



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 04:49 PM UTC

PDB ID : 7EGY / pdb_00007egy
Title : Recombinant head-to-tail dimeric E2 protein
Authors : Ru, Q.X.
Deposited on : 2021-03-27
Resolution : 4.20 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

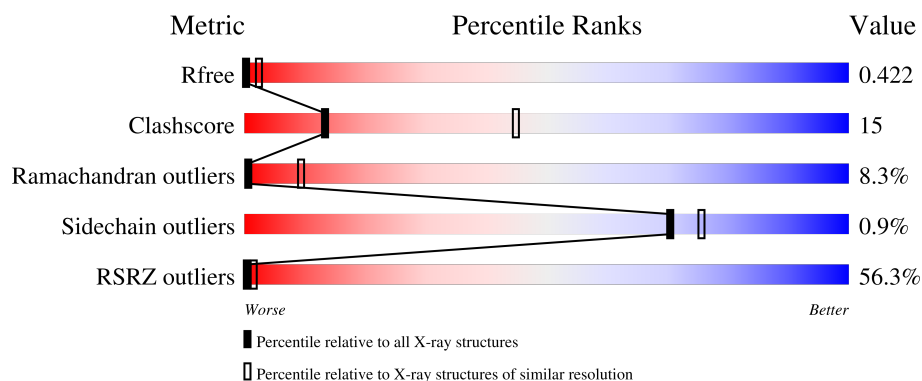
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 4.20 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))
R_{free}	180053	1004 (4.52-3.88)
Clashscore	190562	1019 (4.50-3.90)
Ramachandran outliers	187476	1020 (4.56-3.84)
Sidechain outliers	187428	1006 (4.56-3.84)
RSRZ outliers	180081	1001 (4.52-3.88)

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	342	
1	B	342	

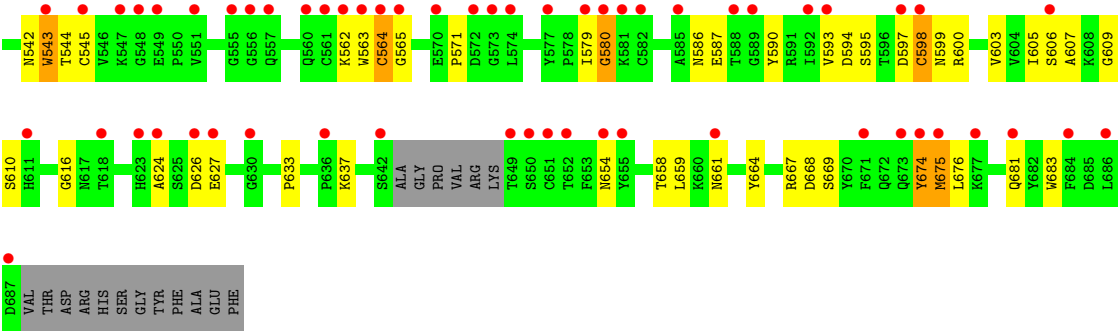
2 Entry composition

There is only 1 type of molecule in this entry. The entry contains 3402 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 E2 protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	238	Total	C	N	O	S	0	0	0
			1701	1082	285	318	16			
1	B	238	Total	C	N	O	S	0	0	0
			1701	1082	285	318	16			



4 Data and refinement statistics

Property	Value	Source
Space group	P 63	Depositor
Cell constants a, b, c, α , β , γ	177.17Å 177.17Å 59.17Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	42.55 – 4.20 42.55 – 4.20	Depositor EDS
% Data completeness (in resolution range)	87.8 (42.55-4.20) 96.7 (42.55-4.20)	Depositor EDS
R_{merge}	0.12	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.12 (at 4.14Å)	Xtriage
Refinement program	PHENIX 1.13_2998	Depositor
R, R_{free}	0.381 , 0.444 0.402 , 0.422	Depositor DCC
R_{free} test set	358 reflections (4.48%)	wwPDB-VP
Wilson B-factor (Å ²)	42.5	Xtriage
Anisotropy	0.589	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.31 , 148.2	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	0.042 for h,-h-k,-l	Xtriage
F_o, F_c correlation	0.52	EDS
Total number of atoms	3402	wwPDB-VP
Average B, all atoms (Å ²)	66.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.63% 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	0.18	0/1737	0.46	0/2350
1	B	0.17	0/1737	0.46	0/2350
All	All	0.17	0/3474	0.46	0/4700

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	1701	0	1478	47	0
1	B	1701	0	1478	47	0
All	All	3402	0	2956	94	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 15.

