



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 20, 2026 – 01:13 PM UTC

PDB ID : 4N43 / pdb_00004n43
Title : Human enterovirus 71 uncoating intermediate captured at atomic resolution
Authors : Chen, R.; Lyu, K.
Deposited on : 2013-10-08
Resolution : 3.80 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
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

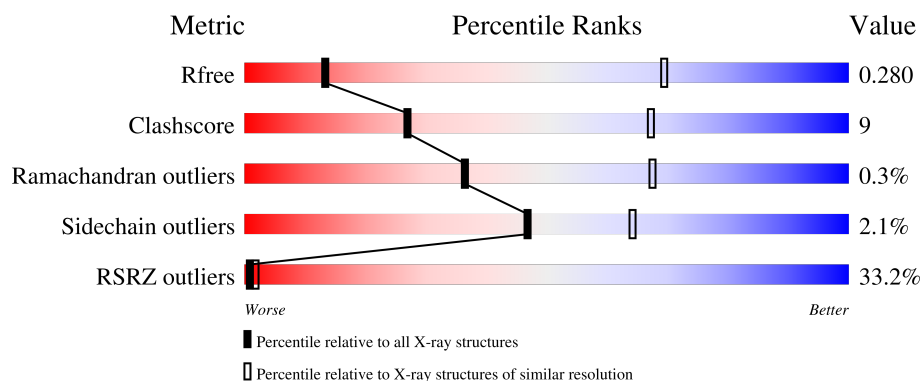
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.80 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}	180053	1065 (3.96-3.64)
Clashscore	190562	1012 (3.94-3.66)
Ramachandran outliers	187476	1048 (3.96-3.64)
Sidechain outliers	187428	1043 (3.96-3.64)
RSRZ outliers	180081	1064 (3.96-3.64)

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	297	24% 61% 14% • 24%
2	B	254	35% 74% 16% 10%
3	C	242	27% 64% 25% • 8%

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 5259 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 Capsid protein VP1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	225	Total	C	N	O	S	0	0	0
			1780	1139	300	330	11			

- Molecule 2 is a protein called Capsid protein VP2.

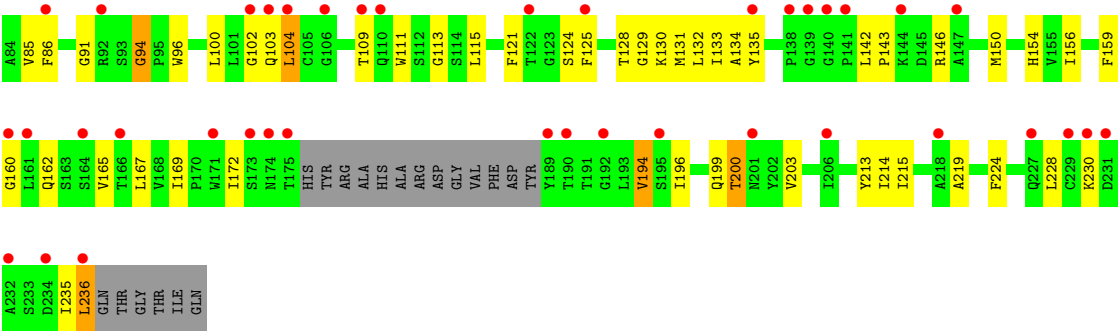
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	229	Total	C	N	O	S	0	0	0
			1777	1143	292	334	8			

- Molecule 3 is a protein called Capsid protein VP3.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	C	223	Total	C	N	O	S	0	0	0
			1702	1097	278	316	11			

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
C	227	GLN	LYS	conflict	UNP Q9WPJ0



