



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 9, 2026 – 04:46 AM UTC

PDB ID : 3E1S / pdb_00003e1s
Title : Structure of an N-terminal truncation of Deinococcus radiodurans RecD2
Authors : Saikrishnan, K.; Griffiths, S.P.; Cook, N.; Court, R.; Wigley, D.B.
Deposited on : 2008-08-04
Resolution : 2.20 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

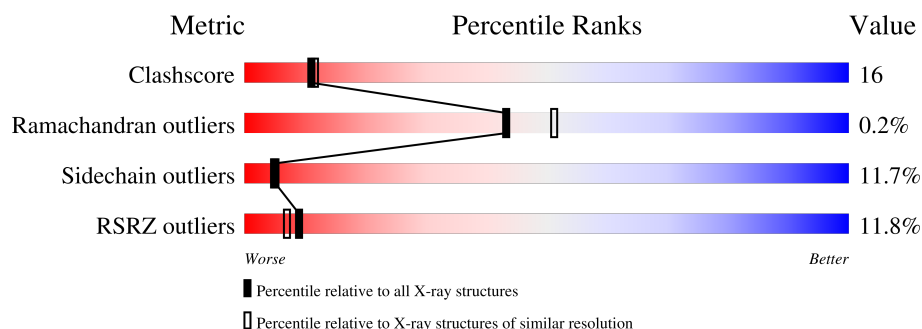
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.20 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	6851 (2.20-2.20)
Ramachandran outliers	187476	6768 (2.20-2.20)
Sidechain outliers	187428	6769 (2.20-2.20)
RSRZ outliers	180081	6166 (2.20-2.20)

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	574	

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 4154 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 Exodeoxyribonuclease V, subunit RecD.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	517	3889	2443	717	719	10	0	0	0

There are 9 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	150	MET	-	expression tag	UNP Q9RT63
A	716	LEU	-	expression tag	UNP Q9RT63
A	717	GLU	-	expression tag	UNP Q9RT63
A	718	HIS	-	expression tag	UNP Q9RT63
A	719	HIS	-	expression tag	UNP Q9RT63
A	720	HIS	-	expression tag	UNP Q9RT63
A	721	HIS	-	expression tag	UNP Q9RT63
A	722	HIS	-	expression tag	UNP Q9RT63
A	723	HIS	-	expression tag	UNP Q9RT63

- Molecule 2 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	265	Total	O	0	0
			265	265		

4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	54.63Å 89.63Å 131.71Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	20.70 – 2.20 20.70 – 2.20	Depositor EDS
% Data completeness (in resolution range)	98.2 (20.70-2.20) 98.0 (20.70-2.20)	Depositor EDS
R_{merge}	0.04	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.02 (at 2.19Å)	Xtriage
Refinement program	REFMAC 5.2.0019	Depositor
R, R_{free}	0.231 , 0.287 (Not available) , (Not available)	Depositor DCC
R_{free} test set	No test flags present.	wwPDB-VP
Wilson B-factor (Å ²)	41.6	Xtriage
Anisotropy	0.613	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.32 , 52.8	EDS
L-test for twinning ²	$\langle L \rangle = 0.47$, $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.91	EDS
Total number of atoms	4154	wwPDB-VP
Average B, all atoms (Å ²)	54.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.25% 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	0.64	1/3962 (0.0%)	0.88	4/5382 (0.1%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	572	ASN	C-N	5.19	1.40	1.33

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	605	GLY	O-C-N	-8.41	113.13	122.55
1	A	352	GLY	O-C-N	-7.31	114.52	122.41
1	A	543	GLY	CA-C-N	5.20	125.25	119.32
1	A	543	GLY	C-N-CA	5.20	125.25	119.32

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	3889	0	3920	128	0
2	A	265	0	0	9	0
All	All	4154	0	3920	128	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 16.

