



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 08:11 PM UTC

PDB ID : 4EDJ / pdb_00004edj
Title : Crystal structure of the GRASP55 GRASP Domain with a phosphomimetic mutation (S189D)
Authors : Truschel, S.T.; Zhang, M.; Bachert, C.; Macbeth, M.R.; Linstedt, A.D.
Deposited on : 2012-03-27
Resolution : 1.90 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

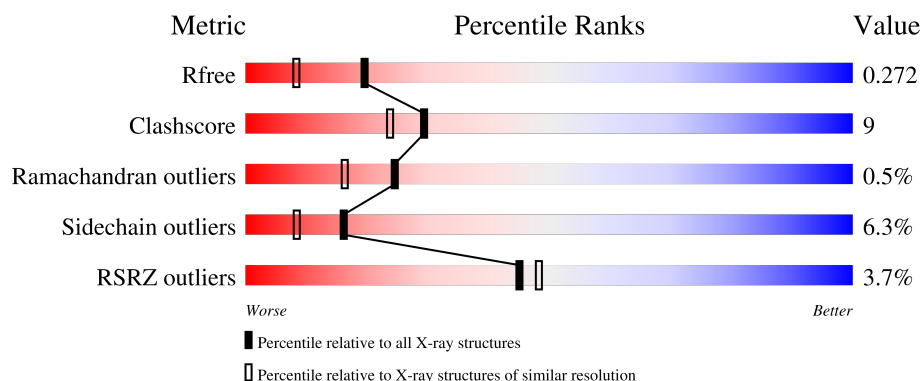
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.90 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	7789 (1.90-1.90)
Clashscore	190562	8410 (1.90-1.90)
Ramachandran outliers	187476	8333 (1.90-1.90)
Sidechain outliers	187428	8333 (1.90-1.90)
RSRZ outliers	180081	7790 (1.90-1.90)

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	209	2% 80% 16% ..
1	B	209	5% 74% 20% ..

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 3471 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 Golgi reassembly-stacking protein 2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	205	Total	C	N	O	S	0	8	0
			1628	1027	276	320	5			
1	B	203	Total	C	N	O	S	0	9	0
			1614	1017	272	319	6			

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	0	GLY	-	expression tag	UNP Q9H8Y8
A	189	ASP	SER	engineered mutation	UNP Q9H8Y8
B	0	GLY	-	expression tag	UNP Q9H8Y8
B	189	ASP	SER	engineered mutation	UNP Q9H8Y8

- Molecule 2 is POTASSIUM ION (CCD ID: K) (formula: K).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	1	Total	K	0	0
			1	1		

- Molecule 3 is water.

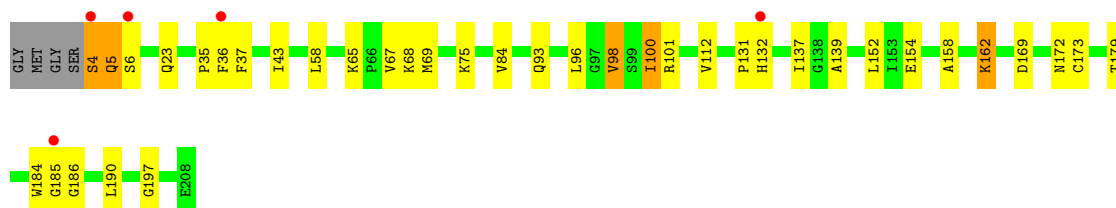
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	136	Total	O	0	0
			136	136		
3	B	92	Total	O	0	0
			92	92		

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.

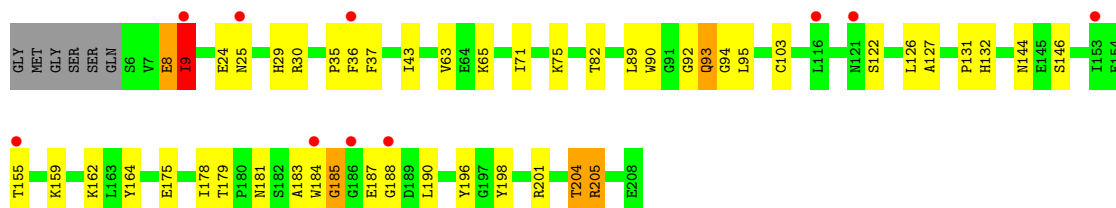
- Molecule 1: Golgi reassembly-stacking protein 2

Chain A:



- Molecule 1: Golgi reassembly-stacking protein 2

Chain B:



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	64.86Å 82.55Å 84.06Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	58.90 – 1.90 58.90 – 1.90	Depositor EDS
% Data completeness (in resolution range)	97.0 (58.90-1.90) 97.0 (58.90-1.90)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.09	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.56 (at 1.91Å)	Xtriage
Refinement program	REFMAC 5.5.0109	Depositor
R, R_{free}	0.209 , 0.271 0.215 , 0.272	Depositor DCC
R_{free} test set	1805 reflections (4.99%)	wwPDB-VP
Wilson B-factor (Å ²)	34.5	Xtriage
Anisotropy	0.083	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.30 , 23.8	EDS
L-test for twinning ²	$\langle L \rangle = 0.51$, $\langle L^2 \rangle = 0.35$	Xtriage
Estimated twinning fraction	0.011 for -h,l,k	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	3471	wwPDB-VP
Average B, all atoms (Å ²)	37.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.50% 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 ⓘ

5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section:
K

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	1.25	3/1682 (0.2%)	1.17	7/2283 (0.3%)
1	B	1.11	0/1668	1.15	8/2264 (0.4%)
All	All	1.18	3/3350 (0.1%)	1.16	15/4547 (0.3%)

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	158	ALA	CA-CB	7.28	1.65	1.53
1	A	139	ALA	CA-CB	6.29	1.62	1.53
1	A	185	GLY	N-CA	5.21	1.53	1.45

All (15) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	186	GLY	N-CA-C	-9.55	93.41	111.66
1	A	184	TRP	CA-C-N	-6.82	107.16	121.06
1	A	184	TRP	C-N-CA	-6.82	107.16	121.06
1	B	9	ILE	N-CA-CB	-6.57	102.01	111.21
1	B	179	THR	CA-C-N	6.33	126.28	119.76
1	B	179	THR	C-N-CA	6.33	126.28	119.76
1	B	204	THR	N-CA-CB	-6.02	101.04	110.44
1	B	127	ALA	N-CA-C	-5.74	106.28	113.28
1	B	198	TYR	N-CA-C	5.56	118.06	111.33
1	A	179	THR	CA-C-N	5.56	125.49	119.76
1	A	179	THR	C-N-CA	5.56	125.49	119.76
1	A	65	LYS	CA-C-N	-5.56	114.25	120.14
1	A	65	LYS	C-N-CA	-5.56	114.25	120.14
1	B	103	CYS	N-CA-C	5.49	115.62	107.88
1	B	201	ARG	CA-CB-CG	-5.02	104.06	114.10

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	1628	0	1593	20	0
1	B	1614	0	1573	35	0
2	A	1	0	0	0	0
3	A	136	0	0	3	0
3	B	92	0	0	3	0
All	All	3471	0	3166	55	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 9.

