A	93	SER	6.2
1	A	177	THR	6.2
1	A	66	VAL	6.2
1	A	180	LYS	6.2
1	A	201	VAL	6.1
1	A	259	GLY	6.1
1	A	150	LYS	6.0
1	A	198	ILE	6.0
1	A	176	LEU	6.0
1	A	116	VAL	5.9
1	A	179	LYS	5.9
1	A	124	THR	5.8
1	A	5	THR	5.8
1	A	35	ILE	5.7
1	A	44	CYS	5.7
1	A	262	HIS	5.6
1	A	231	SER	5.6
1	A	193	LEU	5.6
1	A	3	ARG	5.6
1	A	261	GLY	5.6
1	A	219	VAL	5.5
1	A	166	LYS	5.5
1	A	168	ILE	5.5
1	A	23	VAL	5.4
1	A	138	VAL	5.4
1	A	188	CYS	5.4
1	A	103	GLY	5.4
1	A	4	LEU	5.4
1	A	155	VAL	5.3
1	A	160	TYR	5.3
1	A	167	LYS	5.3
1	A	172	THR	5.3
1	A	83	VAL	5.3

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Mol	Chain	Res	Type	RSRZ
1	A	239	CYS	5.3
1	A	258	LEU	5.2
1	A	94	ILE	5.2
1	A	197	ILE	5.2
1	A	232	PRO	5.2
1	A	125	VAL	5.1
1	A	20	LEU	5.1
1	A	242	TYR	5.1
1	A	50	PRO	5.0
1	A	202	MET	5.0
1	A	207	GLN	5.0
1	A	184	LEU	5.0
1	A	208	LEU	4.9
1	A	264	ASN	4.9
1	A	47	GLY	4.9
1	A	130	TYR	4.9
1	A	136	GLU	4.8
1	A	132	LYS	4.8
1	A	171	GLU	4.8
1	A	247	ALA	4.8
1	A	7	ASN	4.8
1	A	173	LEU	4.8
1	A	271	GLY	4.8
1	A	82	ALA	4.8
1	A	251	GLU	4.7
1	A	209	ILE	4.7
1	A	151	PHE	4.6
1	A	85	LEU	4.6
1	A	59	TRP	4.6
1	A	128	GLN	4.6
1	A	27	LEU	4.5
1	A	265	VAL	4.5
1	A	122	ILE	4.5
1	A	158	ASN	4.5
1	A	165	ALA	4.5
1	A	156	GLU	4.4
1	A	269	GLU	4.4
1	A	89	LYS	4.4
1	A	114	LYS	4.4
1	A	19	GLY	4.4
1	A	157	SER	4.4
1	A	223	LEU	4.4

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Mol	Chain	Res	Type	RSRZ
1	A	110	LYS	4.3
1	A	154	VAL	4.3
1	A	268	ILE	4.3
1	A	76	ALA	4.3
1	A	95	PRO	4.3
1	A	143	VAL	4.3
1	A	18	GLY	4.3
1	A	88	ILE	4.3
1	A	140	GLU	4.3
1	A	141	LEU	4.2
1	A	270	LEU	4.2
1	A	272	GLY	4.2
1	A	257	TRP	4.2
1	A	48	PRO	4.2
1	A	54	VAL	4.2
1	A	113	ASN	4.2
1	A	69	GLY	4.2
1	A	245	GLY	4.2
1	A	213	ALA	4.2
1	A	142	THR	4.2
1	A	120	GLY	4.1
1	A	68	GLN	4.1
1	A	131	GLU	4.1
1	A	146	LEU	4.1
1	A	233	GLN	4.1
1	A	254	ALA	4.1
1	A	56	GLN	4.1
1	A	267	HIS	4.1
1	A	101	LEU	4.1
1	A	111	THR	4.1
1	A	139	PRO	4.0
1	A	87	GLU	4.0
1	A	84	ALA	4.0
1	A	144	THR	4.0
1	A	75	ILE	4.0
1	A	226	PHE	4.0
1	A	41	THR	4.0
1	A	121	THR	4.0
1	A	45	PRO	4.0
1	A	96	VAL	4.0
1	A	241	PHE	4.0
1	A	220	SER	3.9

