

wwPDB EM Validation Summary Report (i)

Mar 9, 2024 – 01:25 PM EST

PDB ID	:	6NRA
EMDB ID	:	EMD-0492
Title	:	hTRiC-hPFD Class1 (No PFD)
Authors	:	Gestaut, D.R.; Roh, S.H.; Ma, B.; Pintilie, G.; Joachimiak, L.A.; Leitner, A.;
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Deposited on	:	2019-01-23
Resolution	:	7.70 Å(reported)

This is a wwPDB EM Validation Summary 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/EMValidationReportHelp with specific help available everywhere you see the (i) 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 (1)) were used in the production of this report:

EMDB validation analysis	:	0.0.1.dev70
MolProbity	:	4.02b-467
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ	:	1.9.13
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: $ELECTRON\ MICROSCOPY$

The reported resolution of this entry is 7.70 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	$egin{array}{c} { m Whole \ archive}\ (\#{ m Entries}) \end{array}$	${ m EM} { m structures} \ (\#{ m Entries})$		
Clashscore	158937	4297		
Ramachandran outliers	154571	4023		
Sidechain outliers	154315	3826		

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the 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 EM map (all-atom inclusion < 40%). The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain		
1	А	534	20%	20%	•••
1	Ι	534	73%	23%	
2	В	509	33%	19%	••
2	J	509	38%	18%	•
3	С	513	72%	23%	••
3	K	513	21%	22%	•••
4	D	514	14%	20%	•••
4	L	514	21%	18%	•

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			Juge	
Mol	Chain	\mathbf{Length}	Quality of chain	
			15%	
5	Ε	517	74%	22% •
			17%	
5	М	517	76%	21% •
			9%	
6	\mathbf{F}	515	77%	20% •
			11%	
6	Ν	515	75%	22% •
			14%	
7	G	514	77%	20% •
			21%	
7	Ο	514	75%	21% •
			9%	
8	Н	514	79%	18% ••
			11%	
8	Р	514	77%	19% ••

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2 Entry composition (i)

There are 8 unique types of molecules in this entry. The entry contains 62802 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, 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 T-complex protein 1 subunit alpha.

Mol	Chain	Residues		At	AltConf	Trace			
1	А	521	Total 3956	C 2479	N 691	O 763	S 23	0	0
1	Ι	534	Total 4056	C 2540	N 709	0 783	S 24	0	0

• Molecule 2 is a protein called T-complex protein 1 subunit beta.

Mol	Chain	Residues		At	AltConf	Trace			
2	В	509	Total 3829	C 2392	N 673	0 745	S 19	0	0
2	J	508	Total 3823	C 2389	N 672	0 743	S 19	0	0

• Molecule 3 is a protein called T-complex protein 1 subunit gamma.

Mol	Chain	Residues		At	AltConf	Trace			
3 C	500	Total	С	Ν	Ο	\mathbf{S}	0	0	
	U	509	3956	2465	697	764	30	0	0
3 K	512	Total	С	Ν	Ο	\mathbf{S}	0	0	
	ĸ	ĸ	515	3985	2481	703	771	30	0

• Molecule 4 is a protein called T-complex protein 1 subunit delta.

Mol	Chain	Residues		At		AltConf	Trace		
4	D	508	Total 3832	C 2398	N 665	0 746	S 23	0	0
4	L	513	Total 3873	C 2422	N 674	0 754	S 23	0	0

• Molecule 5 is a protein called T-complex protein 1 subunit epsilon.



Mol	Chain	Residues		At		AltConf	Trace	
5 E	517	Total	С	Ν	Ο	\mathbf{S}	0	0
		517	3974	2483	692	769	30	0
5 M	517	Total	С	Ν	Ο	\mathbf{S}	0	0
	IVI	517	3974	2483	692	769	30	0

• Molecule 6 is a protein called T-complex protein 1 subunit zeta.

Mol	Chain	Residues		At	AltConf	Trace			
6	F	514	Total	С	Ν	Ο	\mathbf{S}	0	0
0 F	014	3945	2478	690	757	20	0	0	
6	N	512	Total	С	Ν	Ο	\mathbf{S}	0	0
U	IN	515	3940	2476	689	755	20	0	0

• Molecule 7 is a protein called T-complex protein 1 subunit eta.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	G	512	Total 3936	C 2485	N 682	0 746	S 23	0	0
7	О	514	Total 3947	C 2490	N 684	O 750	S 23	0	0

• Molecule 8 is a protein called T-complex protein 1 subunit theta.

