

# CASP12

12th Community Wide Experiment on the Critical Assessment of Techniques for Protein Structure Prediction

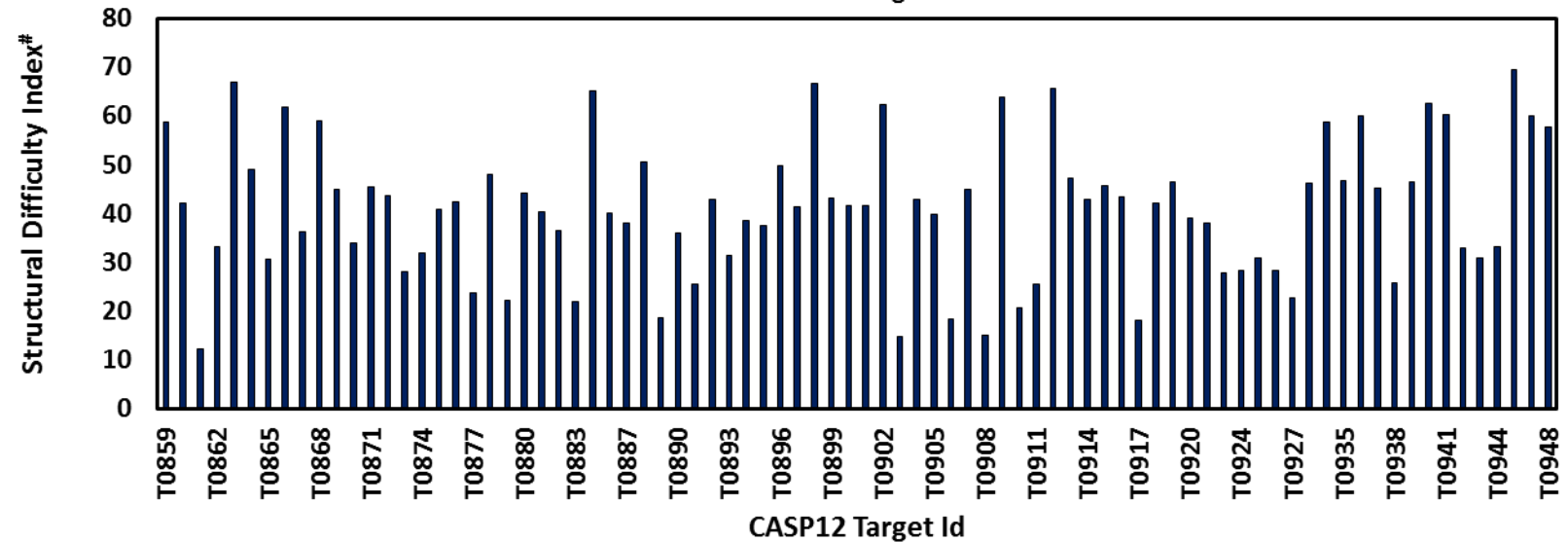
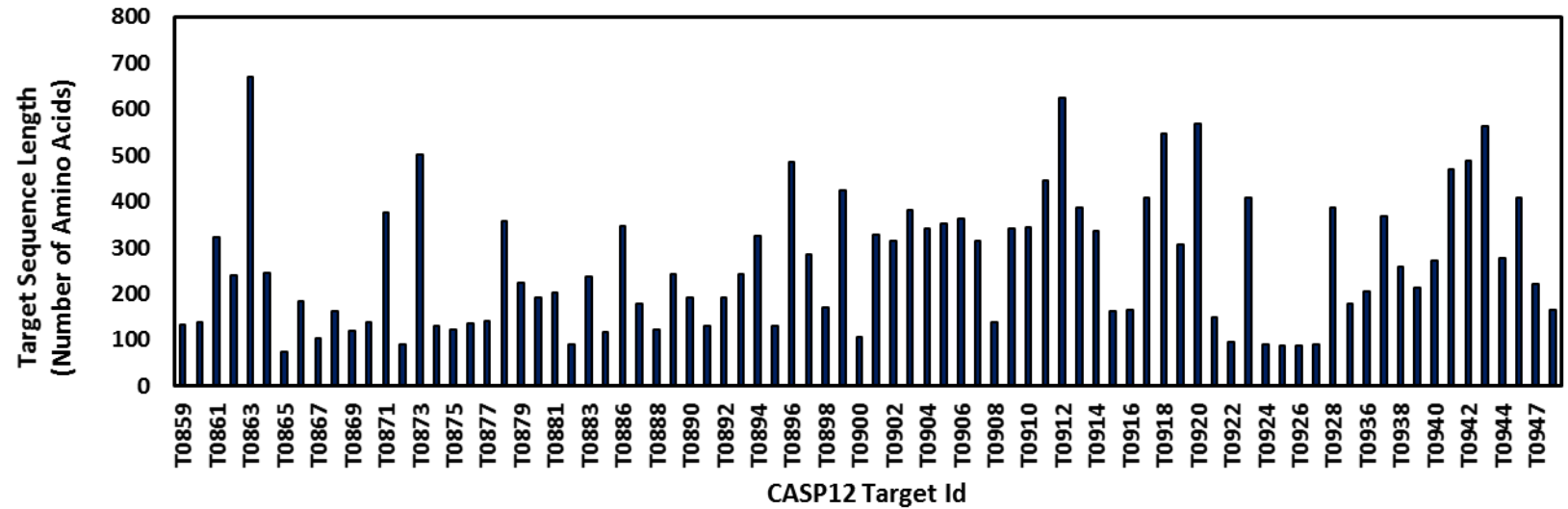
Start Date: 2<sup>nd</sup> May, 2016  
End Date: 12<sup>th</sup> July, 2016

