Full wwPDB X-ray Structure Validation Report (i)

Aug 3, 2023 – 02:54 AM EDT

PDB ID	:	1FYR
Title	:	DIMER FORMATION THROUGH DOMAIN SWAPPING IN THE CRYSTAL STRUCTURE OF THE GRB2-SH2 AC-PYVNV COMPLEX
Authors	:	Schiering, N.; Casale, E.; Caccia, P.; Giordano, P.; Battistini, C.
Deposited on	:	2000-10-03
Resolution	:	2.40 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 (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 (i)) were used in the production of this report:

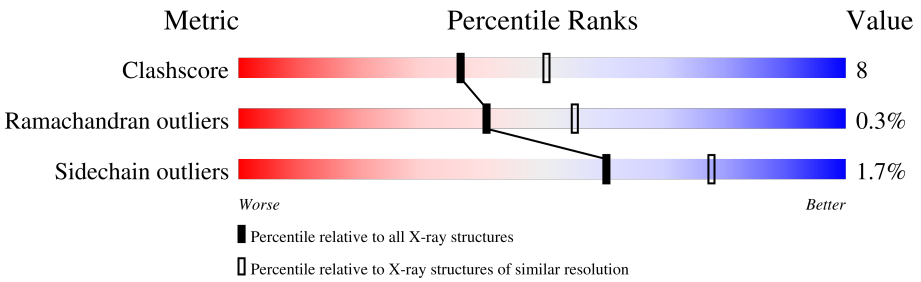
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	NOT EXECUTED
EDS	:	NOT EXECUTED
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.34

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 2.40 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))
Clashscore	141614	4398 (2.40-2.40)
Ramachandran outliers	138981	4318 (2.40-2.40)
Sidechain outliers	138945	4319 (2.40-2.40)

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%

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	A	114	67% 17% 17%
1	B	114	65% 20% • 14%
1	C	114	72% 14% 14%
1	D	114	68% 15% 17%
2	I	5	80% 20%
2	J	5	80% 20%
2	K	5	80% 20%
2	L	5	80% 20%

2 Entry composition (i)

There are 3 unique types of molecules in this entry. The entry contains 3538 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 GROWTH FACTOR RECEPTOR-BOUND PROTEIN 2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	95	785	504	141	139	1	2	0	0
1	B	98	809	520	145	142	2	0	0	0
1	C	98	809	520	145	142	2	0	0	0
1	D	95	785	504	141	139	1	0	0	0

There are 8 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	48	GLY	-	cloning artifact	UNP P08581
A	49	SER	-	cloning artifact	UNP P08581
B	48	GLY	-	cloning artifact	UNP P08581
B	49	SER	-	cloning artifact	UNP P08581
C	48	GLY	-	cloning artifact	UNP P08581
C	49	SER	-	cloning artifact	UNP P08581
D	48	GLY	-	cloning artifact	UNP P08581
D	49	SER	-	cloning artifact	UNP P08581

- Molecule 2 is a protein called HEPATOCYTE GROWTH FACTOR RECEPTOR PEPTIDE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	P			
2	I	5	42	25	5	11	1	0	0	0
2	J	5	42	25	5	11	1	0	0	0
2	K	5	42	25	5	11	1	0	0	0
2	L	5	42	25	5	11	1	0	0	0

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
I	0	PTR	TYR	modified residue	UNP P08581
J	0	PTR	TYR	modified residue	UNP P08581
K	0	PTR	TYR	modified residue	UNP P08581
L	0	PTR	TYR	modified residue	UNP P08581

- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	O		
3	A	41	41	41	0	0
			Total	O		
3	B	49	49	49	0	0
			Total	O		
3	C	34	34	34	0	0
			Total	O		
3	D	43	43	43	0	0
			Total	O		
3	I	2	2	2	0	0
			Total	O		
3	J	5	5	5	0	0
			Total	O		
3	K	5	5	5	0	0
			Total	O		
3	L	3	3	3	0	0

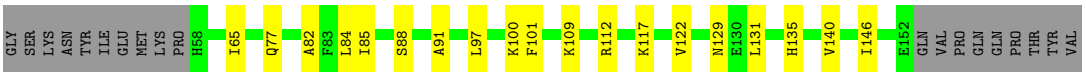
3 Residue-property plots (i)

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. 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. 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.