Mol	Chain	Residues	Atoms				AltConf	Trace	
8	Н	510	Total 3892	C 2451	N 661	0 754	S 26	0	0
8	Р	509	Total 3884	C 2447	N 659	O 752	S 26	0	0



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 atom inclusion in map 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 diamond above a residue indicates a poor fit to the EM map for this residue (all-atom inclusion < 40%). 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: T-complex protein 1 subunit alpha



















D456 0355 1461 0355 7461 0355 7465 0355 6467 0355 6467 0355 6473 0355 6473 0355 6473 0355 6473 0355 6473 0355 6473 0357 6473 0375 6473 0375 6473 0375 6473 0375 6473 0375 6473 0375 6473 0375 6473 0375 6473 0375 6473 0375 6473 0375 648 0385 648 0385 649 0385 649 0385 649 0385 649 0385 649 0385 649 0385 643 0385 643 0426 643 0426 643 0426 643 0426 643 0426 643 0435 643 0435 643 0436 643</t

• Molecule 5: T-complex protein 1 subunit epsilon



• Molecule 5: T-complex protein 1 subunit epsilon







• Molecule 6: T-complex protein 1 subunit zeta













4 Experimental information (i)

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	38323	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE	Depositor
	CORRECTION	
Microscope	JEOL 3200FSC	Depositor
Voltage (kV)	300	Depositor
Electron dose $(e^-/\text{\AA}^2)$	48	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT $(4k \ge 4k)$	Depositor
Maximum map value	0.247	Depositor
Minimum map value	-0.081	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.011	Depositor
Recommended contour level	0.05	Depositor
Map size (Å)	408.0, 408.0, 408.0	wwPDB
Map dimensions	240, 240, 240	wwPDB
Map angles $(^{\circ})$	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.7, 1.7, 1.7	Depositor



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).

Mal	Chain	B	ond lengths	I	Bond angles
	Ullaili	RMSZ	# Z > 5	RMSZ	# Z > 5
1	А	1.65	27/3992~(0.7%)	1.86	78/5389~(1.4%)
1	Ι	1.68	35/4095~(0.9%)	1.93	89/5526~(1.6%)
2	В	2.03	34/3869~(0.9%)	1.93	91/5214~(1.7%)
2	J	2.12	28/3863~(0.7%)	1.90	67/5207~(1.3%)
3	С	1.73	42/4000~(1.1%)	1.94	98/5397~(1.8%)
3	Κ	1.72	36/4029~(0.9%)	1.90	89/5434~(1.6%)
4	D	1.67	27/3863~(0.7%)	1.92	93/5214~(1.8%)
4	L	1.68	34/3904~(0.9%)	1.89	79/5269~(1.5%)
5	Е	1.68	26/4020~(0.6%)	1.91	77/5414 (1.4%)
5	М	1.66	22/4020~(0.5%)	1.85	82/5414~(1.5%)
6	F	1.69	25/3991~(0.6%)	1.85	82/5379~(1.5%)
6	N	1.67	31/3986~(0.8%)	1.90	85/5374~(1.6%)
7	G	1.68	29/3991~(0.7%)	1.88	83/5386~(1.5%)
7	0	1.66	23/4002~(0.6%)	1.91	75/5399~(1.4%)
8	Н	1.68	27/3945~(0.7%)	1.84	71/5331~(1.3%)
8	Р	1.71	38/3937~(1.0%)	1.87	72/5321~(1.4%)
All	All	1.73	484/63507~(0.8%)	1.89	1311/85668~(1.5%)

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	А	0	4
1	Ι	0	9
2	В	0	9
2	J	0	9
3	С	0	10
3	Κ	0	14
4	D	0	7
4	L	0	2
5	Е	0	5

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Mol	Chain	#Chirality outliers	#Planarity outliers
5	М	0	8
6	F	0	12
6	N	0	10
7	G	0	11
7	0	0	12
8	Н	0	9
8	Р	0	10
All	All	0	141

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The worst 5 of 484 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	J	464	GLN	N-CA	79.19	3.04	1.46
2	В	429	PRO	N-CD	41.36	2.05	1.47
2	В	429	PRO	CA-CB	35.04	2.23	1.53
2	В	429	PRO	N-CA	30.94	1.99	1.47
2	В	429	PRO	CG-CD	20.76	2.19	1.50

The worst 5 of 1311 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	$Observed(^{o})$	$Ideal(^{o})$
2	J	179	PHE	CB-CG-CD1	-16.76	109.07	120.80
5	Е	126	ARG	NE-CZ-NH2	-16.45	112.08	120.30
8	Н	304	TYR	CB-CG-CD2	-15.96	111.42	121.00
2	J	179	PHE	CB-CG-CD2	15.96	131.97	120.80
7	G	357	ARG	NE-CZ-NH2	-15.58	112.51	120.30

There are no chirality outliers.