All (94) 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:B:485:VAL:HG11	1:B:543:TRP:HE1	1.44	0.81
1:B:600:ARG:HG3	1:B:633:PRO:HG3	1.69	0.74

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:602:GLY:O	1:A:625:SER:OG	2.06	0.73
1:A:514:ARG:NE	1:A:516:LYS:O	2.20	0.72
1:B:627:GLU:O	1:B:661:ASN:ND2	2.26	0.69
1:A:563:TRP:HB3	1:A:568:PHE:HE2	1.58	0.67
1:B:455:PHE:O	1:B:521:ARG:NH1	2.27	0.67
1:B:528:THR:OG1	1:B:529:VAL:N	2.29	0.66
1:A:628:ARG:O	1:A:662:LYS:NZ	2.27	0.66
1:A:453:ASP:OD1	1:A:514:ARG:NH2	2.26	0.65
1:B:465:SER:O	1:B:497:THR:OG1	2.14	0.64
1:B:668:ASP:OD1	1:B:669:SER:N	2.31	0.63
1:B:542:ASN:O	1:B:544:THR:N	2.31	0.63
1:A:658:THR:OG1	1:A:659:LEU:N	2.31	0.62
1:B:542:ASN:C	1:B:544:THR:H	2.08	0.62
1:A:594:ASP:OD1	1:A:595:SER:N	2.33	0.62
1:B:674:TYR:O	1:B:676:LEU:N	2.34	0.61
1:B:468:VAL:HG21	1:B:475:THR:HG21	1.83	0.61
1:A:503:THR:C	1:A:504:LEU:HD22	2.28	0.58
1:A:664:TYR:O	1:A:681:GLN:NE2	2.37	0.57
1:A:664:TYR:N	1:A:681:GLN:OE1	2.32	0.56
1:B:597:ASP:O	1:B:599:ASN:N	2.39	0.56
1:A:528:THR:OG1	1:A:529:VAL:N	2.40	0.55
1:B:624:ALA:HB2	1:B:659:LEU:HD23	1.87	0.55
1:A:508:VAL:O	1:A:508:VAL:HG13	2.07	0.55
1:B:654:ASN:O	1:B:683:TRP:N	2.39	0.54
1:B:464:THR:O	1:B:466:PRO:HD3	2.08	0.54
1:B:480:SER:OG	1:B:481:ALA:N	2.40	0.54
1:A:658:THR:OG1	1:A:662:LYS:O	2.21	0.53
1:A:627:GLU:O	1:A:661:ASN:ND2	2.40	0.53
1:B:594:ASP:OD1	1:B:595:SER:N	2.40	0.52
1:A:568:PHE:HD1	1:A:618:THR:HG21	1.74	0.52
1:A:595:SER:O	1:A:595:SER:OG	2.27	0.51
1:B:451:MET:O	1:B:514:ARG:NH2	2.44	0.51
1:A:563:TRP:HB3	1:A:568:PHE:CE2	2.44	0.51
1:B:626:ASP:OD1	1:B:627:GLU:N	2.44	0.51
1:A:468:VAL:HG21	1:A:475:THR:HG21	1.93	0.50
1:A:562:LYS:HB3	1:A:581:LYS:HE2	1.94	0.50
1:B:563:TRP:NE1	1:B:564:CYS:SG	2.84	0.50
1:B:514:ARG:NH1	1:B:517:PRO:O	2.45	0.50
1:B:530:GLU:O	1:B:532:GLU:N	2.45	0.49
1:B:476:LEU:HB2	1:B:483:TYR:O	2.12	0.49
1:A:574:LEU:H	1:A:574:LEU:HD12	1.77	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:514:ARG:NH1	1:B:516:LYS:HG3	2.27	0.48
1:B:542:ASN:O	1:B:544:THR:HG23	2.12	0.48
1:B:563:TRP:O	1:B:565:GLY:N	2.47	0.48
1:B:495:GLU:O	1:B:497:THR:N	2.46	0.48
1:B:495:GLU:O	1:B:497:THR:HG23	2.14	0.47
