Full wwPDB X-ray Structure Validation Report ⓘ

Nov 15, 2023 – 03:41 PM JST

PDB ID	:	6JHW
Title	:	Structure of anti-CRISPR AcrIIC3 and NmeCas9 HNH
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Deposited on	:	2019-02-19
Resolution	:	2.04 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:

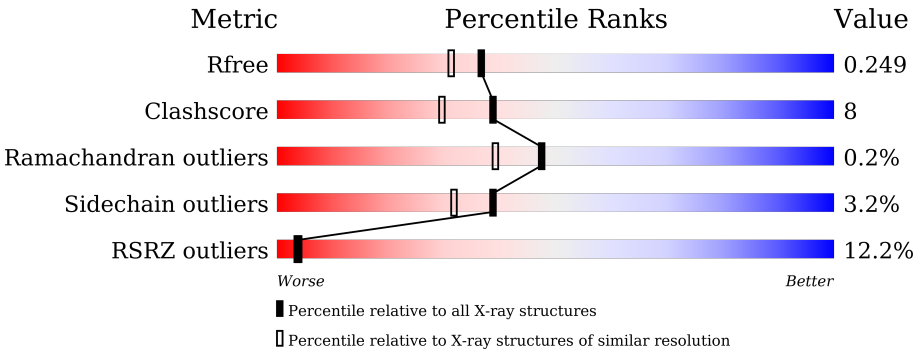
MolProbity	:	4.02b-467
Xtriage (Phenix)	:	1.13
EDS	:	2.36
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.36

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:
X-RAY DIFFRACTION

The reported resolution of this entry is 2.04 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}	130704	1692 (2.04-2.04)
Clashscore	141614	1773 (2.04-2.04)
Ramachandran outliers	138981	1752 (2.04-2.04)
Sidechain outliers	138945	1752 (2.04-2.04)
RSRZ outliers	127900	1672 (2.04-2.04)

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 <=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	117	6% 81% 15%
1	C	117	5% 92% 6%
2	B	139	14% 88% 9%
2	D	139	21% 81% 14%

2 Entry composition (i)

There are 3 unique types of molecules in this entry. The entry contains 4271 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 AcrIIC3.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	116	Total	C	N	O	S	0	0	0
			938	600	162	174	2			
1	C	116	Total	C	N	O	S	0	0	0
			938	600	162	174	2			

- Molecule 2 is a protein called CRISPR-associated endonuclease Cas9.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	138	Total	C	N	O	S	0	0	0
			1161	729	214	217	1			
2	D	138	Total	C	N	O	S	0	0	0
			1161	729	214	217	1			

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	517	GLY	-	expression tag	UNP A0A0T7L299
D	517	GLY	-	expression tag	UNP A0A0T7L299

- Molecule 3 is water.

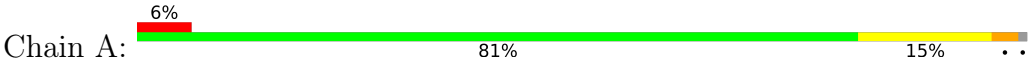
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	23	Total	O	0	0
			23	23		
3	B	16	Total	O	0	0
			16	16		
3	C	17	Total	O	0	0
			17	17		
3	D	17	Total	O	0	0
			17	17		

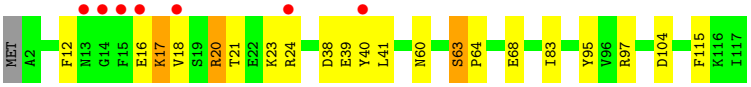
3 Residue-property plots (i)

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: AcrIIC3

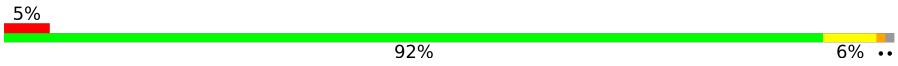
Chain A:

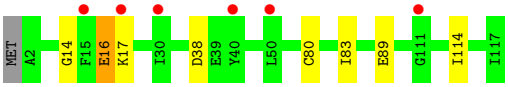




• Molecule 1: AcrIIC3

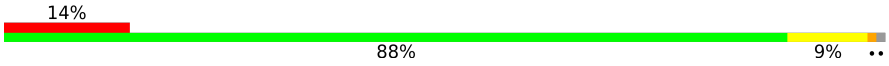
Chain C:

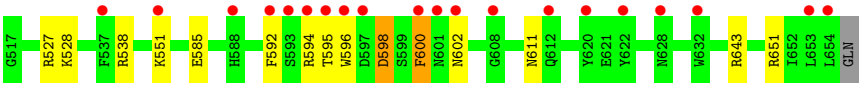




• Molecule 2: CRISPR-associated endonuclease Cas9

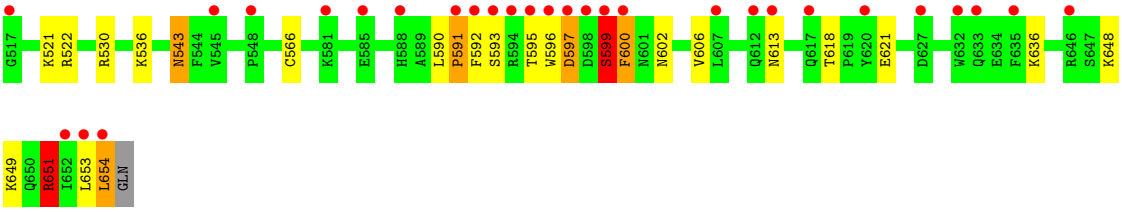
Chain B:





• Molecule 2: CRISPR-associated endonuclease Cas9

Chain D:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 43	Depositor
Cell constants a, b, c, α, β, γ	53.82Å 53.82Å 163.36Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	30.00 – 2.04 38.28 – 2.04	Depositor EDS
% Data completeness (in resolution range)	99.6 (30.00-2.04) 99.6 (38.28-2.04)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	1.17 (at 2.03Å)	Xtriage
Refinement program	REFMAC 5.8.0230	Depositor
R, R_{free}	0.219 , 0.239 0.227 , 0.249	Depositor DCC
R_{free} test set	1420 reflections (4.82%)	wwPDB-VP
Wilson B-factor (Å^2)	39.0	Xtriage
Anisotropy	0.048	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.32 , 25.2	EDS
L-test for twinning[2]	$< \|L\| > = 0.49$, $< L^2 > = 0.33$	Xtriage
Estimated twinning fraction	0.447 for h,-k,-l	Xtriage
F_o,F_c correlation	0.95	EDS
Total number of atoms	4271	wwPDB-VP
Average B, all atoms (Å^2)	46.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.79% of the height of the origin peak. No significant pseudotranslation is detected.*

[1] Intensities estimated from amplitudes.

[2] Theoretical values of $< |L| >$, $< L^2 >$ 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	0.73	1/954 (0.1%)	0.82	0/1280
1	C	0.77	0/954	0.78	0/1280
2	B	0.71	0/1185	0.75	1/1584 (0.1%)
2	D	0.90	2/1185 (0.2%)	0.83	2/1584 (0.1%)
All	All	0.78	3/4278 (0.1%)	0.79	3/5728 (0.1%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand.A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	2
1	C	0	1
2	B	0	1
2	D	0	2
All	All	0	6

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	D	591	PRO	N-CD	-18.76	1.21	1.47
2	D	597	ASP	C-O	5.40	1.33	1.23
1	A	39	GLU	CD-OE2	-5.30	1.19	1.25

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	D	593	SER	C-N-CA	-7.07	104.03	121.70
2	D	591	PRO	CA-N-CD	5.12	118.87	111.70
2	B	600	PHE	CB-CA-C	-5.02	100.36	110.40

There are no chirality outliers.

All (6) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	20	ARG	Sidechain
1	A	97	ARG	Sidechain
2	B	538	ARG	Sidechain
1	C	16	GLU	Peptide
2	D	599	SER	Peptide
2	D	651	ARG	Sidechain

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	938	0	942	18	0
1	C	938	0	942	6	0
2	B	1161	0	1139	19	0
2	D	1161	0	1139	28	0
3	A	23	0	0	0	0
3	B	16	0	0	4	0
3	C	17	0	0	0	0
3	D	17	0	0	1	0
All	All	4271	0	4162	63	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 8.

