



# Full wwPDB X-ray Structure Validation Report ⓘ

Sep 24, 2017 – 08:05 PM EDT

PDB ID : 5N99  
Title : CRYSTAL STRUCTURE OF STREPTAVIDIN with cyclic peptide NQpWQ  
Authors : Lyamichev, V.; Goodrich, L.; Sullivan, E.; Bannen, R.; Benz, J.; Albert, T.; Patel, J.  
Deposited on : unknown  
Resolution : 1.50 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](mailto:validation@mail.wwpdb.org)

A user guide is available at

<http://wwpdb.org/validation/2016/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

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The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity : 4.02b-467  
Mogul : 1.7.2 (RC1), CSD as538be (2017)  
Xtriage (Phenix) : 1.9-1692  
EDS : rb-20029824  
Percentile statistics : 20161228.v01 (using entries in the PDB archive December 28th 2016)  
Refmac : 5.8.0135  
CCP4 : 6.5.0  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : rb-20029824

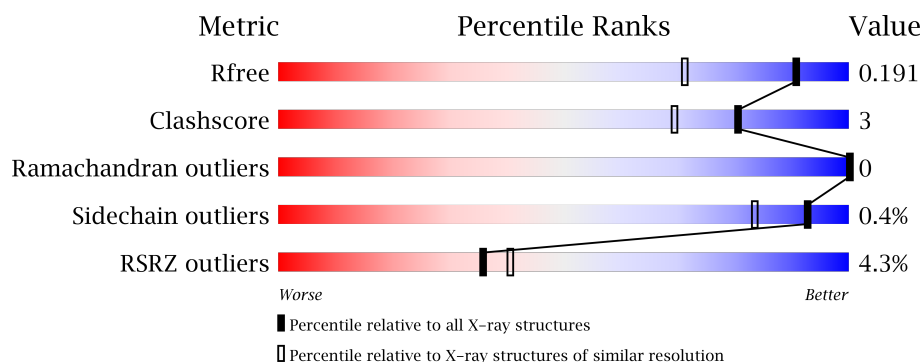
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 1.50 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.






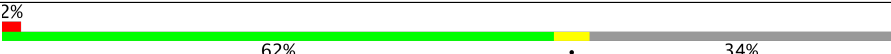
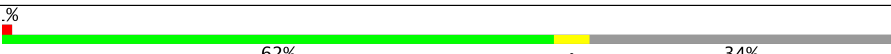
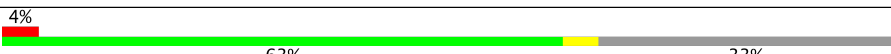
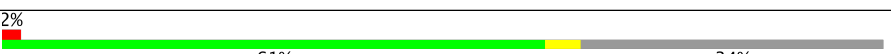
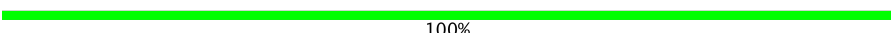

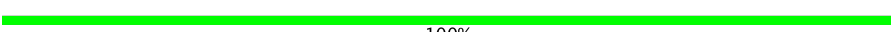
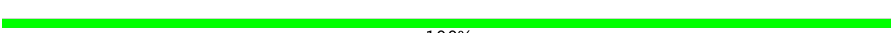








Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
$R_{free}$	100719	2279 (1.50-1.50)
Clashscore	112137	2503 (1.50-1.50)
Ramachandran outliers	110173	2445 (1.50-1.50)
Sidechain outliers	110143	2443 (1.50-1.50)
RSRZ outliers	101464	2305 (1.50-1.50)

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 on the lower bar indicate the fraction of residues that contain outliers for  $\geq 3$ , 2, 1 and 0 types of geometric quality criteria. 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	183	<div> <div>0.1%</div> <div>62%</div> <div>33%</div> </div>
1	B	183	<div> <div>4%</div> <div>63%</div> <div>33%</div> </div>
1	D	183	<div> <div>62%</div> <div>33%</div> </div>
1	G	183	<div> <div>2%</div> <div>61%</div> <div>5%</div> <div>34%</div> </div>
1	I	183	<div> <div>2%</div> <div>61%</div> <div>34%</div> </div>

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Mol	Chain	Length	Quality of chain
1	K	183	
1	M	183	
1	O	183	
1	Q	183	
1	S	183	
1	U	183	
1	Y	183	
2	C	5	
2	E	5	
2	F	5	
2	H	5	
2	J	5	
2	L	5	
2	N	5	
2	P	5	
2	R	5	
2	T	5	
2	V	5	
2	X	5	

## 2 Entry composition [i](#)

There are 3 unique types of molecules in this entry. The entry contains 13995 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 Streptavidin.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
1	A	122	Total	C	N	O	0	10	0
			954	605	158	191			
1	B	123	Total	C	N	O	0	11	0
			966	610	160	196			
1	D	122	Total	C	N	O	0	10	0
			949	600	158	191			
1	G	121	Total	C	N	O	0	9	0
			945	596	157	192			
1	I	120	Total	C	N	O	0	9	0
			939	595	156	188			
1	K	120	Total	C	N	O	0	8	0
			930	587	156	187			
1	M	120	Total	C	N	O	0	9	0
			941	597	156	188			
1	O	120	Total	C	N	O	0	8	0
			930	587	156	187			
1	Q	120	Total	C	N	O	0	9	0
			936	592	156	188			
1	S	121	Total	C	N	O	0	8	0
			937	592	157	188			
1	U	122	Total	C	N	O	0	11	0
			960	608	158	194			
1	Y	120	Total	C	N	O	0	10	0
			940	595	156	189			