1:A:569:ASN:O	1:A:577:TYR:OH	2.25	0.47
1:A:460:CYS:HB2	1:A:480:SER:O	2.13	0.47
1:B:485:VAL:HG11	1:B:543:TRP:NE1	2.22	0.47
1:A:581:LYS:HE3	1:A:590:TYR:CD1	2.50	0.46
1:A:460:CYS:SG	1:A:466:PRO:HG3	2.56	0.46
1:A:522:MET:O	1:A:524:CYS:N	2.48	0.46
1:B:461:PRO:HD2	1:B:496:CYS:SG	2.56	0.46
1:A:530:GLU:O	1:A:532:GLU:N	2.48	0.46
1:A:527:THR:O	1:A:527:THR:OG1	2.28	0.46
1:A:529:VAL:HA	1:A:534:LEU:HA	1.96	0.46
1:B:586:ASN:OD1	1:B:587:GLU:N	2.49	0.46
1:A:455:PHE:O	1:A:521:ARG:NH1	2.48	0.46
1:B:658:THR:OG1	1:B:659:LEU:N	2.49	0.46
1:B:562:LYS:HD2	1:B:590:TYR:HE1	1.81	0.45
1:A:632:MET:HG2	1:A:662:LYS:HB3	1.98	0.45
1:B:444:THR:HA	1:B:445:ASN:HA	1.67	0.45
1:B:563:TRP:C	1:B:565:GLY:H	2.25	0.44
1:B:675:MET:HE1	1:B:683:TRP:HA	1.98	0.44
1:A:609:GLY:HA3	1:A:610:SER:HA	1.65	0.44
1:B:667:ARG:HG3	1:B:674:TYR:CE1	2.52	0.44
1:A:670:TYR:CE1	1:A:686:LEU:HB3	2.52	0.44
1:B:664:TYR:N	1:B:681:GLN:OE1	2.38	0.44
1:A:513:ARG:HG2	1:A:514:ARG:N	2.34	0.43
1:B:579:ILE:HG12	1:B:580:GLY:H	1.82	0.43
1:B:675:MET:HB2	1:B:675:MET:HE3	1.69	0.43
1:B:599:ASN:HA	1:B:603:VAL:O	2.18	0.43
1:B:609:GLY:HA2	1:B:610:SER:HA	1.55	0.43
1:A:504:LEU:HD22	1:A:504:LEU:N	2.33	0.43
1:B:542:ASN:C	1:B:544:THR:N	2.74	0.43
1:A:557:GLN:O	1:A:584:LEU:HD12	2.19	0.42
1:A:575:PRO:HG2	1:A:600:ARG:CZ	2.49	0.42
1:A:586:ASN:OD1	1:A:587:GLU:N	2.51	0.42
1:B:599:ASN:O	1:B:600:ARG:NE	2.47	0.42
1:A:578:PRO:HB2	1:A:582:CYS:SG	2.60	0.42
1:A:641:SER:OG	1:A:654:ASN:OD1	2.36	0.42
1:B:598:CYS:HB3	1:B:605:ILE:HG13	2.02	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:450:GLU:OE2	1:A:513:ARG:HD2	2.20	0.42
1:A:670:TYR:CZ	1:A:686:LEU:O	2.73	0.42
1:B:579:ILE:HG12	1:B:580:GLY:N	2.35	0.41
1:A:597:ASP:C	1:A:599:ASN:H	2.28	0.41
1:A:654:ASN:N	1:A:683:TRP:O	2.30	0.41
1:A:471:LYS:N	1:A:490:TRP:HE1	2.19	0.41
1:A:474:THR:HB	1:A:544:THR:HG21	2.03	0.40
1:A:671:PHE:N	1:A:671:PHE:CD1	2.89	0.40
1:B:606:SER:HB3	1:B:607:ALA:H	1.76	0.40
1:A:536:TYR:N	1:A:549:GLU:O	2.54	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	234/342 (68%)	155 (66%)	58 (25%)	21 (9%)	0	8
1	B	234/342 (68%)	151 (64%)	65 (28%)	18 (8%)	1	10
All	All	468/684 (68%)	306 (65%)	123 (26%)	39 (8%)	0	9