All (63) 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)
2:D:600:PHE:HB3	2:D:651:ARG:CD	1.92	0.99
2:D:600:PHE:CB	2:D:651:ARG:HD3	1.93	0.98
2:D:600:PHE:HB3	2:D:651:ARG:HD3	0.97	0.92
2:B:596:TRP:HE3	2:B:596:TRP:H	1.26	0.82
2:B:551:LYS:HD3	3:B:715:HOH:O	1.81	0.79
1:A:38:ASP:OD2	1:A:41:LEU:HD12	1.85	0.77
2:B:598:ASP:HA	2:B:600:PHE:CE1	2.20	0.77
2:D:592:PHE:HE2	2:D:596:TRP:CE3	2.03	0.75

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:D:596:TRP:HD1	2:D:597:ASP:OD2	1.73	0.72
2:B:551:LYS:CD	3:B:715:HOH:O	2.36	0.70
1:A:40:TYR:CE2	2:B:643:ARG:CZ	2.76	0.69
2:D:653:LEU:O	2:D:654:LEU:HB3	1.90	0.69
2:D:595:THR:HG21	2:D:599:SER:HB3	1.75	0.68
1:A:12:PHE:CD1	1:A:83:ILE:HD13	2.29	0.67
2:D:592:PHE:CZ	2:D:596:TRP:HA	2.30	0.67
2:B:585:GLU:OE1	2:B:611:ASN:ND2	2.26	0.65
2:D:592:PHE:CE2	2:D:596:TRP:CE3	2.85	0.63
2:D:521:LYS:HB3	2:D:522:ARG:HH12	1.64	0.63
2:B:585:GLU:CD	2:B:611:ASN:HD21	2.02	0.61
2:B:598:ASP:HA	2:B:600:PHE:HE1	1.65	0.60
2:B:600:PHE:HD2	2:B:602:ASN:H	1.49	0.60
2:B:551:LYS:CE	3:B:715:HOH:O	2.48	0.59
2:B:551:LYS:HE2	3:B:715:HOH:O	2.03	0.59
2:D:566:CYS:SG	2:D:606:VAL:HG13	2.43	0.58
2:B:600:PHE:HD2	2:B:602:ASN:N	2.00	0.58
2:B:527:ARG:CZ	1:C:114:ILE:HD12	2.34	0.57
2:B:598:ASP:HA	2:B:600:PHE:CD1	2.39	0.57
2:D:592:PHE:HE2	2:D:596:TRP:CZ3	2.23	0.57
2:B:596:TRP:N	2:B:596:TRP:CE3	2.70	0.57
2:D:618:THR:HG23	2:D:621:GLU:H	1.70	0.56
2:D:613:ASN:N	2:D:613:ASN:OD1	2.39	0.55
2:D:649:LYS:O	2:D:653:LEU:HD12	2.07	0.55
1:A:60:ASN:O	1:A:63:SER:OG	2.26	0.54
1:C:16:GLU:HG2	1:C:17:LYS:N	2.24	0.51
1:A:12:PHE:CE1	1:A:83:ILE:HD13	2.45	0.51
2:D:596:TRP:HD1	2:D:597:ASP:CG	2.15	0.50
2:D:649:LYS:O	2:D:653:LEU:CD1	2.60	0.50
1:A:12:PHE:CE1	1:A:83:ILE:CD1	2.95	0.49
2:D:521:LYS:HB3	2:D:522:ARG:NH1	2.27	0.49
1:A:40:TYR:CE2	2:B:643:ARG:NH1	2.81	0.49
2:B:600:PHE:HA	2:B:651:ARG:NH1	2.29	0.47
1:A:115:PHE:C	1:A:115:PHE:CD1	2.88	0.47
1:A:18:VAL:HG23	1:A:23:LYS:HD2	1.98	0.45
1:A:21:THR:HB	2:D:543:ASN:HB3	1.99	0.45
2:D:590:LEU:HA	2:D:591:PRO:HD3	1.71	0.45
2:D:595:THR:OG1	2:D:599:SER:HA	2.17	0.45
1:C:80:CYS:SG	1:C:83:ILE:HB	2.57	0.44
1:A:40:TYR:CD2	2:B:643:ARG:CZ	3.01	0.44
1:A:16:GLU:CD	1:A:16:GLU:H	2.21	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:64:PRO:O	1:A:68:GLU:HG3	2.17	0.44
2:B:595:THR:O	2:B:596:TRP:C	2.54	0.43
1:A:16:GLU:CD	1:A:16:GLU:N	2.72	0.43
1:C:14:GLY:HA3	1:C:17:LYS:HG2	2.00	0.43
1:C:38:ASP:OD1	2:D:536:LYS:NZ	2.51	0.42
1:A:24:ARG:HD2	2:D:543:ASN:OD1	2.19	0.42
2:D:618:THR:HG22	2:D:621:GLU:CD	2.39	0.42
2:D:648:LYS:NZ	3:D:703:HOH:O	2.51	0.42
1:C:89:GLU:HG2	1:C:114:ILE:HD11	2.02	0.42
2:D:596:TRP:CD1	2:D:597:ASP:CG	2.93	0.42
1:A:95:TYR:OH	1:A:104:ASP:OD1	2.31	0.42
1:A:17:LYS:HE3	1:A:17:LYS:HA	2.03	0.41
2:D:595:THR:CG2	2:D:599:SER:HB3	2.44	0.41
1:A:24:ARG:CD	2:D:543:ASN:OD1	2.69	0.40