Total Number of Participants: 189  
80 (Servers) + 109 (Human Group)

Total Number of Countries Involved: 28

Total Number of Unique Targets: 82

Total Number of Domains: 96  
38 (TBM\*) + 39 (FM\*) + 19 (TBM/FM\*)

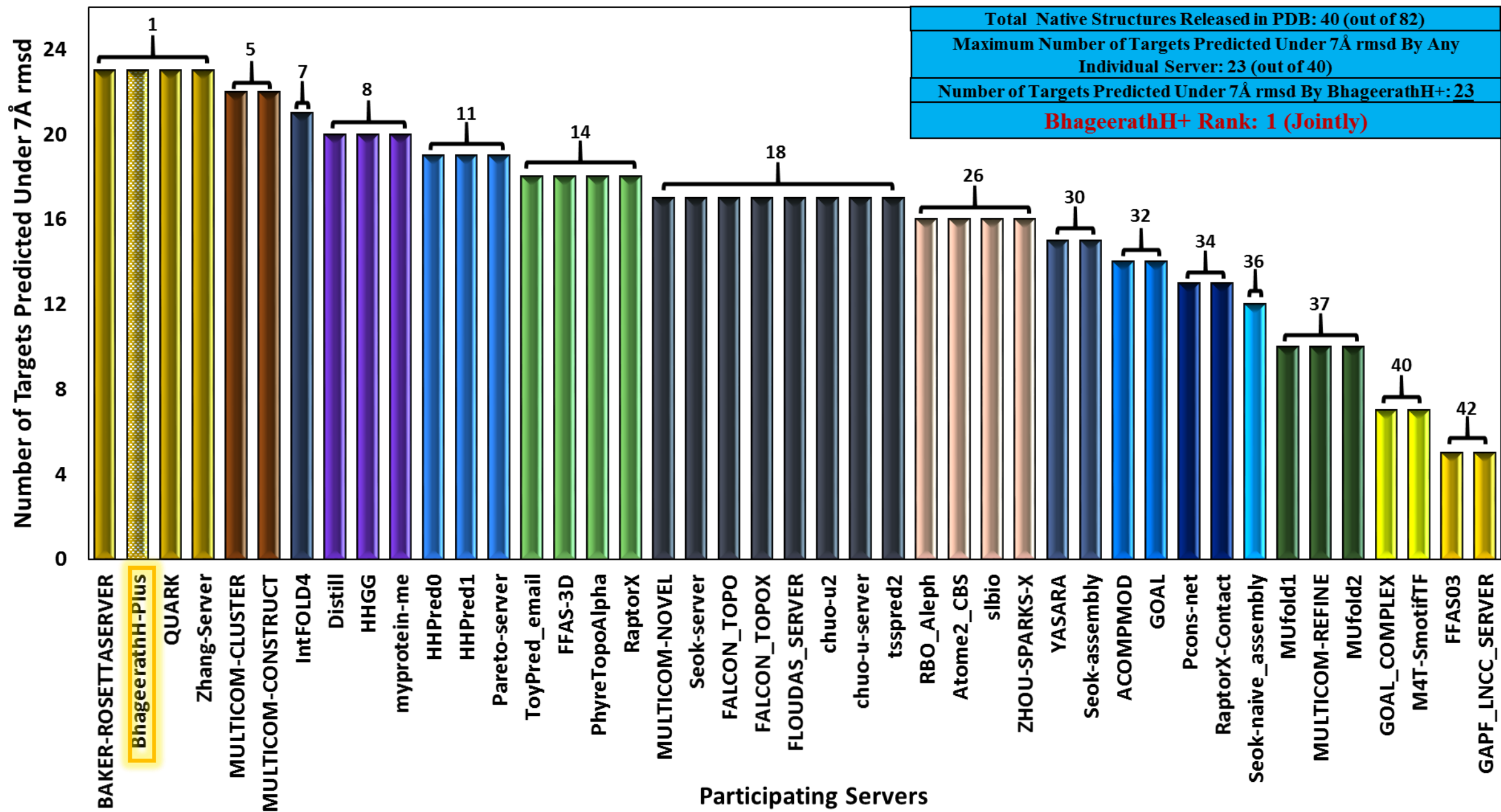