4 Data and refinement statistics

Property	Value	Source
Space group	P 4 ₂ 3 2	Depositor
Cell constants a, b, c, α , β , γ	352.42 Å 352.42 Å 352.42 Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	49.84 – 3.80 49.84 – 3.80	Depositor EDS
% Data completeness (in resolution range)	68.0 (49.84-3.80) 59.4 (49.84-3.80)	Depositor EDS
R_{merge}	0.38	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.68 (at 3.77 Å)	Xtriage
Refinement program	PHENIX	Depositor
R, R_{free}	0.245 , 0.274 0.278 , 0.280	Depositor DCC
R_{free} test set	2000 reflections (3.99%)	wwPDB-VP
Wilson B-factor (Å ²)	53.3	Xtriage
Anisotropy	0.000	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.29 , 0.0	EDS
L-test for twinning ²	$\langle L \rangle = 0.46$, $\langle L^2 \rangle = 0.28$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.21	EDS
Total number of atoms	5259	wwPDB-VP
Average B, all atoms (Å ²)	47.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.01% 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

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	0.27	0/1835	0.74	0/2501
2	B	0.27	0/1830	0.76	0/2509
3	C	0.29	0/1748	0.80	3/2393 (0.1%)
All	All	0.28	0/5413	0.77	3/7403 (0.0%)

There are no bond length outliers.

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	C	160	GLY	N-CA-C	-6.77	106.26	114.66
3	C	94	GLY	CA-C-N	5.87	125.56	119.05
3	C	94	GLY	C-N-CA	5.87	125.56	119.05

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	1780	0	1724	33	0
2	B	1777	0	1712	39	0
3	C	1702	0	1692	43	0
All	All	5259	0	5128	96	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 9.