- Molecule 2 is a protein called ASN-GLN-DPR-TRP-GLN.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
2	C	5	Total	C	N	O	0	0	0
			47	30	9	8			
2	E	5	Total	C	N	O	0	0	0
			47	30	9	8			

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Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
2	F	5	Total	C	N	O	0	0	0
			47	30	9	8			
2	H	5	Total	C	N	O	0	0	0
			47	30	9	8			
2	J	5	Total	C	N	O	0	0	0
			47	30	9	8			
2	L	5	Total	C	N	O	0	0	0
			47	30	9	8			
2	N	5	Total	C	N	O	0	0	0
			47	30	9	8			
2	P	5	Total	C	N	O	0	0	0
			47	30	9	8			
2	R	5	Total	C	N	O	0	0	0
			47	30	9	8			
2	T	5	Total	C	N	O	0	1	0
			53	34	10	9			
2	V	5	Total	C	N	O	0	0	0
			47	30	9	8			
2	X	5	Total	C	N	O	0	0	0
			47	30	9	8			

- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	181	Total	O	0	2
			183	183		
3	B	170	Total	O	0	1
			171	171		
3	C	11	Total	O	0	0
			11	11		
3	D	186	Total	O	0	2
			188	188		
3	E	6	Total	O	0	0
			6	6		
3	F	8	Total	O	0	0
			8	8		
3	G	176	Total	O	0	2
			178	178		
3	H	4	Total	O	0	0
			4	4		
3	I	178	Total	O	0	1
			179	179		

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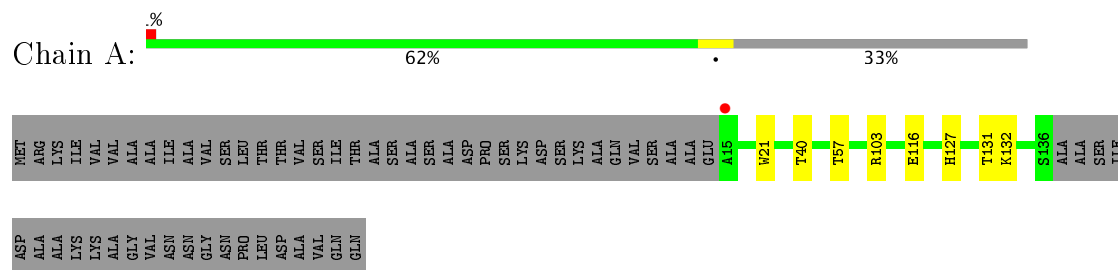
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	J	9	Total 9	O 9	0	0
3	K	162	Total 163	O 163	0	1
3	L	7	Total 7	O 7	0	0
3	M	154	Total 154	O 154	0	0
3	N	4	Total 4	O 4	0	0
3	O	121	Total 121	O 121	0	0
3	P	6	Total 6	O 6	0	0
3	Q	174	Total 175	O 175	0	1
3	R	10	Total 10	O 10	0	0
3	S	180	Total 184	O 184	0	4
3	T	8	Total 8	O 8	0	0
3	U	149	Total 151	O 151	0	2
3	V	8	Total 8	O 8	0	0
3	X	6	Total 6	O 6	0	0
3	Y	162	Total 164	O 164	0	2

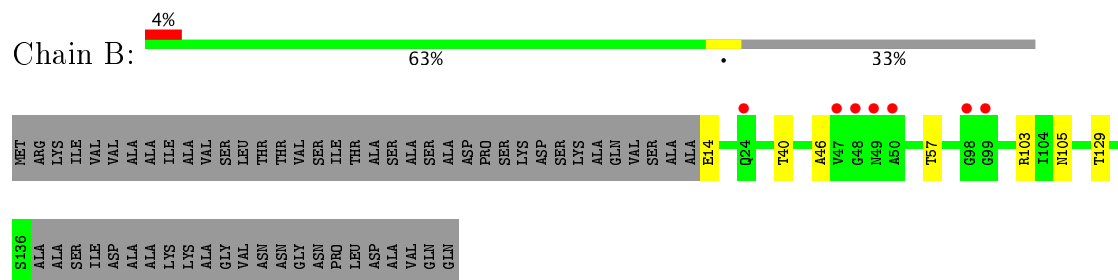
### 3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA and DNA 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.