\*TBM: Template Based Modeling

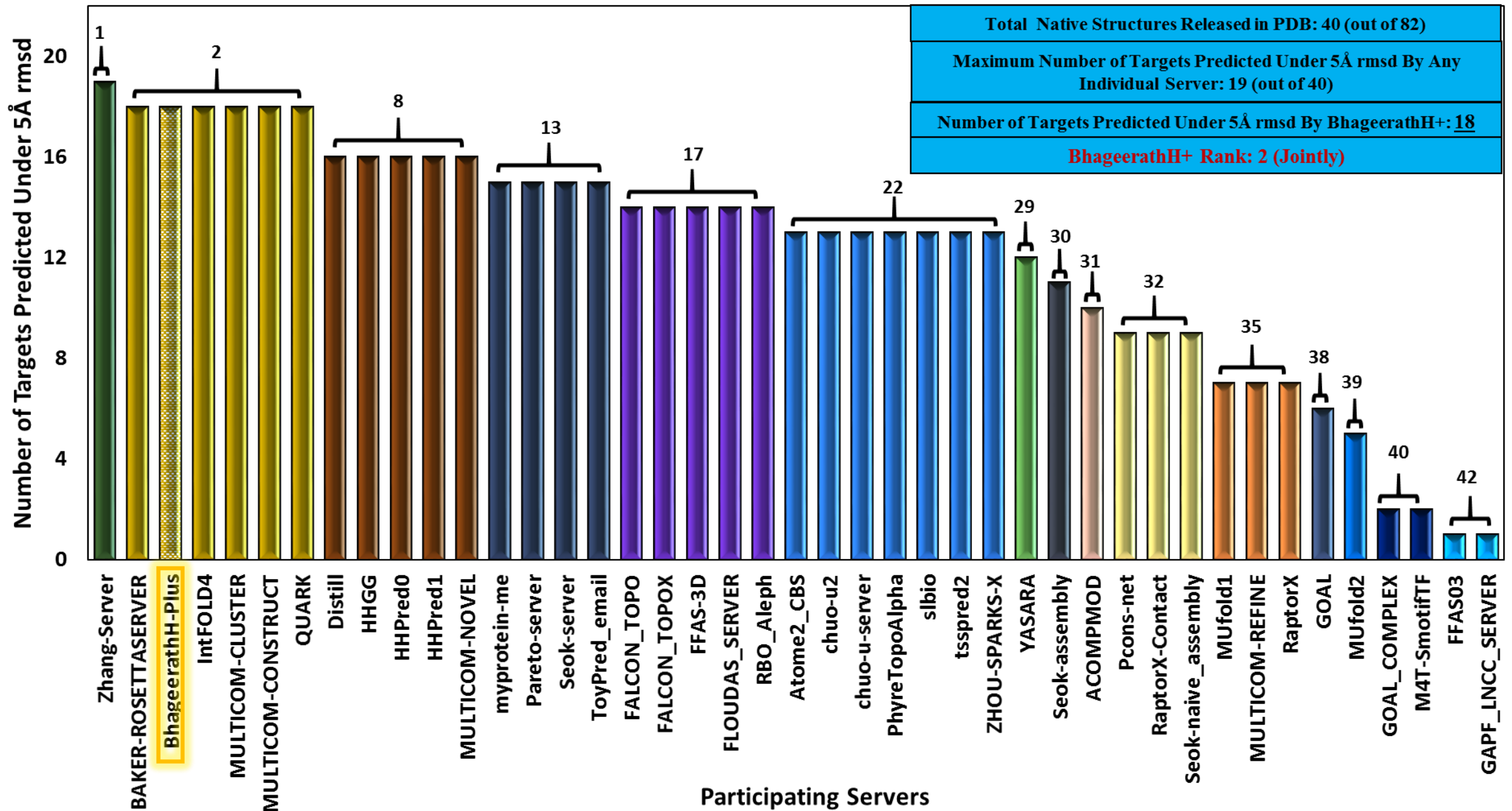
\*FM- Free Modeling

\*Kaushik, R. and Jayaram, B. (2016). Structural difficulty index: A reliable measure for modelability of protein tertiary structures. *PEDS*, 29(9), 391-97