5 of 141 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	А	18	ARG	Sidechain
1	А	242	GLN	Peptide
1	А	283	ALA	Peptide
1	А	443	ARG	Sidechain
2	В	89	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



Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	А	3956	0	4124	19	0
1	Ι	4056	0	4218	11	0
2	В	3829	0	3932	38	0
2	J	3823	0	3927	27	0
3	С	3956	0	4079	14	0
3	Κ	3985	0	4108	8	0
4	D	3832	0	4042	9	0
4	L	3873	0	4086	7	0
5	Ε	3974	0	4084	16	0
5	М	3974	0	4084	15	0
6	F	3945	0	4071	8	0
6	Ν	3940	0	4068	14	0
7	G	3936	0	4029	9	0
7	0	3947	0	4037	15	0
8	Н	3892	0	3949	9	0
8	Р	3884	0	3943	10	0
All	All	62802	0	64781	195	0

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.

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 2.

The worst 5 of 195 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:B:429:PRO:CD	2:J:464:GLN:HA	1.60	1.30
2:B:429:PRO:CA	2:B:429:PRO:N	1.99	1.25
2:B:429:PRO:CD	2:B:429:PRO:N	2.05	1.20
2:B:429:PRO:CD	2:B:429:PRO:CG	2.19	1.19
2:B:429:PRO:CA	2:B:429:PRO:CB	2.23	1.15

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 PDB entries followed by that with respect to all EM entries.



Mol	Chain	Analysed	Favoured	Allowed	Outliers	Per	$\operatorname{centiles}$
1	А	519/534~(97%)	461 (89%)	39~(8%)	19 (4%)	3	24
1	Ι	532/534~(100%)	474 (89%)	40 (8%)	18 (3%)	3	26
2	В	507/509~(100%)	473 (93%)	25~(5%)	9(2%)	8	40
2	J	506/509~(99%)	464 (92%)	32~(6%)	10 (2%)	7	38
3	\mathbf{C}	507/513~(99%)	465~(92%)	28~(6%)	14 (3%)	5	30
3	Κ	511/513~(100%)	462 (90%)	29~(6%)	20~(4%)	3	23
4	D	506/514~(98%)	470 (93%)	24~(5%)	12 (2%)	6	33
4	L	511/514~(99%)	458 (90%)	35~(7%)	18 (4%)	3	25
5	Ε	515/517~(100%)	461 (90%)	36~(7%)	18 (4%)	3	25
5	М	515/517~(100%)	480 (93%)	25~(5%)	10 (2%)	8	38
6	F	512/515~(99%)	474 (93%)	32~(6%)	6 (1%)	13	5 0
6	Ν	511/515~(99%)	483 (94%)	20~(4%)	8 (2%)	9	44
7	G	510/514~(99%)	464 (91%)	33~(6%)	13~(2%)	5	32
7	Ο	512/514~(100%)	471 (92%)	28~(6%)	13~(2%)	5	32
8	Н	508/514~(99%)	466 (92%)	31~(6%)	11 (2%)	6	35
8	Р	$50\overline{7/514}~(99\overline{\%})$	463 (91%)	29~(6%)	15(3%)	4	28
All	All	8189/8260~(99%)	7489 (92%)	486 (6%)	214 (3%)	8	31

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

5 of 214 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	А	49	ILE
1	А	486	ILE
2	В	172	LEU
2	В	250	LYS
2	В	429	PRO

5.3.2 Protein sidechains (i)

In the following table, the Percentiles column shows the percent side chain outliers of the chain as a percentile score with respect to all PDB entries followed by that with respect to all EM entries.

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	А	434/445~(98%)	423~(98%)	11 (2%)	47	68
1	Ι	445/445~(100%)	419 (94%)	26~(6%)	20	45
2	В	405/405~(100%)	390~(96%)	15~(4%)	34	58
2	J	405/405~(100%)	390~(96%)	15~(4%)	34	58
3	С	441/444 (99%)	425~(96%)	16 (4%)	35	59
3	Κ	444/444~(100%)	430~(97%)	14 (3%)	39	61
4	D	433/439~(99%)	422 (98%)	11 (2%)	47	68
4	L	438/439~(100%)	429~(98%)	9(2%)	53	72
5	Ε	436/436~(100%)	419 (96%)	17 (4%)	32	56
5	М	436/436~(100%)	424 (97%)	12 (3%)	43	65
6	F	429/429~(100%)	410 (96%)	19 (4%)	28	53
6	Ν	429/429~(100%)	416 (97%)	13 (3%)	41	63
7	G	420/421~(100%)	408~(97%)	12 (3%)	42	64
7	Ο	421/421~(100%)	406 (96%)	15~(4%)	35	59
8	Н	423/426~(99%)	410 (97%)	13 (3%)	40	62
8	Р	$42\overline{2}/426~(99\%)$	411 (97%)	11 (3%)	46	66
All	All	6861/6890 (100%)	6632 (97%)	229 (3%)	41	61

5 of 229 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	Ι	55	THR
8	Р	239	ILE
2	J	77	ASP
8	Р	67	ASN
6	Ν	487	MET

Sometimes side chains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 86 such side chains are listed below:

Mol	Mol Chain Res		Type
5	М	85	HIS
6	N	470	HIS
5	М	236	HIS
6	N	37	ASN
7	0	151	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 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 Map visualisation (i)

This section contains visualisations of the EMDB entry EMD-0492. These allow visual inspection of the internal detail of the map and identification of artifacts.

Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections (i)

6.1.1 Primary map



6.1.2 Raw map



The images above show the map projected in three orthogonal directions.



6.2 Central slices (i)

6.2.1 Primary map







Y Index: 120



Z Index: 120

6.2.2 Raw map



X Index: 120

Y Index: 120

Z Index: 120

The images above show central slices of the map in three orthogonal directions.



6.3 Largest variance slices (i)

6.3.1 Primary map



X Index: 98





Z Index: 142

6.3.2 Raw map



X Index: 98

Y Index: 128

Z Index: 148

The images above show the largest variance slices of the map in three orthogonal directions.



6.4 Orthogonal standard-deviation projections (False-color) (i)

6.4.1 Primary map



6.4.2 Raw map



The images above show the map standard deviation projections with false color in three orthogonal directions. Minimum values are shown in green, max in blue, and dark to light orange shades represent small to large values respectively.



6.5 Orthogonal surface views (i)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.05. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.5.2 Raw map



These images show the 3D surface of the raw map. The raw map's contour level was selected so that its surface encloses the same volume as the primary map does at its recommended contour level.

6.6 Mask visualisation (i)

This section was not generated. No masks/segmentation were deposited.



7 Map analysis (i)

This section contains the results of statistical analysis of the map.

7.1 Map-value distribution (i)



The map-value distribution is plotted in 128 intervals along the x-axis. The y-axis is logarithmic. A spike in this graph at zero usually indicates that the volume has been masked.



7.2 Volume estimate (i)



The volume at the recommended contour level is 683 nm^3 ; this corresponds to an approximate mass of 617 kDa.

The volume estimate graph shows how the enclosed volume varies with the contour level. The recommended contour level is shown as a vertical line and the intersection between the line and the curve gives the volume of the enclosed surface at the given level.



7.3 Rotationally averaged power spectrum (i)



*Reported resolution corresponds to spatial frequency of 0.130 ${\rm \AA^{-1}}$



8 Fourier-Shell correlation (i)

Fourier-Shell Correlation (FSC) is the most commonly used method to estimate the resolution of single-particle and subtomogram-averaged maps. The shape of the curve depends on the imposed symmetry, mask and whether or not the two 3D reconstructions used were processed from a common reference. The reported resolution is shown as a black line. A curve is displayed for the half-bit criterion in addition to lines showing the 0.143 gold standard cut-off and 0.5 cut-off.

8.1 FSC (i)



*Reported resolution corresponds to spatial frequency of 0.130 $\mathrm{\AA^{-1}}$



8.2 Resolution estimates (i)

$\mathbf{Bosolution} \text{ ostimato } (\mathbf{\hat{\lambda}})$	Estimation criterion (FSC cut-off)		
Resolution estimate (A)	0.143	0.5	Half-bit
Reported by author	7.70	-	-
Author-provided FSC curve	6.58	7.52	6.82
Unmasked-calculated*	7.59	9.13	7.76

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from author-provided FSC intersecting FSC 0.143 CUT-OFF 6.58 differs from the reported value 7.7 by more than 10 %



9 Map-model fit (i)

This section contains information regarding the fit between EMDB map EMD-0492 and PDB model 6NRA. Per-residue inclusion information can be found in section 3 on page 6.

9.1 Map-model overlay (i)



The images above show the 3D surface view of the map at the recommended contour level 0.05 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.



9.2 Q-score mapped to coordinate model (i)



The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions at which atoms can be resolved. Low Q-score values may therefore be expected for many entries.

9.3 Atom inclusion mapped to coordinate model (i)



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.05).



9.4 Atom inclusion (i)



At the recommended contour level, 82% of all backbone atoms, 63% of all non-hydrogen atoms, are inside the map.



9.5 Map-model fit summary (i)

The table lists the average atom inclusion at the recommended contour level (0.05) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score	
All	0.6340	0.1010	
A	0.6100	0.0910	
В	0.5230	0.0950	— 10
С	0.6490	0.1070	1.0
D	0.6630	0.1150	
E	0.6760	0.0980	
F	0.7010	0.1150	
G	0.6650	0.1010	
Н	0.7000	0.1140	
Ι	0.6060	0.0860	
J	0.4700	0.0880	
K	0.6080	0.0880	0.0
L	0.6300	0.1050	<0.0
М	0.6570	0.1040	
N	0.6800	0.1090]
0	0.6110	0.0950	
Р	0.6970	0.1110	