All (128) 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:665:MET:CE	1:A:668:LEU:HD12	1.83	1.08
1:A:480:ALA:HA	1:A:485:THR:HG21	1.56	0.86
1:A:220:PRO:O	1:A:224:THR:HG23	1.77	0.84
1:A:665:MET:HE1	1:A:668:LEU:HD12	1.61	0.83
1:A:340:SER:H	1:A:343:GLN:HE21	1.28	0.82
1:A:564:ASN:HD21	1:A:642:ALA:H	1.30	0.80
1:A:665:MET:HE3	1:A:665:MET:HA	1.65	0.79
1:A:619:THR:HG22	1:A:628:GLU:HG2	1.65	0.79
1:A:603:PHE:HD1	1:A:604:ASN:H	1.31	0.79
1:A:558:LEU:HB3	1:A:659:VAL:HG11	1.65	0.78
1:A:417:GLN:HB2	2:A:798:HOH:O	1.86	0.76
1:A:592:VAL:HG22	1:A:607:LEU:HD23	1.68	0.76
1:A:483:ALA:O	1:A:485:THR:HG23	1.86	0.75
1:A:665:MET:HE3	1:A:668:LEU:HD12	1.66	0.75
1:A:553:MET:HE2	1:A:667:MET:CG	2.18	0.74
1:A:417:GLN:NE2	1:A:418:GLY:O	2.20	0.74
1:A:387:CYS:SG	1:A:408:VAL:HA	2.33	0.69
1:A:226:ALA:HB1	1:A:256:THR:HG21	1.73	0.68
1:A:417:GLN:CB	2:A:798:HOH:O	2.41	0.68
1:A:553:MET:HE2	1:A:667:MET:HG3	1.75	0.68
1:A:259:THR:H	1:A:262:GLN:HE21	1.42	0.68
1:A:452:VAL:HG21	1:A:458:VAL:HG21	1.77	0.67
1:A:329:TRP:HA	1:A:380:LEU:HD13	1.77	0.67
1:A:233:LEU:HD23	1:A:255:TYR:CZ	2.30	0.67
1:A:271:VAL:HG11	1:A:278:GLU:CG	2.25	0.66
1:A:226:ALA:CB	1:A:256:THR:HG21	2.25	0.66
1:A:523:THR:HG23	2:A:790:HOH:O	1.96	0.65
1:A:578:VAL:HG23	1:A:613:ALA:HB1	1.77	0.64
1:A:313:ARG:HE	1:A:314:THR:HG22	1.63	0.64
1:A:609:MET:O	1:A:611:LEU:HD22	1.97	0.64
1:A:271:VAL:HG11	1:A:278:GLU:HG3	1.81	0.63
1:A:553:MET:HE3	1:A:664:HIS:HB3	1.81	0.62
1:A:337:LYS:HE3	2:A:882:HOH:O	1.99	0.62
1:A:564:ASN:ND2	1:A:642:ALA:H	1.98	0.62
1:A:665:MET:HE1	1:A:695:ILE:HG21	1.81	0.61
1:A:310:SER:O	1:A:314:THR:HG23	2.01	0.61
1:A:434:VAL:HG21	1:A:448:LEU:HD21	1.83	0.60
1:A:417:GLN:HA	2:A:798:HOH:O	2.00	0.60

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:302:LEU:HD22	1:A:306:LYS:HD2	1.82	0.59
1:A:350:LEU:O	1:A:457:ARG:NH1	2.35	0.59
1:A:665:MET:CE	1:A:665:MET:HA	2.32	0.59
1:A:469:PRO:O	1:A:704:ARG:NH2	2.34	0.59
1:A:655:THR:HG22	2:A:727:HOH:O	2.02	0.58
1:A:357:VAL:HB	1:A:485:THR:HG22	1.85	0.58
1:A:386:LEU:HD23	1:A:397:LEU:HD22	1.86	0.57
1:A:204:LEU:H	1:A:204:LEU:HD12	1.68	0.57
1:A:342:GLU:OE2	1:A:489:THR:HG22	2.04	0.57
1:A:655:THR:HG21	1:A:683:ARG:HH21	1.71	0.55
1:A:387:CYS:SG	1:A:408:VAL:HG22	2.47	0.55
1:A:271:VAL:CG1	1:A:278:GLU:HG3	2.36	0.54
1:A:417:GLN:CA	2:A:798:HOH:O	2.56	0.54
1:A:538:VAL:HG13	1:A:547:VAL:CG1	2.37	0.54
1:A:554:ARG:HG3	1:A:560:MET:HE2	1.90	0.54
1:A:627:VAL:HG22	1:A:629:LEU:HD13	1.90	0.53
1:A:655:THR:HB	1:A:683:ARG:HB2	1.91	0.53
1:A:408:VAL:HG11	1:A:444:LEU:HD12	1.90	0.53
1:A:603:PHE:HD1	1:A:604:ASN:N	2.04	0.52
1:A:434:VAL:HG21	1:A:448:LEU:CD2	2.40	0.52
1:A:407:THR:HG23	1:A:410:ARG:HH11	1.75	0.52
1:A:271:VAL:HG21	1:A:278:GLU:HG2	1.91	0.52
1:A:495:ALA:HB1	1:A:501:ILE:HD12	1.91	0.51
1:A:336:ARG:HA	1:A:339:LEU:HD22	1.92	0.51
1:A:591:VAL:HG11	1:A:637:LEU:HG	1.92	0.51
1:A:390:THR:CG2	1:A:439:MET:HE1	2.41	0.50
1:A:553:MET:HE3	1:A:664:HIS:CA	2.42	0.50
1:A:553:MET:HE3	1:A:664:HIS:HA	1.93	0.50
1:A:627:VAL:HG22	1:A:629:LEU:CD1	2.42	0.50
1:A:553:MET:HE3	1:A:664:HIS:CB	2.41	0.50
1:A:371:LYS:HG3	1:A:401:THR:HA	1.93	0.49
1:A:363:GLY:HA3	1:A:491:VAL:HG13	1.94	0.49
1:A:630:THR:CA	1:A:634:LEU:HD13	2.42	0.49
1:A:480:ALA:CA	1:A:485:THR:HG21	2.35	0.49
1:A:231:LEU:O	1:A:234:ALA:HB3	2.12	0.49
1:A:630:THR:HA	1:A:634:LEU:HD13	1.95	0.49
1:A:329:TRP:CZ2	1:A:376:LEU:HD12	2.47	0.49
1:A:322:ASP:N	1:A:326:ASN:OD1	2.41	0.48
1:A:223:LEU:CD2	1:A:258:VAL:HG11	2.43	0.48
1:A:271:VAL:HG11	1:A:278:GLU:CD	2.38	0.48
1:A:592:VAL:HG22	1:A:607:LEU:CD2	2.41	0.48