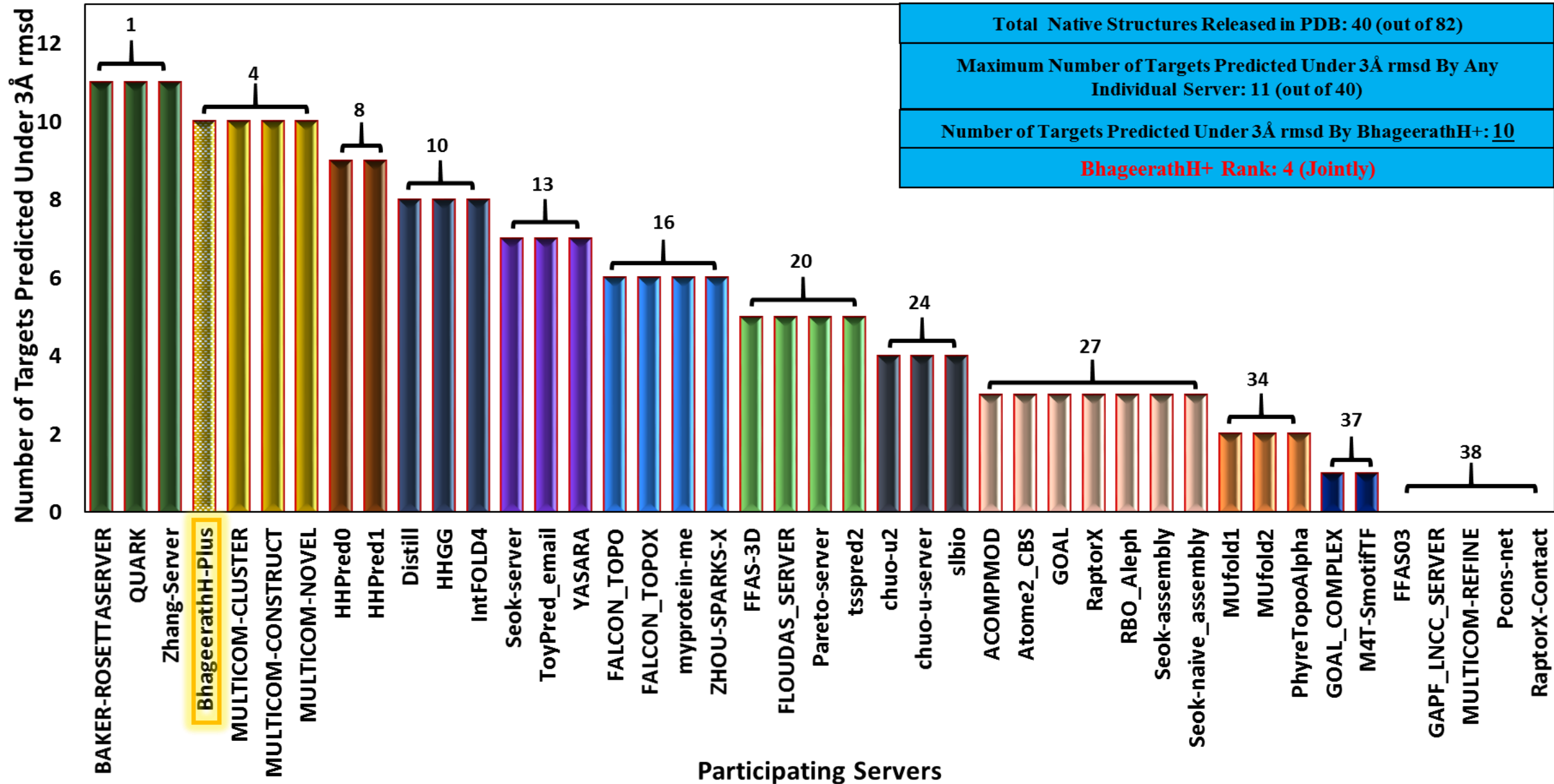
# ANALYSIS BASED ON NATIVE STRUCTURES RELEASED IN PDB AS FULL LENGTH TARGETS



# ANALYSIS BASED ON NATIVE STRUCTURES RELEASED IN PDB AS FULL LENGTH TARGETS



# ANALYSIS BASED ON NATIVE STRUCTURES RELEASED IN PDB AS FULL LENGTH TARGETS



**TS Analysis : Group performance based on combined z-scores**

[Results Home](#)   [Table Browser](#)   [Estimate of Model Accuracy Results](#)   [RR Assessment Results](#)

The cumulative z-scores in this table are calculated according to the following procedure (example for the "first" models):  
 1. Calculate z-scores from the raw scores for all "first" models (corresponding values from the main result table);  
 2. Remove outliers - models with zscores below the tolerance threshold (set to -2.0);  
 3. Recalculate z-scores on the reduced dataset;  
 4. Assign z-scores below the penalty threshold (either -2.0 or 0.0) to the value of this threshold.