All (39) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	446	PRO
1	A	461	PRO
1	B	446	PRO
1	B	461	PRO
1	B	543	TRP
1	B	564	CYS
1	A	531	ASN
1	B	496	CYS

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Mol	Chain	Res	Type
1	B	523	ASP
1	B	531	ASN
1	B	580	GLY
1	B	593	VAL
1	B	598	CYS
1	B	674	TYR
1	B	675	MET
1	A	487	PRO
1	A	502	THR
1	A	559	LYS
1	A	660	LYS
1	B	483	TYR
1	B	637	LYS
1	A	463	ASP
1	A	543	TRP
1	A	554	THR
1	A	572	ASP
1	A	651	CYS
1	B	545	CYS
1	A	618	THR
1	A	625	SER
1	A	670	TYR
1	A	592	ILE
1	A	598	CYS
1	A	601	ASP
1	B	456	GLY
1	B	502	THR
1	B	616	GLY
1	A	456	GLY
1	A	633	PRO
1	A	486	CYS

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.

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	158/295 (54%)	157 (99%)	1 (1%)	78	80
1	B	159/295 (54%)	157 (99%)	2 (1%)	61	71
All	All	317/590 (54%)	314 (99%)	3 (1%)	70	75

All (3) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	571	PRO
1	B	501	PRO
1	B	571	PRO

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (3) such sidechains are listed below:

Mol	Chain	Res	Type
1	B	473	ASN
1	B	478	ASN
1	B	672	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](#)

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	238/342 (69%)	2.42	132 (55%) 0 1	29, 62, 95, 133	0
1	B	238/342 (69%)	2.58	136 (57%) 0 1	31, 70, 106, 147	0
All	All	476/684 (69%)	2.50	268 (56%) 0 1	29, 66, 102, 147	0

All (268) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	462	PHE	11.6
1	B	515	GLU	10.2
1	A	642	SER	9.7
1	A	528	THR	8.7
1	B	649	THR	8.4
1	B	444	THR	7.9
1	B	484	LEU	7.8
1	A	650	SER	7.6
1	A	686	LEU	7.3
1	B	499	VAL	7.3
1	A	610	SER	7.3
1	A	557	GLN	7.2
1	B	519	PRO	7.0
1	A	649	THR	6.7
1	B	459	LEU	6.3
1	B	524	CYS	5.9
1	B	489	GLY	5.6
1	B	504	LEU	5.6
1	A	523	ASP	5.6
1	A	598	CYS	5.6
1	A	448	THR	5.5
1	B	449	GLU	5.3
1	A	525	VAL	5.3
1	B	687	ASP	5.3