Note EDS was not executed.

• Molecule 1: GROWTH FACTOR RECEPTOR-BOUND PROTEIN 2

Chain A:



• Molecule 1: GROWTH FACTOR RECEPTOR-BOUND PROTEIN 2

Chain B:

• Molecule 1: GROWTH FACTOR RECEPTOR-BOUND PROTEIN 2

Chain C:

• Molecule 1: GROWTH FACTOR RECEPTOR-BOUND PROTEIN 2

Chain D:

• Molecule 2: HEPATOCYTE GROWTH FACTOR RECEPTOR PEPTIDE

Chain I:

• Molecule 2: HEPATOCYTE GROWTH FACTOR RECEPTOR PEPTIDE

Chain J:

• Molecule 2: HEPATOCYTE GROWTH FACTOR RECEPTOR PEPTIDE

Chain K:

• Molecule 2: HEPATOCYTE GROWTH FACTOR RECEPTOR PEPTIDE

Chain L:

4 Data and refinement statistics (i)

Xtriage (Phenix) and EDS were not executed - this section is therefore incomplete.

Property	Value	Source
Space group	P 43 21 2	Depositor
Cell constants a, b, c, α, β, γ	77.61Å 77.61Å 183.47Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	20.00 – 2.40	Depositor
% Data completeness (in resolution range)	98.7 (20.00-2.40)	Depositor
R_{merge}	0.09	Depositor
R_{sym}	(Not available)	Depositor
Refinement program	CNX	Depositor
R, R_{free}	0.217 , 0.270	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	3538	wwPDB-VP
Average B, all atoms ($Å^2$)	35.0	wwPDB-VP

5 Model quality (i)

5.1 Standard geometry (i)

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

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	0.41	0/806	0.62	0/1083
1	B	0.38	0/831	0.62	0/1116
1	C	0.41	0/831	0.62	0/1116
1	D	0.40	0/806	0.58	0/1083
2	I	0.47	0/22	0.74	0/28
2	J	0.51	0/22	0.86	0/28
2	K	0.51	0/22	0.82	0/28
2	L	0.56	0/22	0.65	0/28
All	All	0.40	0/3362	0.62	0/4510