All (96) 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:149:GLN:HG2	1:A:247:LEU:HD11	1.64	0.79
1:A:271:TYR:H	3:C:235:ILE:HG12	1.49	0.78
2:B:151:THR:HG22	2:B:152:GLN:HG3	1.74	0.70
2:B:122:LEU:HB2	2:B:183:ILE:HB	1.74	0.68
2:B:186:ARG:NH1	3:C:124:SER:O	2.27	0.67
1:A:268:ASN:HB2	2:B:171:PRO:HD3	1.79	0.65
2:B:134:THR:HG23	2:B:146:PRO:HG3	1.78	0.64
3:C:85:VAL:HB	3:C:194:VAL:HG13	1.80	0.64
3:C:59:PRO:HD2	3:C:68:ARG:HD3	1.80	0.63
3:C:142:LEU:HD12	3:C:143:PRO:HD2	1.81	0.62
1:A:262:ILE:HG21	2:B:128:PRO:HG2	1.83	0.61
3:C:146:ARG:NH1	3:C:199:GLN:OE1	2.34	0.61
1:A:181:VAL:HG11	1:A:188:ALA:HB2	1.83	0.61
3:C:115:LEU:HB2	3:C:169:ILE:HD11	1.83	0.60
2:B:85:VAL:HG23	2:B:86:LEU:HG	1.85	0.59
1:A:113:ILE:HG23	1:A:253:MET:HE1	1.83	0.59
2:B:80:TRP:HB3	2:B:85:VAL:HG11	1.85	0.59
1:A:265:PRO:HB3	2:B:174:GLN:HB2	1.85	0.59
2:B:177:VAL:HG11	3:C:100:LEU:HD22	1.85	0.58
2:B:71:TRP:HD1	2:B:232:ILE:HB	1.68	0.58
1:A:287:THR:HG21	3:C:94:GLY:H	1.68	0.58
1:A:291:ARG:HH11	1:A:291:ARG:H	1.51	0.58
2:B:23:ILE:HG21	2:B:237:THR:HG21	1.87	0.57
2:B:71:TRP:NE1	2:B:222:LEU:HB2	2.20	0.56
1:A:155:PHE:HB3	1:A:177:PRO:HG2	1.87	0.56
2:B:87:THR:O	2:B:97:GLN:NE2	2.36	0.56
1:A:127:THR:HG22	1:A:264:ARG:HE	1.70	0.56
2:B:186:ARG:NH2	3:C:159:PHE:O	2.39	0.56
1:A:93:ILE:HD11	1:A:109:TRP:HB2	1.88	0.56
1:A:278:ASN:OD1	2:B:134:THR:N	2.38	0.55
2:B:71:TRP:CD1	2:B:232:ILE:HB	2.41	0.54
1:A:210:THR:O	2:B:208:ASN:ND2	2.40	0.54
2:B:184:ASN:O	2:B:188:ASN:N	2.41	0.54
3:C:57:ASN:HA	3:C:68:ARG:HD2	1.89	0.53
2:B:71:TRP:CZ3	2:B:218:PRO:HB3	2.43	0.53
3:C:59:PRO:HG2	3:C:67:GLU:HB2	1.92	0.52
1:A:276:ASN:OD1	1:A:278:ASN:ND2	2.43	0.51
1:A:106:TYR:OH	1:A:164:ASP:O	2.23	0.51
2:B:174:GLN:HE22	3:C:103:GLN:HG3	1.74	0.51
1:A:128:TYR:HB2	1:A:261:TRP:HB2	1.93	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:156:VAL:HB	1:A:232:THR:HG23	1.94	0.50
2:B:97:GLN:HA	2:B:207:LEU:HD11	1.92	0.50
3:C:130:LYS:HB2	3:C:200:THR:HB	1.93	0.50
1:A:131:PHE:HB3	1:A:258:VAL:HG12	1.94	0.49
3:C:121:PHE:HA	3:C:214:ILE:HG22	1.95	0.49
2:B:32:ILE:HD11	2:B:193:ILE:HG12	1.95	0.49
3:C:109:THR:OG1	3:C:228:LEU:HB3	2.13	0.48
1:A:116:TYR:HD2	1:A:119:MET:HB2	1.79	0.48
2:B:177:VAL:HG12	3:C:49:VAL:HG21	1.96	0.48
2:B:186:ARG:HG3	3:C:125:PHE:HA	1.96	0.48