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Mol	Chain	Res	Type	RSRZ
1	A	527	THR	5.2
1	A	590	TYR	4.8
1	A	450	GLU	4.8
1	B	598	CYS	4.8
1	B	482	PHE	4.7
1	A	687	ASP	4.7
1	A	569	ASN	4.7
1	A	597	ASP	4.6
1	B	472	TYR	4.6
1	A	565	GLY	4.5
1	B	513	ARG	4.5
1	A	505	ARG	4.5
1	A	581	LYS	4.5
1	B	478	ASN	4.4
1	B	557	GLN	4.4
1	B	470	GLY	4.3
1	B	506	THR	4.3
1	B	503	THR	4.3
1	B	501	PRO	4.3
1	B	496	CYS	4.3
1	B	476	LEU	4.2
1	A	554	THR	4.2
1	A	638	GLU	4.2
1	B	507	GLU	4.2
1	A	685	ASP	4.2
1	A	669	SER	4.1
1	B	486	CYS	4.1
1	B	466	PRO	4.1
1	A	679	GLU	4.0
1	A	567	ASP	4.0
1	A	673	GLN	4.0
1	B	505	ARG	4.0
1	A	444	THR	4.0
1	B	477	LEU	3.9
1	B	453	ASP	3.9
1	A	675	MET	3.8
1	B	460	CYS	3.8
1	A	475	THR	3.8
1	A	502	THR	3.8
1	A	588	THR	3.8
1	A	684	PHE	3.8
1	B	461	PRO	3.8

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Mol	Chain	Res	Type	RSRZ
1	B	500	SER	3.8
1	A	578	PRO	3.8
1	B	517	PRO	3.8
1	A	460	CYS	3.7
1	A	608	LYS	3.7
1	A	553	TYR	3.7
1	B	588	THR	3.7
1	B	521	ARG	3.7
1	B	650	SER	3.7
1	B	502	THR	3.7
1	B	675	MET	3.7
1	B	580	GLY	3.7
1	A	641	SER	3.6
1	A	652	THR	3.6
1	B	488	ILE	3.6
1	B	611	HIS	3.6
1	B	545	CYS	3.6
1	A	520	HIS	3.5
1	B	511	THR	3.5
1	B	543	TRP	3.5
1	A	459	LEU	3.5
1	B	445	ASN	3.5
1	B	520	HIS	3.5
1	B	485	VAL	3.5
1	B	448	THR	3.5
1	A	504	LEU	3.4
1	B	495	GLU	3.4
1	B	457	PHE	3.4
1	A	667	ARG	3.4
1	B	467	VAL	3.3
1	B	618	THR	3.3
1	A	461	PRO	3.3
1	A	571	PRO	3.3
1	A	507	GLU	3.3
1	A	556	GLY	3.3
1	B	516	LYS	3.3
1	B	518	PHE	3.3
1	A	534	LEU	3.3
1	A	582	CYS	3.3
1	B	592	ILE	3.3
1	A	503	THR	3.3
1	B	623	HIS	3.3

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Mol	Chain	Res	Type	RSRZ
1	A	589	GLY	3.2
1	B	458	GLY	3.2
1	A	626	ASP	3.2
1	B	498	ALA	3.2
1	B	464	THR	3.2
1	A	530	GLU	3.2
1	A	509	VAL	3.2
1	B	565	GLY	3.2
1	A	572	ASP	3.2
1	B	538	LYS	3.1
1	B	465	SER	3.1
1	B	539	LEU	3.1
1	B	574	LEU	3.1
1	B	483	TYR	3.1
1	A	570	GLU	3.1
1	B	456	GLY	3.1
1	B	536	TYR	3.0
1	A	506	THR	3.0
1	A	492	GLY	3.0
1	A	464	THR	3.0
1	B	487	PRO	3.0
1	A	609	GLY	3.0
1	A	617	ASN	3.0
1	B	525	VAL	2.9
1	B	581	LYS	2.9
1	B	533	ASP	2.9
1	B	468	VAL	2.9
1	A	619	THR	2.9
1	B	479	GLY	2.9
1	B	531	ASN	2.9
1	B	534	LEU	2.9
1	A	545	CYS	2.8
1	B	526	THR	2.8
1	B	512	PHE	2.8
1	A	555	GLY	2.8
1	A	607	ALA	2.8
1	A	654	ASN	2.8
1	B	491	THR	2.8
1	B	450	GLU	2.7
1	A	536	TYR	2.7
1	A	622	VAL	2.7
1	B	497	THR	2.7