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Mol	Chain	Res	Type	RSRZ
1	A	46	TYR	3.9
1	A	38	VAL	3.9
1	A	218	GLU	3.9
1	A	148	CYS	3.9
1	A	70	ILE	3.8
1	A	211	SER	3.8
1	A	229	SER	3.8
1	A	79	THR	3.8
1	A	52	GLU	3.8
1	A	86	GLU	3.8
1	A	118	ILE	3.8
1	A	22	VAL	3.8
1	A	115	GLN	3.7
1	A	250	PHE	3.7
1	A	49	ARG	3.7
1	A	13	ILE	3.7
1	A	55	ILE	3.7
1	A	107	ALA	3.7
1	A	147	ALA	3.7
1	A	63	ASP	3.7
1	A	77	CYS	3.7
1	A	119	ILE	3.7
1	A	235	GLY	3.7
1	A	137	LYS	3.7
1	A	53	GLN	3.6
1	A	199	GLN	3.6
1	A	106	ALA	3.6
1	A	57	TYR	3.6
1	A	228	LEU	3.6
1	A	90	ALA	3.5
1	A	134	LEU	3.6
1	A	234	ASN	3.5
1	A	187	GLY	3.5
1	A	81	THR	3.5
1	A	104	THR	3.5
1	A	43	ARG	3.5
1	A	105	ARG	3.5
1	A	266	GLU	3.5
1	A	186	LEU	3.5
1	A	248	LYS	3.5
1	A	97	ILE	3.5
1	A	36	LEU	3.5

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Mol	Chain	Res	Type	RSRZ
1	A	80	ALA	3.5
1	A	133	ALA	3.5
1	A	98	GLY	3.5
1	A	263	LEU	3.5
1	A	195	ARG	3.4
1	A	15	SER	3.4
1	A	182	ASP	3.4
1	A	252	GLU	3.4
1	A	135	LYS	3.3
1	A	217	GLY	3.3
1	A	32	ASN	3.3
1	A	42	ALA	3.3
1	A	65	LEU	3.3
1	A	243	THR	3.3
1	A	28	LYS	3.3
1	A	12	PHE	3.3
1	A	126	LYS	3.3
1	A	185	ILE	3.2
1	A	225	TYR	3.2
1	A	31	PRO	3.2
1	A	37	PHE	3.2
1	A	227	ASN	3.2
1	A	14	ASP	3.2
1	A	221	MET	3.2
1	A	10	ILE	3.2
1	A	246	SER	3.2
1	A	191	TYR	3.1
1	A	224	ASP	3.1
1	A	78	ASN	3.1
1	A	183	THR	3.1
1	A	30	LEU	3.1
1	A	255	GLU	3.0
1	A	8	ARG	3.0
1	A	145	SER	3.0
1	A	40	ASP	3.0
1	A	210	ASP	3.0
1	A	215	THR	3.0
1	A	196	PRO	3.0
1	A	91	ALA	3.0
1	A	152	VAL	2.9
1	A	123	GLY	2.9
1	A	236	ARG	2.9

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Mol	Chain	Res	Type	RSRZ
1	A	16	GLY	2.9
1	A	117	GLY	2.9
1	A	159	GLU	2.8
1	A	73	LEU	2.7
1	A	244	THR	2.7
1	A	64	TYR	2.6
1	A	58	THR	2.6
1	A	153	SER	2.6
1	A	67	GLU	2.6
1	A	212	GLY	2.5
1	A	192	PRO	2.5
1	A	240	GLN	2.5
1	A	26	ALA	2.4
1	A	102	PRO	2.4
1	A	190	HIS	2.2
1	A	214	GLU	2.2
1	A	237	THR	2.2
1	A	11	GLY	2.2
1	A	24	LYS	2.2
1	A	62	THR	2.1
1	A	29	GLN	2.1
1	A	189	THR	2.1
1	A	72	MET	2.1
1	A	34	ASN	2.1

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
2	PO4	A	1274	5/5	0.54	0.52	39,40,40,40	0
2	PO4	A	1273	5/5	0.58	0.31	41,41,41,41	0

6.5 Other polymers [i](#)

There are no such residues in this entry.