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:231:LEU:HD21	1:A:296:ILE:HD11	1.94	0.47
1:A:259:THR:HG23	1:A:262:GLN:NE2	2.29	0.47
1:A:507:LEU:HD11	1:A:677:LEU:HD22	1.94	0.47
1:A:286:ALA:O	1:A:290:ALA:N	2.48	0.47
1:A:226:ALA:HB1	1:A:256:THR:CG2	2.41	0.47
1:A:665:MET:HE2	1:A:699:ARG:NH2	2.31	0.46
1:A:201:ILE:H	1:A:201:ILE:HD12	1.81	0.45
1:A:655:THR:CG2	2:A:727:HOH:O	2.61	0.45
1:A:452:VAL:HG21	1:A:458:VAL:CG2	2.45	0.45
1:A:617:ARG:HE	1:A:628:GLU:HB3	1.82	0.45
1:A:415:GLY:N	1:A:417:GLN:HE22	2.13	0.45
1:A:434:VAL:O	1:A:461:VAL:HG13	2.17	0.44
1:A:437:VAL:HG13	1:A:445:MET:HE3	1.98	0.44
1:A:466:GLN:NE2	1:A:675:THR:OG1	2.51	0.44
1:A:466:GLN:HE22	1:A:675:THR:HA	1.82	0.44
1:A:580:ILE:HD13	1:A:585:ALA:HB2	2.00	0.44
1:A:233:LEU:HD23	1:A:255:TYR:CE1	2.54	0.43
1:A:435:ASP:OD2	1:A:461:VAL:HG22	2.19	0.43
1:A:474:LEU:HD22	1:A:477:LEU:HD22	2.00	0.43
1:A:665:MET:HE3	1:A:668:LEU:CD1	2.43	0.43
1:A:376:LEU:C	1:A:376:LEU:HD13	2.43	0.43
1:A:277:SER:O	1:A:296:ILE:HA	2.19	0.43
1:A:196:THR:HG23	1:A:203:PHE:HB2	2.01	0.43
1:A:223:LEU:HD23	1:A:258:VAL:HG11	2.01	0.42
1:A:408:VAL:HG11	1:A:444:LEU:CD1	2.49	0.42
1:A:326:ASN:ND2	1:A:327:ASP:O	2.53	0.42
1:A:220:PRO:HA	1:A:223:LEU:HD12	2.02	0.42
1:A:460:LEU:CD1	1:A:479:LEU:HD13	2.50	0.42
1:A:611:LEU:HD21	1:A:621:ASP:HB2	2.01	0.42
1:A:313:ARG:NE	1:A:314:THR:HG22	2.31	0.42
1:A:233:LEU:HD23	1:A:255:TYR:CE2	2.54	0.42
1:A:440:MET:CE	1:A:445:MET:HE2	2.50	0.42
1:A:223:LEU:HB3	1:A:266:ALA:HB2	2.01	0.42
1:A:553:MET:HE2	1:A:667:MET:HG2	1.99	0.42
1:A:553:MET:CE	1:A:664:HIS:HA	2.50	0.42
1:A:474:LEU:N	1:A:475:PRO:HD3	2.35	0.41
1:A:568:GLN:CD	1:A:639:LEU:HD21	2.45	0.41
1:A:238:ALA:HB3	1:A:240:HIS:CD2	2.55	0.41
1:A:538:VAL:HG13	1:A:547:VAL:HG13	2.02	0.41
1:A:429:TYR:CD2	1:A:432:LEU:HD21	2.54	0.41
1:A:580:ILE:O	1:A:581:ALA:C	2.63	0.41