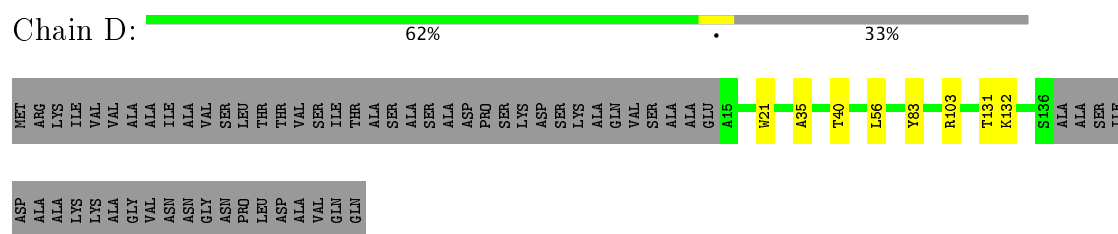
- Molecule 1: Streptavidin



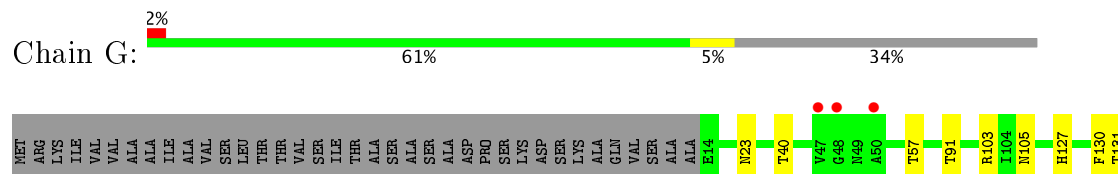
- Molecule 1: Streptavidin



- Molecule 1: Streptavidin

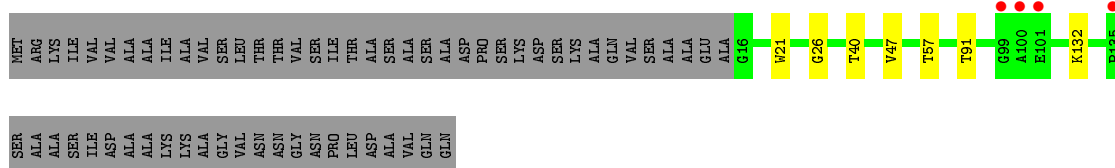


- Molecule 1: Streptavidin

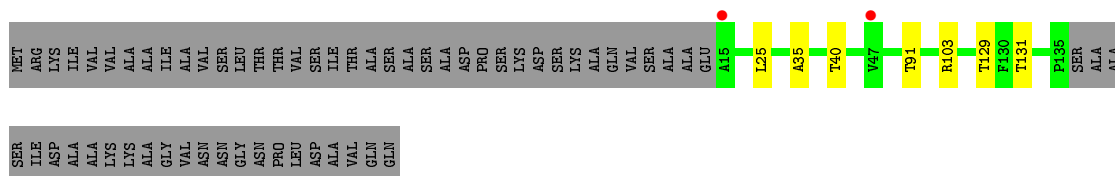




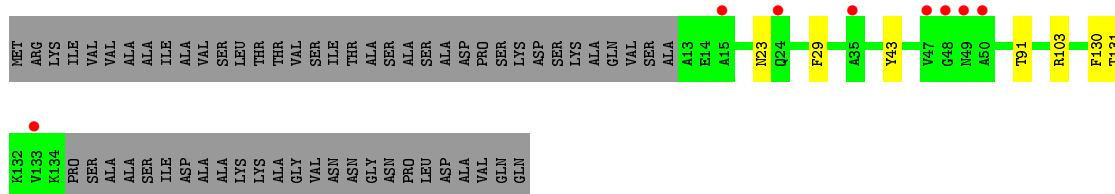




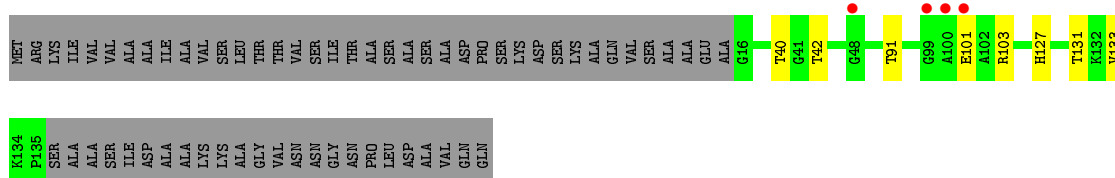
- Molecule 1: Streptavidin



- Molecule 1: Streptavidin



- Molecule 1: Streptavidin



- Molecule 2: ASN-GLN-DPR-TRP-GLN



There are no outlier residues recorded for this chain.

- Molecule 2: ASN-GLN-DPR-TRP-GLN



- Molecule 2: ASN-GLN-DPR-TRP-GLN

Chain F:  100%

There are no outlier residues recorded for this chain.

- Molecule 2: ASN-GLN-DPR-TRP-GLN

Chain H:  100%

There are no outlier residues recorded for this chain.

- Molecule 2: ASN-GLN-DPR-TRP-GLN

Chain J:  100%

There are no outlier residues recorded for this chain.

- Molecule 2: ASN-GLN-DPR-TRP-GLN

Chain L:  100%

There are no outlier residues recorded for this chain.