1:A:166:ARG:NH2	1:A:237:THR:O	2.46	0.48
3:C:135:TYR:HB2	3:C:167:LEU:HD21	1.95	0.48
1:A:192:VAL:HG22	3:C:24:ILE:HG21	1.96	0.47
3:C:72:PRO:HB3	3:C:213:TYR:CE1	2.49	0.47
3:C:235:ILE:HA	3:C:236:LEU:HA	1.55	0.47
2:B:126:VAL:HG13	2:B:212:PHE:CD1	2.50	0.46
2:B:97:GLN:HG2	2:B:207:LEU:HD21	1.99	0.45
1:A:126:PHE:CG	1:A:260:ALA:HB1	2.52	0.45
1:A:164:ASP:OD1	1:A:164:ASP:N	2.47	0.45
1:A:284:ILE:HG22	1:A:285:LYS:H	1.81	0.45
1:A:113:ILE:HG13	1:A:230:MET:HE1	1.98	0.44
1:A:191:SER:OG	3:C:21:SER:OG	2.35	0.44
3:C:46:LEU:O	3:C:49:VAL:HG22	2.17	0.44
2:B:71:TRP:CH2	2:B:218:PRO:HB3	2.53	0.44
3:C:78:GLY:O	3:C:79:LYS:HG2	2.18	0.44
3:C:82:LEU:HD22	3:C:131:MET:HE2	1.99	0.44
3:C:150:MET:HE3	3:C:150:MET:HB3	1.94	0.44
1:A:211:PHE:HA	2:B:208:ASN:ND2	2.33	0.44
2:B:136:ALA:HB2	2:B:143:ASP:HB3	1.98	0.44
2:B:122:LEU:HD22	2:B:216:VAL:HG12	2.00	0.43
2:B:186:ARG:HE	3:C:162:GLN:HG3	1.82	0.43
3:C:91:GLY:HA3	3:C:111:TRP:CH2	2.53	0.43
1:A:261:TRP:HA	3:C:39:GLU:HA	2.00	0.43
2:B:89:THR:HG21	2:B:155:ALA:HB2	2.00	0.43
2:B:95:ASN:O	2:B:99:HIS:ND1	2.41	0.43
3:C:115:LEU:HG	3:C:172:ILE:HD13	1.99	0.43
1:A:268:ASN:HB2	2:B:171:PRO:CD	2.48	0.43
3:C:96:TRP:O	3:C:102:GLY:HA3	2.19	0.43
2:B:71:TRP:HB3	2:B:232:ILE:O	2.19	0.42
3:C:134:ALA:HA	3:C:154:HIS:HA	2.01	0.42
3:C:109:THR:HG22	3:C:230:LYS:HE3	2.00	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:29:HIS:HA	3:C:30:PRO:HD2	1.93	0.42
1:A:282:ASN:O	1:A:282:ASN:ND2	2.52	0.42
3:C:128:THR:OG1	3:C:129:GLY:N	2.53	0.42
1:A:196:SER:HB2	1:A:201:TYR:CE1	2.55	0.42
3:C:132:LEU:HB2	3:C:199:GLN:HB2	2.02	0.41
3:C:133:ILE:HG12	3:C:196:ILE:HG23	2.02	0.41
2:B:81:LYS:HE2	2:B:130:TYR:HB3	2.01	0.41
2:B:249:ARG:H	2:B:249:ARG:HD2	1.84	0.41
3:C:113:GLY:HA3	3:C:224:PHE:HA	2.02	0.41
3:C:104:LEU:HD13	3:C:104:LEU:HA	1.92	0.41
3:C:132:LEU:HD23	3:C:156:ILE:HD13	2.02	0.41
3:C:50:GLU:HA	3:C:219:ALA:HB2	2.03	0.41
1:A:291:ARG:H	1:A:291:ARG:HD2	1.86	0.40
2:B:81:LYS:O	2:B:85:VAL:HG13	2.20	0.40
3:C:58:VAL:HB	3:C:59:PRO:HD3	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	223/297 (75%)	202 (91%)	21 (9%)	0	100	100
2	B	225/254 (89%)	209 (93%)	16 (7%)	0	100	100
3	C	219/242 (90%)	201 (92%)	16 (7%)	2 (1%)	14	45
All	All	667/793 (84%)	612 (92%)	53 (8%)	2 (0%)	36	67