**GDT\_TS based**   **Assessors' formula**

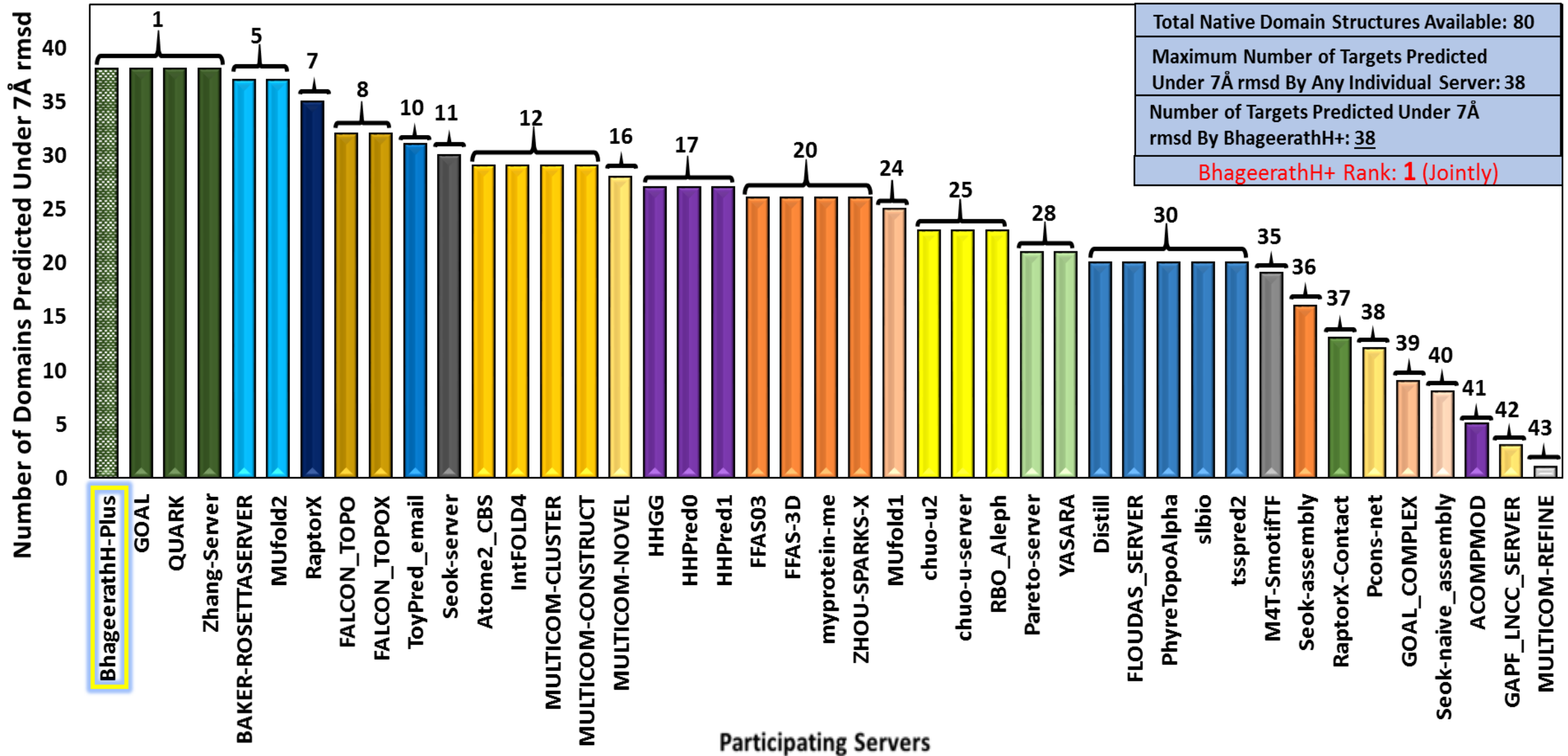
- Analysis on the models designated as "1"
- Analysis on the models with the best scores
  
- All groups on 'all groups' targets
- Server groups on 'all groups' + 'server only' targets
  
- The ranking of the groups is based on the analysis of zscores for **GDT\_TS**.
  - TBM
  - TBM/FM
  - FM