- Molecule 2: ASN-GLN-DPR-TRP-GLN

Chain N:  20% 100%



- Molecule 2: ASN-GLN-DPR-TRP-GLN

Chain P:  100%


There are no outlier residues recorded for this chain.

- Molecule 2: ASN-GLN-DPR-TRP-GLN

Chain R:  100%

There are no outlier residues recorded for this chain.

- Molecule 2: ASN-GLN-DPR-TRP-GLN

Chain T:  80% 20%



- Molecule 2: ASN-GLN-DPR-TRP-GLN

Chain V:  100%

There are no outlier residues recorded for this chain.

- Molecule 2: ASN-GLN-DPR-TRP-GLN

Chain X:  100%

There are no outlier residues recorded for this chain.

## 4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	67.74Å 115.31Å 210.37Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	48.72 – 1.50 48.72 – 1.50	Depositor EDS
% Data completeness (in resolution range)	99.5 (48.72-1.50) 99.7 (48.72-1.50)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	0.08	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.47 (at 1.50Å)	Xtriage
Refinement program	BUSTER 2.11.6	Depositor
R, $R_{free}$	0.167 , 0.192 0.168 , 0.191	Depositor DCC
$R_{free}$ test set	12914 reflections (5.20%)	DCC
Wilson B-factor (Å <sup>2</sup> )	16.5	Xtriage
Anisotropy	0.319	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.31 , 43.0	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.49$ , $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.97	EDS
Total number of atoms	13995	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	23.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.23% of the height of the origin peak. No significant pseudotranslation is detected.*

<sup>1</sup>Intensities estimated from amplitudes.

<sup>2</sup>Theoretical 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: DPR

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	0.56	0/1006	0.72	0/1379
1	B	0.53	0/1023	0.71	0/1402
1	D	0.52	0/1000	0.69	0/1371
1	G	0.54	0/992	0.71	0/1358
1	I	0.54	0/987	0.69	0/1352
1	K	0.53	0/974	0.71	0/1334
1	M	0.50	0/990	0.70	0/1357
1	O	0.46	0/974	0.67	0/1334
1	Q	0.49	0/984	0.67	0/1349
1	S	0.51	0/982	0.69	0/1346
1	U	0.49	0/1014	0.68	0/1389
1	Y	0.50	0/991	0.66	0/1359
2	C	0.55	0/40	0.68	0/52
2	E	0.54	0/40	0.70	0/52
2	F	0.47	0/40	0.66	0/52
2	H	0.52	0/40	0.63	0/52
2	J	0.56	0/40	0.66	0/52
2	L	0.43	0/40	0.60	0/52
2	N	0.43	0/40	0.63	0/52
2	P	0.44	0/40	0.65	0/52
2	R	0.57	0/40	0.77	0/52
2	T	0.44	0/48	0.91	0/61
2	V	0.42	0/40	0.67	0/52
2	X	0.49	0/40	0.76	0/52
All	All	0.51	0/12405	0.69	0/16963

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 ⓘ

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	954	0	913	8	0
1	B	966	0	929	10	0
1	D	949	0	911	4	0
1	G	945	0	902	8	0
1	I	939	0	899	8	0
1	K	930	0	890	3	0
1	M	941	0	901	8	0
1	O	930	0	890	4	0
1	Q	936	0	899	6	0
1	S	937	0	897	7	0
1	U	960	0	922	4	0
1	Y	940	0	906	7	0
2	C	47	0	39	0	0
2	E	47	0	39	1	0
2	F	47	0	39	0	0
2	H	47	0	39	0	0
2	J	47	0	39	0	0
2	L	47	0	39	0	0
2	N	47	0	39	0	0
2	P	47	0	39	0	0
2	R	47	0	39	0	0
2	T	53	0	47	1	0
2	V	47	0	39	0	0
2	X	47	0	39	0	0
3	A	183	0	0	4	0
3	B	171	0	0	1	0
3	C	11	0	0	0	0
3	D	188	0	0	2	0
3	E	6	0	0	0	0
3	F	8	0	0	0	0
3	G	178	0	0	2	0
3	H	4	0	0	0	0
3	I	179	0	0	3	0
3	J	9	0	0	0	0
3	K	163	0	0	2	0
3	L	7	0	0	0	0
3	M	154	0	0	2	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	N	4	0	0	0	0
3	O	121	0	0	1	0
3	P	6	0	0	0	0
3	Q	175	0	0	2	0
3	R	10	0	0	0	0
3	S	184	0	0	1	0
3	T	8	0	0	0	0
3	U	151	0	0	0	0
3	V	8	0	0	0	0
3	X	6	0	0	0	0
3	Y	164	0	0	4	0
All	All	13995	0	11335	71	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 3.