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
3	C	82	LEU
3	C	58	VAL

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	193/251 (77%)	190 (98%)	3 (2%)	55	68
2	B	195/214 (91%)	194 (100%)	1 (0%)	81	81
3	C	187/202 (93%)	179 (96%)	8 (4%)	26	50
All	All	575/667 (86%)	563 (98%)	12 (2%)	47	64

All (12) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	284	ILE
1	A	285	LYS
1	A	291	ARG
2	B	60	VAL
3	C	86	PHE
3	C	104	LEU
3	C	165	VAL
3	C	194	VAL
3	C	200	THR
3	C	203	VAL
3	C	215	ILE
3	C	236	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (4) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	73	HIS
1	A	282	ASN
2	B	211	ASN
3	C	97	GLN

5.3.3 RNA ⓘ

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](#)

There are no ligands in this entry.

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	225/297 (75%)	1.73	70 (31%)  	20, 38, 96, 127	0
2	B	229/254 (90%)	2.07	89 (38%)  	20, 47, 117, 173	0
3	C	223/242 (92%)	1.57	66 (29%)  	21, 37, 64, 105	0
All	All	677/793 (85%)	1.79	225 (33%)  	20, 39, 102, 173	0

All (225) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	B	47	ALA	8.8
1	A	213	GLU	8.2
2	B	139	THR	8.0
2	B	16	LEU	7.8
3	C	175	THR	7.4
1	A	212	GLY	7.3
1	A	209	PRO	6.9
1	A	214	HIS	6.7
2	B	137	GLY	6.6
1	A	217	GLU	6.2
2	B	46	ASP	6.2
1	A	216	GLN	6.1
2	B	142	GLU	6.1
2	B	144	SER	5.8
2	B	58	VAL	5.7
3	C	141	PRO	5.7
3	C	171	TRP	5.6
1	A	104	ASN	5.4
3	C	140	GLY	5.4
2	B	141	THR	5.3
2	B	43	SER	5.2
2	B	45	SER	5.2
3	C	1	GLY	5.2

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Mol	Chain	Res	Type	RSRZ
1	A	219	ASP	5.1
3	C	173	SER	5.0
2	B	30	ASN	5.0
1	A	73	HIS	4.9
1	A	76	ALA	4.9
1	A	215	LYS	4.8
2	B	89	THR	4.7
2	B	152	GLN	4.7
2	B	44	ASP	4.7
1	A	218	LYS	4.6
1	A	210	THR	4.6
2	B	149	LYS	4.6
3	C	19	GLY	4.5
3	C	29	HIS	4.5
1	A	221	GLU	4.5
1	A	220	LEU	4.4
2	B	88	GLU	4.4
2	B	59	SER	4.4
2	B	91	VAL	4.3
1	A	98	GLU	4.3
2	B	21	SER	4.3
2	B	180	HIS	4.3
1	A	289	ALA	4.2
2	B	244	GLU	4.2
2	B	250	GLN	4.2
3	C	3	PRO	4.1
2	B	143	ASP	4.1
2	B	94	GLN	4.0
2	B	246	ALA	4.0
1	A	99	GLY	4.0
2	B	40	SER	4.0
2	B	136	ALA	3.9
2	B	90	GLY	3.9
2	B	17	THR	3.9
1	A	293	ALA	3.9
2	B	189	ASN	3.9
1	A	223	GLY	3.8
1	A	239	GLY	3.8
2	B	242	CYS	3.8
1	A	72	SER	3.8
2	B	138	GLY	3.8
3	C	27	ASN	3.8

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Mol	Chain	Res	Type	RSRZ
2	B	19	GLY	3.8
2	B	134	THR	3.7
3	C	76	GLN	3.7
2	B	145	HIS	3.7
1	A	162	LYS	3.7
2	B	151	THR	3.7
2	B	61	ASN	3.7
2	B	173	SER	3.6
3	C	164	SER	3.6
3	C	234	ASP	3.6
1	A	100	THR	3.6
3	C	60	THR	3.6
1	A	240	THR	3.6
2	B	97	GLN	3.5
1	A	78	THR	3.5
1	A	225	CYS	3.5
2	B	42	CYS	3.5
1	A	224	ALA	3.5
1	A	77	GLU	3.4
2	B	27	GLU	3.4
2	B	60	VAL	3.4
3	C	92	ARG	3.4
3	C	236	LEU	3.4
1	A	296	THR	3.3
2	B	140	GLY	3.3
3	C	122	THR	3.3
2	B	153	PRO	3.3
3	C	195	SER	3.3
1	A	208	TYR	3.3
1	A	211	PHE	3.2
2	B	245	PHE	3.2
2	B	41	TYR	3.2
2	B	18	ILE	3.2
3	C	189	TYR	3.2
1	A	242	LYS	3.2
2	B	26	GLN	3.2
2	B	249	ARG	3.2
2	B	210	CYS	3.1
2	B	31	ILE	3.1
3	C	83	CYS	3.1
2	B	148	TYR	3.1
2	B	208	ASN	3.1