#	GR code	GR name	Domains Count	SUM Zscore (>-2.0)	Rank SUM Zscore (>-2.0)
1	005	BAKER-ROSETTASERVER	77	89.7904	1
2	479	Zhang-Server	77	87.7028	2
3	183	QUARK	77	83.0551	3
4	220	GOAL	75	70.8140	4
5	092	RaptorX	77	34.2029	5
6	048	ToyPred_email	76	30.9512	6
7	236	MULTICOM-CONSTRUCT	77	28.1152	7
8	287	MULTICOM-CLUSTER	77	27.1435	8
9	345	MULTICOM-NOVEL	77	26.5875	9
10	405	IntFOLD4	77	10.6896	10
11	444	BhageerathH-Plus	77	6.8231	11
12	250	Seok-server	77	4.8007	12
13	452	ZHOU-SPARKS-X	71	-0.2518	13
14	313	HHGG	77	-0.2736	14
15	425	FALCON_TOPOX	77	-1.0520	15
16	077	FALCON_TOPO	77	-1.6145	16
17	421	MUfold2	72	-3.1090	17
18	119	HHPred0	77	-4.8296	18
19	349	HHPred1	77	-5.0120	19
20	380	chuo-u-server	77	-7.4725	20
21	026	chuo-u2	77	-7.4725	20

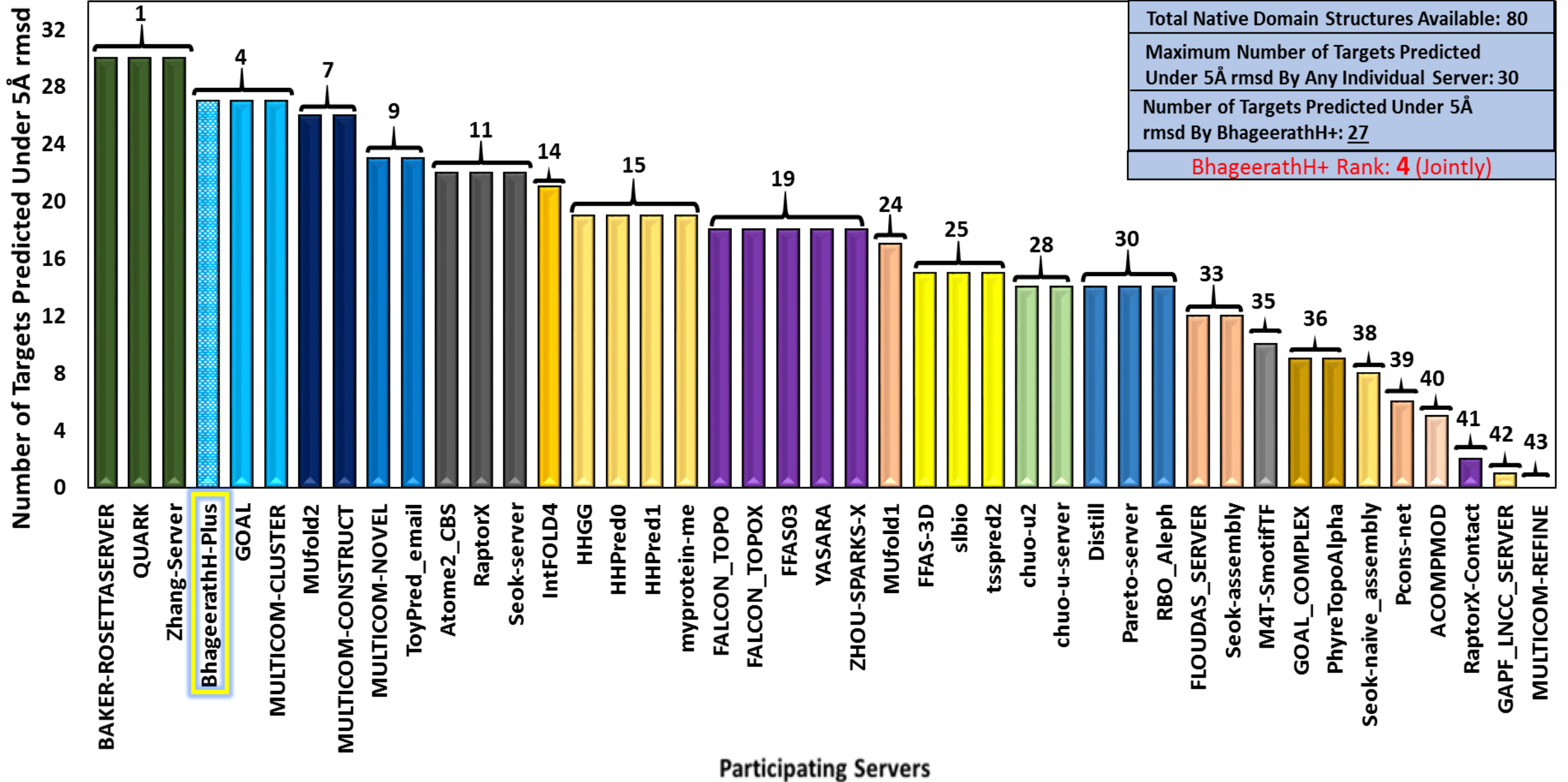
#	GR code	GR name	Domains Count	SUM Zscore (>-2.0)	Rank SUM Zscore (>-2.0)
22	446	YASARA	73	-14.2711	22
23	016	FFAS-3D	77	-14.6048	23
24	251	myprotein-me	73	-15.4033	24
25	407	Distill	74	-15.9574	25
26	464	tspred2	77	-20.9155	26
27	467	Pareto-server	75	-22.1108	27
28	359	Atome2_CBS	72	-24.7460	28
29	258	MUfold1	77	-25.1083	29
30	382	RBO_Aleph	76	-26.2241	30
31	275	sibio	74	-31.6197	31
32	180	PhyreTopoAlpha	77	-39.7043	32
33	451	RaptorX-Contact	75	-51.2500	33
34	166	FFAS03	63	-57.9242	34
35	357	FLOUDAS_SERVER	76	-59.0852	35
36	434	MULTICOM-REFINE	77	-75.9047	36
37	432	Poons-net	57	-76.8753	37
38	495	Seok-assembly	37	-79.4542	38
39	321	GAPF_LNCC_SERVER	74	-91.2282	39
40	028	M4T-SmotITF	51	-98.2998	40
41	455	ACOMPMOD	71	-98.5272	41
42	430	GOAL_COMPLEX	12	-126.7949	42
43	284	Seok-naive_assembly	14	-132.4145	43