All (71) 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:103:ARG:HH21	1:B:129[B]:THR:CG2	1.85	0.88
3:K:282:HOH:O	1:Q:57[B]:THR:HG21	1.85	0.76
1:A:57[B]:THR:HG21	3:M:268:HOH:O	1.86	0.76
1:B:103:ARG:HH21	1:B:129[B]:THR:HG22	1.50	0.74
1:B:57[B]:THR:HG21	3:D:315:HOH:O	1.91	0.70
1:B:103:ARG:HH21	1:B:129[B]:THR:HG21	1.55	0.70
1:G:103:ARG:HE	1:G:105:ASN:HD21	1.38	0.69
1:M:103:ARG:HH21	1:M:129[B]:THR:CG2	2.10	0.65
1:Y:42[A]:THR:HG22	3:Y:336:HOH:O	1.98	0.63
1:S:103:ARG:HG2	1:S:131[A]:THR:HG22	1.82	0.60
1:Q:40[A]:THR:HG22	3:Q:220:HOH:O	2.02	0.59
1:S:103:ARG:HE	1:S:129[B]:THR:CG2	2.15	0.58
1:A:103:ARG:HG2	1:A:131:THR:HG22	1.85	0.58
1:I:103:ARG:HH21	1:I:129[B]:THR:CG2	2.16	0.58
1:I:103:ARG:HG2	1:I:131:THR:HG22	1.84	0.58
1:B:103:ARG:NH2	1:B:129[B]:THR:CG2	2.64	0.57
1:Y:131[B]:THR:HG22	1:Y:133:VAL:H	1.70	0.57
1:Q:57[B]:THR:HG22	3:Q:328:HOH:O	2.05	0.56
1:B:103:ARG:NH2	1:B:129[B]:THR:HG21	2.21	0.56
1:G:40[B]:THR:HG23	3:G:222:HOH:O	2.06	0.56
1:U:103:ARG:CD	1:U:131[A]:THR:HG22	2.37	0.54
1:S:103:ARG:HE	1:S:129[B]:THR:HG21	1.73	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:M:103:ARG:HH21	1:M:129[B]:THR:HG22	1.72	0.53
1:M:103:ARG:HG2	1:M:131:THR:HG22	1.90	0.52
1:A:57[B]:THR:HG22	3:A:258:HOH:O	2.10	0.52
1:I:40[B]:THR:HG23	3:I:223:HOH:O	2.09	0.52
1:G:131:THR:OG1	1:G:133:VAL:HG22	2.10	0.51
1:Y:131[B]:THR:HG21	3:Y:309:HOH:O	2.10	0.51
1:M:21:TRP:CZ2	1:M:132:LYS:HE3	2.45	0.51
1:B:40[B]:THR:HG23	3:B:236:HOH:O	2.11	0.50
1:S:40[B]:THR:HG23	3:S:287:HOH:O	2.11	0.50
1:Y:127:HIS:HD2	3:Y:324:HOH:O	1.94	0.50
1:B:105:ASN:OD1	1:B:129[B]:THR:HG23	2.12	0.49
1:K:40[A]:THR:HG22	3:K:218[A]:HOH:O	2.12	0.49
1:D:103:ARG:HG2	1:D:131[A]:THR:HG22	1.94	0.48
1:B:103:ARG:NH2	1:B:129[B]:THR:HG22	2.24	0.48
1:D:40[B]:THR:HG23	3:D:266:HOH:O	2.12	0.48
1:M:103:ARG:HH21	1:M:129[B]:THR:HG21	1.79	0.47
1:A:21:TRP:CZ2	1:A:132:LYS:HE3	2.50	0.47
1:G:57[A]:THR:HG21	3:I:304:HOH:O	2.15	0.47
1:I:103:ARG:HH21	1:I:129[B]:THR:HG21	1.78	0.46
1:G:103:ARG:NE	1:G:105:ASN:HD21	2.10	0.46
1:K:91:THR:HB	1:Q:91:THR:HB	1.97	0.46
1:U:29:PHE:HB3	1:U:43[A]:TYR:CD1	2.51	0.45
1:O:91:THR:HB	1:Y:91:THR:HB	1.99	0.45
1:A:40[B]:THR:HG23	3:A:258:HOH:O	2.16	0.45
1:I:103:ARG:HH21	1:I:129[B]:THR:HG22	1.80	0.45
1:I:28:THR:HG22	3:I:255:HOH:O	2.17	0.45
3:A:299:HOH:O	1:M:57[B]:THR:HG21	2.15	0.45
1:M:23:ASN:HB3	1:M:130:PHE:CE2	2.51	0.45
1:S:91:THR:HB	1:U:91:THR:HB	2.00	0.44
1:A:116:GLU:HG2	3:M:328:HOH:O	2.16	0.44
1:A:127:HIS:HD2	3:A:340:HOH:O	2.00	0.44
1:O:127:HIS:HD2	3:O:293:HOH:O	2.01	0.43
1:D:35:ALA:HB1	1:S:35:ALA:HB1	2.00	0.43
1:G:23:ASN:HB3	1:G:130:PHE:CE2	2.54	0.43
1:A:57[B]:THR:HG23	1:M:59:ARG:HD3	2.00	0.43
1:D:21:TRP:CZ2	1:D:132:LYS:HE3	2.54	0.43
1:Q:21:TRP:CZ2	1:Q:132:LYS:HE3	2.54	0.42
1:O:23:ASN:HB3	1:O:130:PHE:CE2	2.54	0.42
1:Q:26:GLY:O	1:Q:47:VAL:HG23	2.20	0.42
1:U:23:ASN:HB3	1:U:130:PHE:CE2	2.55	0.42
1:O:21:TRP:CZ2	1:O:132:LYS:HE3	2.54	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:91:THR:HB	1:I:91:THR:HB	2.02	0.42
1:I:29:PHE:HB3	1:I:43[A]:TYR:CD1	2.54	0.42
1:K:23:ASN:HB3	1:K:130:PHE:CE2	2.55	0.41
1:Y:103:ARG:HG2	1:Y:131[A]:THR:HG22	2.02	0.41
1:B:46:ALA:HB2	2:E:3:DPR:HG2	2.03	0.40
1:S:25:LEU:HD13	2:T:2[B]:GLN:HE21	1.85	0.40
1:Y:40[B]:THR:HG23	3:Y:221:HOH:O	2.21	0.40
1:G:127:HIS:HD2	3:G:323:HOH:O	2.04	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	129/183 (70%)	128 (99%)	1 (1%)	0	100	100
1	B	132/183 (72%)	130 (98%)	2 (2%)	0	100	100
1	D	129/183 (70%)	127 (98%)	2 (2%)	0	100	100
1	G	127/183 (69%)	127 (100%)	0	0	100	100
1	I	126/183 (69%)	125 (99%)	1 (1%)	0	100	100
1	K	125/183 (68%)	122 (98%)	3 (2%)	0	100	100
1	M	126/183 (69%)	125 (99%)	1 (1%)	0	100	100
1	O	125/183 (68%)	123 (98%)	2 (2%)	0	100	100
1	Q	126/183 (69%)	123 (98%)	3 (2%)	0	100	100
1	S	126/183 (69%)	126 (100%)	0	0	100	100
1	U	130/183 (71%)	128 (98%)	2 (2%)	0	100	100
1	Y	127/183 (69%)	124 (98%)	3 (2%)	0	100	100
2	C	2/5 (40%)	2 (100%)	0	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	E	2/5 (40%)	2 (100%)	0	0	100	100
2	F	2/5 (40%)	2 (100%)	0	0	100	100
2	H	2/5 (40%)	2 (100%)	0	0	100	100
2	J	2/5 (40%)	2 (100%)	0	0	100	100
2	L	2/5 (40%)	2 (100%)	0	0	100	100
2	N	2/5 (40%)	2 (100%)	0	0	100	100
2	P	2/5 (40%)	2 (100%)	0	0	100	100
2	R	2/5 (40%)	2 (100%)	0	0	100	100
2	T	3/5 (60%)	3 (100%)	0	0	100	100
2	V	2/5 (40%)	2 (100%)	0	0	100	100
2	X	2/5 (40%)	2 (100%)	0	0	100	100
All	All	1553/2256 (69%)	1533 (99%)	20 (1%)	0	100	100