All (55) 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:36:PHE:HZ	1:B:164:TYR:CD2	1.92	0.88
1:B:25:ASN:H	1:B:29:HIS:HD2	1.21	0.86
1:B:9:ILE:HD13	3:B:387:HOH:O	1.75	0.86
1:B:36:PHE:CZ	1:B:164:TYR:CD2	2.68	0.81
1:B:36:PHE:CZ	1:B:164:TYR:CG	2.75	0.75
1:A:5:GLN:O	1:A:5:GLN:HG2	1.85	0.75
1:B:162:LYS:HE3	3:B:388:HOH:O	1.87	0.75
1:B:25:ASN:H	1:B:29:HIS:CD2	2.10	0.66
1:B:35:PRO:O	1:B:36:PHE:HB2	1.97	0.63
1:A:35:PRO:O	1:A:36:PHE:HB2	2.01	0.60
1:B:184:TRP:HE1	1:B:188:GLY:H	1.47	0.60
1:A:169:ASP:OD1	3:A:508:HOH:O	2.17	0.60
1:A:23:GLN:HE22	1:A:93:GLN:H	1.52	0.58
1:B:8:GLU:H	1:B:8:GLU:CD	2.12	0.58
1:A:4:SER:O	1:A:6:SER:N	2.30	0.58
1:A:5:GLN:O	1:A:5:GLN:CG	2.49	0.57
1:B:63:VAL:HG12	1:B:95:LEU:HD13	1.89	0.55
1:A:172[A]:ASN:OD1	3:A:472:HOH:O	2.18	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:137:ILE:HD11	1:A:173:CYS:SG	2.49	0.53
1:A:98:VAL:HG12	1:A:100:ILE:HG23	1.90	0.52
1:B:30:ARG:HD2	3:B:392:HOH:O	2.09	0.52
1:B:36:PHE:CE2	1:B:164:TYR:CG	2.98	0.51
1:B:146:SER:HB2	1:B:196:TYR:CE2	2.46	0.51
1:B:36:PHE:CE2	1:B:164:TYR:CB	2.94	0.50
1:B:183:ALA:O	1:B:184:TRP:C	2.54	0.50
1:B:181:ASN:HD21	1:B:183:ALA:HB3	1.77	0.50
1:B:24:GLU:O	1:B:25:ASN:HB2	2.12	0.49
1:A:112:VAL:HG12	1:A:137:ILE:HG22	1.95	0.49
1:B:71:ILE:HD11	1:B:82:THR:HG22	1.95	0.49
1:B:131:PRO:O	1:B:132:HIS:HB2	2.12	0.49
1:A:84:VAL:HG21	1:A:96:LEU:CD2	2.43	0.48
1:A:84:VAL:HG21	1:A:96:LEU:HD21	1.94	0.48
1:B:122:SER:O	1:B:126:LEU:HG	2.14	0.48
1:A:131:PRO:O	1:A:132:HIS:HB2	2.14	0.47
1:B:90:TRP:CZ3	1:B:92:GLY:HA3	2.49	0.47
1:B:37:PHE:CD1	1:B:75:LYS:HB2	2.50	0.46
1:A:37:PHE:CD2	1:A:75:LYS:HE2	2.50	0.46
1:B:8:GLU:CD	1:B:8:GLU:N	2.74	0.45
1:B:184:TRP:HE1	1:B:188:GLY:N	2.13	0.45
1:B:93[B]:GLN:OE1	1:B:94:GLY:N	2.50	0.44
1:B:183:ALA:O	1:B:185:GLY:N	2.50	0.44
1:B:63:VAL:CG1	1:B:95:LEU:HD13	2.47	0.44
1:A:69:MET:HE3	1:A:84:VAL:HG11	1.99	0.43
1:A:43:ILE:HG23	1:A:58:LEU:HD12	2.00	0.43
1:B:36:PHE:HZ	1:B:164:TYR:CG	2.23	0.42
1:B:205:ARG:O	1:B:205:ARG:HG3	2.20	0.42
1:B:36:PHE:CE2	1:B:164:TYR:HB3	2.55	0.41
1:B:71:ILE:CD1	1:B:82:THR:HG22	2.50	0.41
1:A:36:PHE:HB3	1:A:137:ILE:HD12	2.01	0.41
1:B:93[A]:GLN:HE21	1:B:93[A]:GLN:HB3	1.72	0.41
1:A:197:GLY:HA2	3:A:462:HOH:O	2.21	0.41
1:A:162[B]:LYS:HE2	1:A:162[B]:LYS:HB2	1.11	0.40
1:B:178:ILE:CD1	1:B:190:LEU:HD22	2.51	0.40
1:A:98:VAL:CG1	1:A:100:ILE:HG23	2.51	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	211/209 (101%)	204 (97%)	6 (3%)	1 (0%)	24	16
1	B	210/209 (100%)	196 (93%)	13 (6%)	1 (0%)	24	16
All	All	421/418 (101%)	400 (95%)	19 (4%)	2 (0%)	24	16

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	5	GLN
1	B	185	GLY

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.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	183/177 (103%)	172 (94%)	11 (6%)	17	9
1	B	182/177 (103%)	168 (92%)	14 (8%)	12	5
All	All	365/354 (103%)	340 (93%)	25 (7%)	16	7

All (25) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	4	SER
1	A	67	VAL
1	A	68	LYS
1	A	98	VAL

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Mol	Chain	Res	Type
1	A	100	ILE
1	A	101	ARG
1	A	152	LEU
1	A	154	GLU
1	A	162[A]	LYS
1	A	162[B]	LYS
1	A	190	LEU
1	B	8	GLU
1	B	9	ILE
1	B	43[A]	ILE
1	B	43[B]	ILE
1	B	65	LYS
1	B	89	LEU
1	B	93[A]	GLN
1	B	93[B]	GLN
1	B	144	ASN
1	B	159	LYS
1	B	175	GLU
1	B	187	GLU
1	B	204	THR
1	B	205	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (4) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	23	GLN
1	B	25	ASN
1	B	29	HIS
1	B	181	ASN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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](#)

Of 1 ligands modelled in this entry, 1 is monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

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, 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	205/209 (98%)	0.07	5 (2%) 59 63	14, 32, 44, 77	8 (3%)
1	B	203/209 (97%)	0.40	10 (4%) 35 37	14, 39, 61, 75	9 (4%)
All	All	408/418 (97%)	0.23	15 (3%) 45 48	14, 35, 59, 77	17 (4%)

All (15) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	132	HIS	3.0
1	B	188	GLY	2.9
1	B	36	PHE	2.8
1	B	184	TRP	2.7
1	A	36	PHE	2.6
1	A	4	SER	2.6
1	B	121	ASN	2.5
1	B	25	ASN	2.4
1	B	153	ILE	2.3
1	A	185	GLY	2.3
1	B	9	ILE	2.2
1	A	6	SER	2.2
1	B	186	GLY	2.1
1	B	116	LEU	2.1
1	B	155	THR	2.1

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 oligosaccharides in this entry.

6.4 Ligands [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. The B-factors column lists the minimum, median, 95th 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	B-factors($\text{\AA}^2$)	Q<0.9
2	K	A	301	1/1	0.93	0.09	59,59,59,59	0

6.5 Other polymers [i](#)

There are no such residues in this entry.