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	114/117 (97%)	113 (99%)	1 (1%)	0	100	100
1	C	114/117 (97%)	109 (96%)	5 (4%)	0	100	100
2	B	136/139 (98%)	130 (96%)	6 (4%)	0	100	100
2	D	136/139 (98%)	127 (93%)	8 (6%)	1 (1%)	22	12
All	All	500/512 (98%)	479 (96%)	20 (4%)	1 (0%)	47	39

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	D	600	PHE

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	97/98 (99%)	94 (97%)	3 (3%)	40	33
1	C	97/98 (99%)	97 (100%)	0	100	100
2	B	124/125 (99%)	120 (97%)	4 (3%)	39	32
2	D	124/125 (99%)	117 (94%)	7 (6%)	21	12
All	All	442/446 (99%)	428 (97%)	14 (3%)	39	32

All (14) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	17	LYS
1	A	20	ARG
1	A	63	SER
2	B	528	LYS
2	B	592	PHE
2	B	594	ARG
2	B	598	ASP
2	D	530	ARG
2	D	543	ASN
2	D	599	SER
2	D	602	ASN
2	D	636	LYS
2	D	651	ARG
2	D	654	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (1) such sidechains are listed below:

Mol	Chain	Res	Type
2	D	601	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 monosaccharides 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, 95^{th} 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	116/117 (99%)	0.73	7 (6%)	21	23	28, 39, 57, 111	0
1	C	116/117 (99%)	0.58	6 (5%)	27	29	28, 39, 57, 82	0
2	B	138/139 (99%)	1.19	20 (14%)	2	2	30, 48, 77, 108	0
2	D	138/139 (99%)	1.25	29 (21%)	1	0	31, 47, 80, 96	0
All	All	508/512 (99%)	0.96	62 (12%)	4	3	28, 43, 73, 111	0

All (62) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	B	596	TRP	12.2
1	A	15	PHE	11.7
2	D	593	SER	9.6
2	B	600	PHE	9.5
2	D	596	TRP	8.6
2	D	597	ASP	7.8
2	B	595	THR	7.3
2	B	597	ASP	6.8
2	B	594	ARG	6.3
2	B	592	PHE	5.9
2	D	654	LEU	5.2
2	B	593	SER	4.8
2	D	598	ASP	4.7
2	B	608	GLY	4.2
2	D	653	LEU	4.1
1	A	18	VAL	3.8
2	D	592	PHE	3.7
2	D	612	GLN	3.5
1	C	40	TYR	3.5
2	D	652	ILE	3.3
1	C	17	LYS	3.2

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Mol	Chain	Res	Type	RSRZ
2	D	585	GLU	3.1
2	D	632	TRP	3.1
2	D	594	ARG	3.0
2	D	599	SER	3.0
2	D	591	PRO	2.8
2	D	613	ASN	2.8
1	C	15	PHE	2.8
2	B	612	GLN	2.8
1	A	14	GLY	2.8
1	A	13	ASN	2.6
2	B	602	ASN	2.5
2	D	627	ASP	2.5
2	B	601	ASN	2.5
2	D	548	PRO	2.5
1	C	30	ILE	2.5
2	D	595	THR	2.5
1	C	50	LEU	2.5
2	D	600	PHE	2.5
2	B	588	HIS	2.4
2	B	620	TYR	2.4
2	D	517	GLY	2.4
2	B	537	PHE	2.3
2	D	646	ARG	2.3
1	A	40	TYR	2.3
2	B	654	LEU	2.3
2	D	607	LEU	2.3
2	B	628	ASN	2.2
2	B	551	LYS	2.2
2	D	545	VAL	2.2
1	C	111	GLY	2.2
2	D	633	GLN	2.1
2	B	632	TRP	2.1
2	D	635	PHE	2.1
2	D	581	LYS	2.1
1	A	24	ARG	2.1
2	D	588	HIS	2.1
2	B	653	LEU	2.1
1	A	16	GLU	2.1
2	B	622	TYR	2.0
2	D	617	GLN	2.0
2	D	620	TYR	2.0

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 monosaccharides 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.