There are no Ramachandran outliers to report.

### 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	98/134 (73%)	98 (100%)	0	100	100
1	B	101/134 (75%)	100 (99%)	1 (1%)	80	60
1	D	98/134 (73%)	96 (98%)	2 (2%)	60	28
1	G	97/134 (72%)	97 (100%)	0	100	100
1	I	96/134 (72%)	96 (100%)	0	100	100
1	K	95/134 (71%)	95 (100%)	0	100	100
1	M	97/134 (72%)	97 (100%)	0	100	100
1	O	95/134 (71%)	95 (100%)	0	100	100
1	Q	97/134 (72%)	97 (100%)	0	100	100
1	S	96/134 (72%)	96 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	U	99/134 (74%)	99 (100%)	0	100	100
1	Y	98/134 (73%)	97 (99%)	1 (1%)	80	60
2	C	4/4 (100%)	4 (100%)	0	100	100
2	E	4/4 (100%)	4 (100%)	0	100	100
2	F	4/4 (100%)	4 (100%)	0	100	100
2	H	4/4 (100%)	4 (100%)	0	100	100
2	J	4/4 (100%)	4 (100%)	0	100	100
2	L	4/4 (100%)	4 (100%)	0	100	100
2	N	4/4 (100%)	4 (100%)	0	100	100
2	P	4/4 (100%)	4 (100%)	0	100	100
2	R	4/4 (100%)	4 (100%)	0	100	100
2	T	5/4 (125%)	5 (100%)	0	100	100
2	V	4/4 (100%)	4 (100%)	0	100	100
2	X	4/4 (100%)	4 (100%)	0	100	100
All	All	1216/1656 (73%)	1212 (100%)	4 (0%)	93	86

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

Mol	Chain	Res	Type
1	B	14	GLU
1	D	56	LEU
1	D	83	TYR
1	Y	101	GLU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (32) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	24	GLN
1	A	82	ASN
1	A	127	HIS
1	B	82	ASN
2	C	5	GLN
1	D	82	ASN
2	E	5	GLN
2	F	5	GLN
1	G	82	ASN