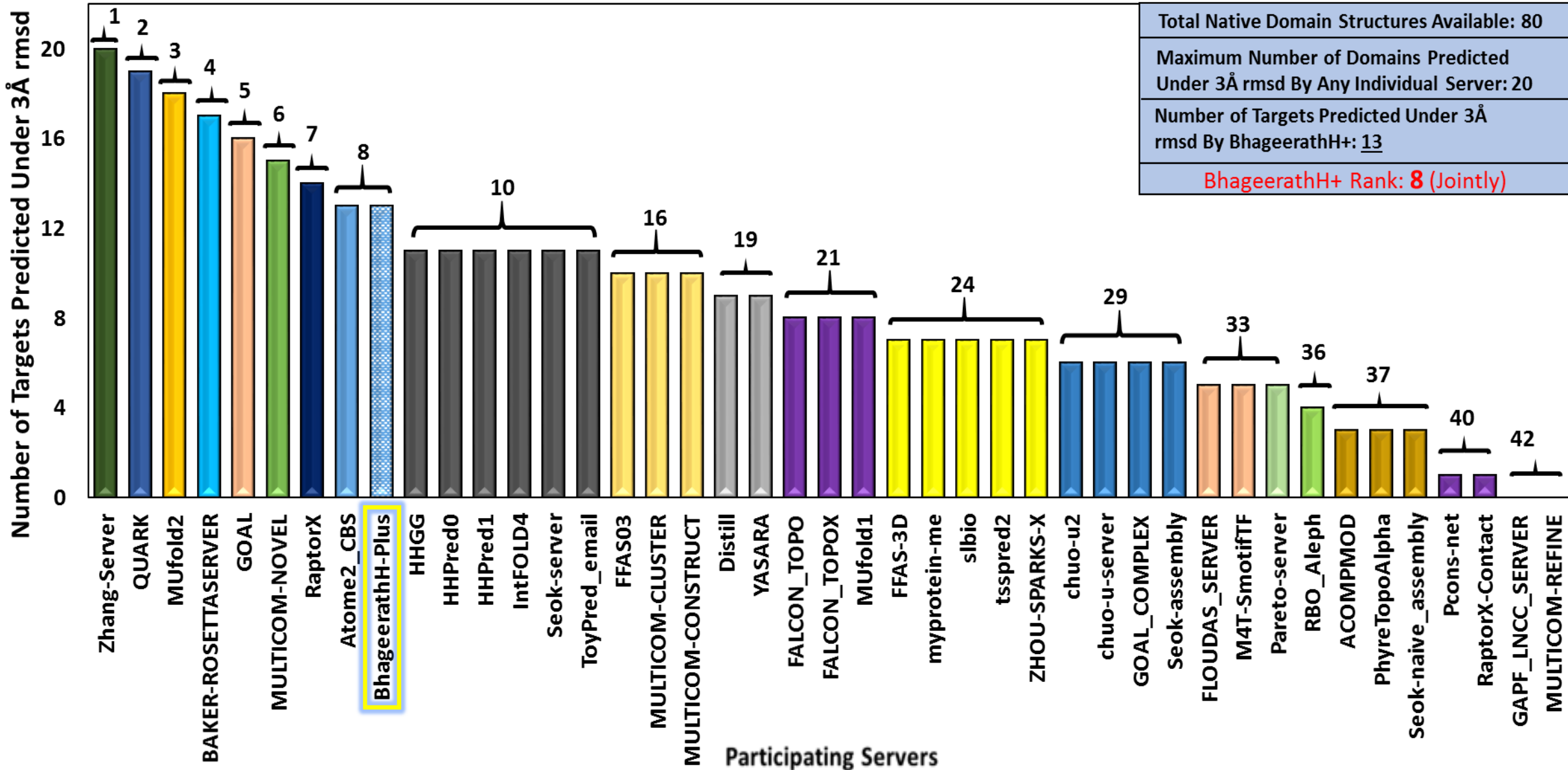
# ANALYSIS BASED ON NATIVE DOMAIN STRUCTURES AVAILABLE TO SELECTED GROUPS ON REQUEST