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Mol	Chain	Res	Type	RSRZ
3	C	11	ASN	3.0
1	A	198	ALA	3.0
3	C	33	CYS	3.0
2	B	57	ASP	3.0
3	C	26	PRO	3.0
2	B	28	ALA	3.0
1	A	238	VAL	2.9
2	B	147	PRO	2.9
2	B	161	GLN	2.9
3	C	106	GLY	2.9
2	B	54	THR	2.9
2	B	29	ALA	2.9
1	A	262	ILE	2.9
1	A	222	TYR	2.9
3	C	138	PRO	2.9
2	B	184	ASN	2.9
2	B	67	ASP	2.8
3	C	161	LEU	2.8
1	A	74	SER	2.8
3	C	64	SER	2.8
2	B	96	ALA	2.8
2	B	95	ASN	2.8
1	A	101	THR	2.8
2	B	232	ILE	2.8
3	C	56	ASN	2.8
2	B	55	ARG	2.7
3	C	104	LEU	2.7
1	A	82	SER	2.7
3	C	23	PRO	2.7
3	C	54	GLU	2.7
1	A	103	PRO	2.7
2	B	209	HIS	2.7
2	B	135	VAL	2.7
2	B	86	LEU	2.7
1	A	87	ALA	2.7
2	B	22	THR	2.7
3	C	166	THR	2.7
2	B	156	ASP	2.7
3	C	230	LYS	2.7
3	C	231	ASP	2.7
3	C	147	ALA	2.6
2	B	202	PRO	2.6

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Mol	Chain	Res	Type	RSRZ
3	C	35	HIS	2.6
1	A	114	THR	2.6
3	C	37	PRO	2.6
1	A	79	THR	2.6
3	C	227	GLN	2.6
3	C	139	GLY	2.6
3	C	67	GLU	2.5
1	A	117	ALA	2.5
2	B	233	PRO	2.5
1	A	267	ARG	2.5
2	B	188	ASN	2.5
2	B	84	ASP	2.5
1	A	90	VAL	2.5
1	A	270	ASN	2.5
1	A	254	ARG	2.5
1	A	118	GLN	2.5
3	C	12	GLN	2.5
3	C	192	GLY	2.5
2	B	20	ASN	2.4
1	A	166	ARG	2.4
1	A	257	HIS	2.4
1	A	259	ARG	2.4
1	A	175	THR	2.4
1	A	178	SER	2.4
2	B	205	SER	2.4
3	C	174	ASN	2.4
3	C	144	LYS	2.4
1	A	260	ALA	2.4
1	A	274	LYS	2.4
3	C	160	GLY	2.4
3	C	190	THR	2.4
2	B	241	MET	2.4
3	C	232	ALA	2.4
3	C	61	ASN	2.3
3	C	110	GLN	2.3
1	A	273	PHE	2.3
2	B	99	HIS	2.3
2	B	157	GLY	2.3
3	C	103	GLN	2.3
3	C	2	PHE	2.3
3	C	218	ALA	2.3
2	B	83	PRO	2.3

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Mol	Chain	Res	Type	RSRZ
2	B	101	LEU	2.2
2	B	63	PHE	2.2
2	B	220	SER	2.2
3	C	45	GLU	2.2
3	C	86	PHE	2.2
2	B	117	PHE	2.2
3	C	102	GLY	2.2
1	A	204	PHE	2.2
1	A	164	ASP	2.1
1	A	282	ASN	2.1
2	B	206	ALA	2.1
3	C	77	ALA	2.1
3	C	109	THR	2.1
1	A	120	ARG	2.1
2	B	98	PHE	2.1
3	C	135	TYR	2.1
3	C	229	CYS	2.1
3	C	201	ASN	2.1
2	B	158	PHE	2.1
1	A	207	GLY	2.1
1	A	258	VAL	2.1
3	C	80	GLY	2.1
3	C	10	THR	2.1
3	C	206	ILE	2.1
1	A	107	ALA	2.1
2	B	150	GLN	2.1
1	A	169	LEU	2.1
1	A	91	GLY	2.0
1	A	243	SER	2.0
1	A	286	PRO	2.0
3	C	125	PHE	2.0
3	C	48	GLN	2.0
1	A	158	PRO	2.0
3	C	30	PRO	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.