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Mol	Chain	Res	Type
1	G	105	ASN
1	G	127	HIS
2	H	5	GLN
1	I	127	HIS
2	J	5	GLN
1	K	82	ASN
2	L	5	GLN
1	M	82	ASN
1	M	127	HIS
2	N	5	GLN
1	O	49	ASN
1	O	127	HIS
2	P	5	GLN
1	Q	82	ASN
2	R	5	GLN
1	S	82	ASN
2	T	5	GLN
1	U	82	ASN
1	U	127	HIS
2	V	5	GLN
2	X	5	GLN
1	Y	82	ASN
1	Y	127	HIS

### 5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

12 non-standard protein/DNA/RNA residues 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	DPR	C	3	2	6,7,8	0.88	0	7,8,10	1.29	2 (28%)
2	DPR	E	3	2	6,7,8	0.82	0	7,8,10	1.32	1 (14%)
2	DPR	F	3	2	6,7,8	0.95	0	7,8,10	1.31	1 (14%)
2	DPR	H	3	2	6,7,8	0.92	0	7,8,10	1.20	1 (14%)
2	DPR	J	3	2	6,7,8	0.98	0	7,8,10	1.11	0
2	DPR	L	3	2	6,7,8	1.12	1 (16%)	7,8,10	1.14	1 (14%)
2	DPR	N	3	2	6,7,8	1.10	1 (16%)	7,8,10	1.16	0
2	DPR	P	3	2	6,7,8	1.17	1 (16%)	7,8,10	1.14	0
2	DPR	R	3	2	6,7,8	0.67	0	7,8,10	1.22	1 (14%)
2	DPR	T	3	2	6,7,8	0.70	0	7,8,10	1.34	1 (14%)
2	DPR	V	3	2	6,7,8	0.95	0	7,8,10	1.18	0
2	DPR	X	3	2	6,7,8	0.99	0	7,8,10	1.25	0

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the chemical component dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	DPR	C	3	2	-	0/0/9/11	0/1/1/1
2	DPR	E	3	2	-	0/0/9/11	0/1/1/1
2	DPR	F	3	2	-	0/0/9/11	0/1/1/1
2	DPR	H	3	2	-	0/0/9/11	0/1/1/1
2	DPR	J	3	2	-	0/0/9/11	0/1/1/1
2	DPR	L	3	2	-	0/0/9/11	0/1/1/1
2	DPR	N	3	2	-	0/0/9/11	0/1/1/1
2	DPR	P	3	2	-	0/0/9/11	0/1/1/1
2	DPR	R	3	2	-	0/0/9/11	0/1/1/1
2	DPR	T	3	2	-	0/0/9/11	0/1/1/1
2	DPR	V	3	2	-	0/0/9/11	0/1/1/1
2	DPR	X	3	2	-	0/0/9/11	0/1/1/1

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	L	3	DPR	CA-C	2.27	1.53	1.50
2	N	3	DPR	CA-C	2.50	1.53	1.50

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	P	3	DPR	CA-C	2.50	1.53	1.50

All (8) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	T	3	DPR	O-C-CA	-2.44	119.45	125.15
2	F	3	DPR	O-C-CA	-2.24	119.93	125.15
2	H	3	DPR	O-C-CA	-2.15	120.13	125.15
2	C	3	DPR	O-C-CA	-2.05	120.37	125.15
2	L	3	DPR	O-C-CA	-2.01	120.47	125.15
2	R	3	DPR	CD-N-CA	2.07	112.69	107.13
2	C	3	DPR	CD-N-CA	2.09	112.75	107.13
2	E	3	DPR	CD-N-CA	2.17	112.98	107.13

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	E	3	DPR	1	0

## 5.5 Carbohydrates [i](#)

There are no carbohydrates 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 i

### 6.1 Protein, DNA and RNA chains i

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<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
1	A	122/183 (66%)	-0.25	1 (0%) 86 88	11, 16, 35, 63	2 (1%)
1	B	123/183 (67%)	-0.02	7 (5%) 24 28	11, 18, 41, 61	2 (1%)
1	D	122/183 (66%)	-0.29	0 100 100	11, 16, 29, 62	2 (1%)
1	G	121/183 (66%)	-0.05	4 (3%) 47 52	11, 17, 40, 70	2 (1%)
1	I	120/183 (65%)	-0.21	4 (3%) 47 52	11, 16, 32, 80	2 (1%)
1	K	120/183 (65%)	-0.02	8 (6%) 19 21	12, 20, 48, 76	2 (1%)
1	M	120/183 (65%)	0.22	10 (8%) 12 14	13, 20, 50, 63	2 (1%)
1	O	120/183 (65%)	0.19	12 (10%) 8 9	14, 25, 58, 74	2 (1%)
1	Q	120/183 (65%)	-0.17	4 (3%) 47 52	12, 20, 40, 57	2 (1%)
1	S	121/183 (66%)	-0.36	2 (1%) 70 75	13, 18, 29, 47	2 (1%)
1	U	122/183 (66%)	0.12	8 (6%) 19 22	13, 20, 48, 86	2 (1%)
1	Y	120/183 (65%)	-0.17	4 (3%) 47 52	13, 21, 40, 57	2 (1%)
2	C	4/5 (80%)	-0.30	0 100 100	13, 14, 14, 21	0
2	E	4/5 (80%)	-0.35	0 100 100	16, 16, 23, 30	0
2	F	4/5 (80%)	-0.29	0 100 100	14, 16, 16, 23	0
2	H	4/5 (80%)	-0.18	0 100 100	16, 18, 23, 28	0
2	J	4/5 (80%)	-0.45	0 100 100	16, 17, 20, 26	0
2	L	4/5 (80%)	-0.38	0 100 100	19, 22, 28, 29	0
2	N	4/5 (80%)	0.45	1 (25%) 1 1	21, 23, 29, 34	0
2	P	4/5 (80%)	-0.03	0 100 100	24, 25, 30, 39	0
2	R	4/5 (80%)	-0.52	0 100 100	14, 14, 15, 29	0
2	T	4/5 (80%)	-0.37	0 100 100	16, 17, 21, 27	0
2	V	4/5 (80%)	0.10	0 100 100	20, 21, 28, 36	0
2	X	4/5 (80%)	-0.43	0 100 100	16, 18, 18, 30	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2		OWAB(Å <sup>2</sup> )	Q<0.9
All	All	1499/2256 (66%)	-0.09	65 (4%)	36 41	11, 19, 42, 86	24 (1%)