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:611:LEU:HD21	1:A:621:ASP:CB	2.50	0.41
1:A:550:LEU:HA	1:A:643:LEU:O	2.21	0.41
1:A:358:LEU:O	1:A:461:VAL:HA	2.21	0.41
1:A:452:VAL:CG2	1:A:458:VAL:HG21	2.47	0.41
1:A:332:PRO:HG2	1:A:335:ALA:HB2	2.02	0.41
1:A:591:VAL:CG1	1:A:637:LEU:HG	2.51	0.41
1:A:330:ALA:O	1:A:376:LEU:HD21	2.21	0.41
1:A:646:HIS:HE1	2:A:783:HOH:O	2.04	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	509/574 (89%)	491 (96%)	17 (3%)	1 (0%)	43	51

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	662	GLU

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	393/435 (90%)	347 (88%)	46 (12%)	5 5

All (46) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	197	GLU
1	A	201	ILE
1	A	219	ASP
1	A	224	THR
1	A	233	LEU
1	A	254	HIS
1	A	256	THR
1	A	278	GLU
1	A	296	ILE
1	A	302	LEU
1	A	308	LEU
1	A	311	LEU
1	A	313	ARG
1	A	314	THR
1	A	322	ASP
1	A	341	GLU
1	A	349	GLN
1	A	350	LEU
1	A	355	LEU
1	A	358	LEU
1	A	397	LEU
1	A	444	LEU
1	A	445	MET
1	A	459	LEU
1	A	461	VAL
1	A	501	ILE
1	A	520	LEU
1	A	567	LEU
1	A	570	LEU
1	A	582	GLU
1	A	591	VAL
1	A	603	PHE
1	A	609	MET
1	A	629	LEU
1	A	633	GLU
1	A	634	LEU
1	A	637	LEU
1	A	639	LEU

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	A	647	ARG
1	A	655	THR
1	A	665	MET
1	A	709	LEU
1	A	716	LEU
1	A	718	HIS
1	A	719	HIS
1	A	720	HIS

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	262	GLN
1	A	343	GLN
1	A	349	GLN
1	A	417	GLN
1	A	466	GLN
1	A	490	GLN
1	A	502	GLN
1	A	521	ASN
1	A	564	ASN
1	A	566	HIS
1	A	568	GLN
1	A	572	ASN
1	A	593	GLN
1	A	625	ASN
1	A	646	HIS
1	A	671	ASN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates ⓘ

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	517/574 (90%)	0.99	61 (11%) 9 7	39, 54, 62, 76	2 (0%)

All (61) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	325	GLY	4.7
1	A	327	ASP	4.7
1	A	331	VAL	4.6
1	A	441	GLY	3.9
1	A	713	ARG	3.4
1	A	335	ALA	3.4
1	A	352	GLY	3.3
1	A	324	ALA	3.3
1	A	256	THR	3.3
1	A	351	ALA	3.1
1	A	472	ALA	3.1
1	A	242	PHE	2.7
1	A	326	ASN	2.7
1	A	418	GLY	2.6
1	A	467	LEU	2.6
1	A	474	LEU	2.6
1	A	414	TYR	2.6
1	A	241	SER	2.6
1	A	322	ASP	2.6
1	A	468	PRO	2.6
1	A	271	VAL	2.5
1	A	301	VAL	2.5
1	A	410	ARG	2.5
1	A	204	LEU	2.5
1	A	448	LEU	2.5
1	A	296	ILE	2.5
1	A	336	ARG	2.5

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	A	470	VAL	2.4
1	A	329	TRP	2.4
1	A	206	ALA	2.4
1	A	238	ALA	2.3
1	A	330	ALA	2.3
1	A	720	HIS	2.3
1	A	328	ASP	2.3
1	A	338	GLY	2.3
1	A	332	PRO	2.3
1	A	209	LEU	2.2
1	A	244	PRO	2.2
1	A	392	LYS	2.2
1	A	719	HIS	2.2
1	A	703	ALA	2.2
1	A	382	LEU	2.2
1	A	337	LYS	2.2
1	A	495	ALA	2.2
1	A	496	ALA	2.2
1	A	504	ALA	2.2
1	A	424	LEU	2.1
1	A	473	GLY	2.1
1	A	647	ARG	2.1
1	A	492	TYR	2.1
1	A	639	LEU	2.1
1	A	210	TRP	2.1
1	A	267	VAL	2.1
1	A	525	ILE	2.1
1	A	239	GLY	2.1
1	A	198	VAL	2.1
1	A	437	VAL	2.1
1	A	442	ASP	2.0
1	A	304	ALA	2.0
1	A	463	ASP	2.0
1	A	629	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.