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Mol	Chain	Res	Type	RSRZ
1	A	463	ASP	2.7
1	A	547	LYS	2.7
1	A	635	ARG	2.7
1	B	471	LYS	2.7
1	A	678	GLY	2.7
1	A	670	TYR	2.7
1	B	686	LEU	2.7
1	B	561	CYS	2.7
1	B	626	ASP	2.6
1	A	529	VAL	2.6
1	A	604	VAL	2.6
1	B	684	PHE	2.6
1	A	624	ALA	2.6
1	B	630	GLY	2.6
1	B	528	THR	2.6
1	B	510	LYS	2.6
1	B	556	GLY	2.6
1	A	549	GLU	2.6
1	A	606	SER	2.5
1	B	677	LYS	2.5
1	B	560	GLN	2.5
1	B	681	GLN	2.5
1	A	651	CYS	2.5
1	A	532	GLU	2.5
1	B	674	TYR	2.5
1	A	574	LEU	2.5
1	B	589	GLY	2.5
1	B	532	GLU	2.5
1	B	636	PRO	2.5
1	A	599	ASN	2.5
1	B	642	SER	2.5
1	B	597	ASP	2.5
1	B	549	GLU	2.4
1	B	537	CYS	2.4
1	B	564	CYS	2.4
1	B	469	LYS	2.4
1	B	547	LYS	2.4
1	B	572	ASP	2.4
1	A	445	ASN	2.4
1	B	473	ASN	2.4
1	A	480	SER	2.4
1	B	651	CYS	2.4

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Mol	Chain	Res	Type	RSRZ
1	A	668	ASP	2.4
1	A	449	GLU	2.4
1	A	636	PRO	2.4
1	B	555	GLY	2.4
1	B	624	ALA	2.4
1	A	657	LYS	2.4
1	A	584	LEU	2.4
1	A	543	TRP	2.4
1	A	672	GLN	2.3
1	A	548	GLY	2.3
1	B	455	PHE	2.3
1	B	570	GLU	2.3
1	A	623	HIS	2.3
1	B	535	PHE	2.3
1	A	491	THR	2.3
1	A	677	LYS	2.3
1	A	612	GLU	2.3
1	A	562	LYS	2.3
1	B	606	SER	2.3
1	A	611	HIS	2.3
1	A	493	VAL	2.3
1	A	676	LEU	2.3
1	A	625	SER	2.3
1	A	499	VAL	2.3
1	A	666	PRO	2.3
1	B	452	GLY	2.3
1	B	551	VAL	2.3
1	A	591	ARG	2.3
1	B	451	MET	2.3
1	A	457	PHE	2.2
1	A	661	ASN	2.2
1	A	524	CYS	2.2
1	B	582	CYS	2.2
1	B	548	GLY	2.2
1	A	535	PHE	2.2
1	A	614	LEU	2.2
1	A	526	THR	2.2
1	B	593	VAL	2.2
1	B	579	ILE	2.2
1	B	563	TRP	2.2
1	A	542	ASN	2.2
1	B	481	ALA	2.2

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Mol	Chain	Res	Type	RSRZ
1	A	483	TYR	2.2
1	B	652	THR	2.2
1	A	462	PHE	2.2
1	B	671	PHE	2.2
1	B	577	TYR	2.2
1	A	585	ALA	2.2
1	B	654	ASN	2.2
1	A	637	LYS	2.2
1	B	673	GLN	2.2
1	A	452	GLY	2.1
1	A	472	TYR	2.1
1	A	632	MET	2.1
1	A	513	ARG	2.1
1	B	627	GLU	2.1
1	A	488	ILE	2.1
1	B	661	ASN	2.1
1	A	454	ASP	2.1
1	A	456	GLY	2.1
1	A	500	SER	2.1
1	A	628	ARG	2.1
1	A	621	LYS	2.1
1	B	585	ALA	2.1
1	B	523	ASP	2.1
1	A	613	CYS	2.1
1	B	655	TYR	2.1
1	A	568	PHE	2.1
1	A	501	PRO	2.0
1	A	540	GLY	2.0
1	B	492	GLY	2.0
1	A	531	ASN	2.0
1	A	593	VAL	2.0
1	A	577	TYR	2.0
1	B	573	GLY	2.0
1	B	562	LYS	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.