# ANALYSIS BASED ON NATIVE DOMAIN STRUCTURES AVAILABLE TO SELECTED GROUPS ON REQUEST



# ANALYSIS BASED ON NATIVE DOMAIN STRUCTURES AVAILABLE TO SELECTED GROUPS ON REQUEST





## Assessment of CASP12: Predictions By Participating Servers in Different Range of GDT-TS

Server Name	GDT $\geq$ 25*	GDT $\geq$ 50*	GDT $\geq$ 75*	Server Name	GDT $\geq$ 25*	GDT $\geq$ 50*	GDT $\geq$ 75*
Zhang-Server	33 (1)	23 (1)	8 (7)	ROSETTA	25 (23)	19 (16)	6 (16)
QUARK	32 (2)	22 (6)	9 (2)	FFAS-3D	25 (23)	18 (19)	6 (16)
<b>BhageerathH+</b>	<b>32 (2)</b>	<b>23 (1)</b>	<b>8 (7)</b>	chuo-u-server	25 (23)	14 (26)	3 (26)
MULTICOM-CLUST	31 (4)	21 (10)	8 (7)	chuo-u2	25 (23)	14 (26)	3 (26)
MULTICOM-CONSTR	31 (4)	19 (16)	8 (7)	ZHOU-SPARKS-X	24 (27)	17 (23)	5 (20)
IntFOLD4	31 (4)	23 (1)	7 (12)	Pareto-server	22 (28)	12 (29)	3 (26)
RaptorX	31 (4)	23 (1)	7 (12)	PhyreTopoAlpha	21 (29)	9 (31)	3 (26)
ToyPred_email	31 (4)	22 (6)	7 (12)	RaptorX-Contact	21 (29)	1 (41)	0 (40)
MULTICOM-NOVEL	30 (9)	21 (10)	10 (1)	MUfold1	17 (31)	13 (28)	4 (24)
GOAL	30 (9)	23 (1)	9 (2)	Pcons-net	17 (31)	4 (37)	0 (40)
Seok-server	30 (9)	20 (15)	7 (12)	YASARA	16 (33)	11 (30)	3 (26)
HHGG	29 (12)	21 (10)	9 (2)	Atome2_CBS	15 (34)	8 (32)	6 (16)
HHPred0	29 (12)	21 (10)	9 (2)	Seok-assembly	10 (35)	6 (34)	2 (33)
HHPred1	29 (12)	21 (10)	9 (2)	MUfold2	8 (36)	7 (33)	2 (33)
Distill	29 (12)	18 (19)	8 (7)	ACOMPMOD	8 (36)	5 (35)	2 (33)
RBO_Aleph	29 (12)	16 (24)	4 (24)	Seok-naive_assembly	7 (38)	3 (38)	1 (39)
FALCON_TOPO	28 (17)	22 (6)	5 (20)	MULTICOM-REFINE	7 (38)	1 (41)	0 (40)
FALCON_TOPOX	28 (17)	22 (10)	5 (20)	GOAL_COMPLEX	6 (40)	3 (38)	3 (26)
myprotein-me	28 (17)	18(19)	3 (26)	GAPF_LNCC	6 (40)	0 (43)	0 (40)
slbio	27 (20)	18 (19)	6 (16)	M4T-SmotifTF	5 (42)	5 (35)	2 (33)
tsspred2	27 (20)	19 (16)	5 (20)	FFAS03	3 (43)	3 (38)	2 (33)
FLOUDAS	26 (22)	16 (24)	2 (33)				

\*Relative rankings are indicated in parenthesis



# Acknowledgement

The BhageerathH+ team is very thankful to the CASP organizing committee for providing such a wonderful platform. We are grateful to the organizers for providing the native domain structures for the CASP12 targets which are yet to be released in PDB.