All (65) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	U	47	VAL	11.6
1	U	48	GLY	11.0
1	G	47	VAL	9.5
1	M	47	VAL	9.4
1	O	47	VAL	8.9
1	M	48	GLY	8.7
1	Y	100	ALA	7.6
1	K	47	VAL	7.0
1	G	48	GLY	7.0
1	Q	100	ALA	6.0
1	O	100	ALA	5.4
1	K	48	GLY	5.4
1	O	15	ALA	4.8
1	O	48	GLY	4.4
1	S	15	ALA	4.3
1	A	15	ALA	4.2
1	K	50	ALA	4.1
1	U	50	ALA	3.9
1	M	134	LYS	3.7
1	B	24	GLN	3.6
1	G	133	VAL	3.6
1	B	50	ALA	3.5
1	I	24	GLN	3.5
1	K	26	GLY	3.4
1	M	26	GLY	3.4
1	O	24	GLN	3.3
1	U	24	GLN	3.3
1	U	133	VAL	3.3
1	M	50	ALA	3.3
1	M	46	ALA	3.2
1	M	135	PRO	3.2
1	M	49	ASN	3.1
1	B	99	GLY	3.0
1	B	49	ASN	3.0
1	G	50	ALA	3.0
1	B	47	VAL	3.0
1	B	48	GLY	2.9

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Mol	Chain	Res	Type	RSRZ
1	Y	101	GLU	2.9
1	K	15	ALA	2.8
1	M	100	ALA	2.8
1	O	101	GLU	2.7
1	I	47	VAL	2.6
1	Y	48	GLY	2.6
1	O	99	GLY	2.5
1	O	51	GLU	2.4
1	Q	99	GLY	2.4
1	Y	99	GLY	2.4
1	M	29	PHE	2.4
2	N	4	TRP	2.4
1	I	48	GLY	2.4
1	Q	101	GLU	2.3
1	U	49	ASN	2.3
1	O	29	PHE	2.3
1	O	35	ALA	2.3
1	K	49	ASN	2.3
1	Q	135	PRO	2.2
1	O	50	ALA	2.2
1	O	133	VAL	2.2
1	K	29	PHE	2.1
1	U	15	ALA	2.1
1	I	134	LYS	2.0
1	U	35	ALA	2.0
1	B	98	GLY	2.0
1	S	47	VAL	2.0
1	K	35	ALA	2.0

## 6.2 Non-standard residues in protein, DNA, RNA chains [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. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. The B-factors column lists the minimum, median, 95<sup>th</sup> 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	LLDF	B-factors(Å <sup>2</sup> )	Q<0.9
2	DPR	H	3	7/8	0.96	0.16	-	23,24,26,31	0
2	DPR	L	3	7/8	0.93	0.11	-	25,27,28,32	0
2	DPR	V	3	7/8	0.97	0.09	-	26,27,29,32	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors( $\text{\AA}^2$ )	Q<0.9
2	DPR	P	3	7/8	0.86	0.17	-	29,30,31,34	0
2	DPR	J	3	7/8	0.95	0.09	-	16,18,19,23	0
2	DPR	T	3	7/8	0.96	0.06	-	18,19,20,26	0
2	DPR	X	3	7/8	0.96	0.06	-	17,18,20,25	0
2	DPR	R	3	7/8	0.97	0.06	-	15,16,18,23	0
2	DPR	F	3	7/8	0.96	0.07	-	14,16,18,21	0
2	DPR	C	3	7/8	0.97	0.08	-	13,14,16,20	0
2	DPR	E	3	7/8	0.97	0.08	-	19,22,23,26	0
2	DPR	N	3	7/8	0.93	0.17	-	27,28,29,33	0

### 6.3 Carbohydrates [i](#)

There are no carbohydrates 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.