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 (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	785	0	764	15	0
1	B	809	0	793	16	0
1	C	809	0	793	14	0
1	D	785	0	764	12	0
2	I	42	0	34	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	J	42	0	34	0	0
2	K	42	0	34	0	0
2	L	42	0	34	0	0
3	A	41	0	0	2	0
3	B	49	0	0	4	0
3	C	34	0	0	4	0
3	D	43	0	0	0	0
3	I	2	0	0	0	0
3	J	5	0	0	0	0
3	K	5	0	0	0	0
3	L	3	0	0	0	0
All	All	3538	0	3250	52	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 (52) 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:C:59:PRO:HD3	3:C:1166:HOH:O	1.80	0.81
1:D:77:GLN:O	1:D:100:LYS:HE3	1.85	0.76
1:B:66:PRO:HD2	1:B:69:LYS:HD2	1.70	0.71
1:C:59:PRO:CD	3:C:1166:HOH:O	2.39	0.66
1:B:78:ARG:HG3	1:B:79:HIS:ND1	2.13	0.64
1:D:69:LYS:N	1:D:69:LYS:HD2	2.14	0.62
1:C:122:VAL:HG23	1:C:122:VAL:O	2.02	0.58
1:D:112:ARG:HA	1:D:117:LYS:O	2.03	0.57
1:A:77:GLN:CD	1:B:151:ILE:HG23	2.26	0.55
1:A:112:ARG:HA	1:A:117:LYS:O	2.07	0.55
1:B:77:GLN:O	1:B:100:LYS:HE2	2.06	0.55
1:A:140:VAL:HG22	1:A:146:ILE:HB	1.88	0.54
1:C:129:ASN:HD21	1:D:58:HIS:CE1	2.24	0.54
1:C:77:GLN:CD	1:D:151:ILE:HG23	2.28	0.54
1:B:128:LEU:O	1:B:132:VAL:HG23	2.08	0.52
1:C:77:GLN:O	1:C:100:LYS:HE2	2.10	0.51
1:B:112:ARG:HA	1:B:117:LYS:O	2.12	0.50
1:A:85:ILE:HD13	1:A:97:LEU:HA	1.93	0.49
1:D:143:ASN:OD1	1:D:144:GLN:HG3	2.12	0.48
1:B:104:ASP:HB2	3:B:1047:HOH:O	2.13	0.48
1:B:135:HIS:CG	1:B:140:VAL:HG12	2.48	0.48
1:C:67:ARG:HD3	3:C:1050:HOH:O	2.13	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:85:ILE:HD11	1:A:97:LEU:HD13	1.94	0.48
1:A:122:VAL:O	1:A:122:VAL:HG23	2.12	0.48
1:C:112:ARG:NH1	3:C:1129:HOH:O	2.47	0.48
1:B:56:LYS:HB3	1:B:56:LYS:NZ	2.29	0.47
1:C:112:ARG:HA	1:C:117:LYS:O	2.15	0.47
1:D:69:LYS:HD2	1:D:69:LYS:H	1.81	0.46
1:A:100:LYS:HG2	1:A:101:PHE:N	2.31	0.46
1:B:109:LYS:HG3	3:B:1017:HOH:O	2.15	0.46
1:D:122:VAL:O	1:D:122:VAL:HG23	2.17	0.45
1:B:65:ILE:O	1:B:65:ILE:HG13	2.15	0.45
1:C:78:ARG:HG3	1:C:79:HIS:CE1	2.51	0.45
1:D:91:ALA:HB1	1:D:94:ASP:OD2	2.16	0.45
1:A:82:ALA:HA	1:B:149:ARG:O	2.16	0.45
1:D:131:LEU:C	1:D:131:LEU:HD23	2.38	0.45
1:B:78:ARG:HG3	1:B:79:HIS:CE1	2.52	0.44
1:C:140:VAL:HG11	1:C:148:LEU:HD21	2.00	0.43
1:A:131:LEU:C	1:A:131:LEU:HD23	2.39	0.43
1:C:122:VAL:O	1:C:122:VAL:CG2	2.65	0.43
1:C:142:ARG:HB2	1:D:121:TRP:CE3	2.54	0.42
1:A:109:LYS:NZ	3:A:1158:HOH:O	2.47	0.42
1:D:84:LEU:C	1:D:84:LEU:HD12	2.40	0.42
1:A:84:LEU:C	1:A:84:LEU:HD12	2.40	0.42
1:B:111:LEU:O	1:B:112:ARG:HD2	2.20	0.42
1:B:64:LYS:HE2	3:B:1146:HOH:O	2.19	0.41
1:C:135:HIS:HD2	1:C:138:THR:O	2.03	0.41
1:A:65:ILE:O	1:A:65:ILE:HG23	2.21	0.41
1:A:122:VAL:HG22	3:A:1124:HOH:O	2.21	0.41
1:A:135:HIS:HE1	3:B:1088:HOH:O	2.03	0.40
1:B:97:LEU:O	1:B:107:HIS:HA	2.22	0.40
1:A:88:SER:HB3	1:A:91:ALA:O	2.21	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	93/114 (82%)	90 (97%)	3 (3%)	0	100	100
1	B	96/114 (84%)	94 (98%)	1 (1%)	1 (1%)	15	23
1	C	96/114 (84%)	93 (97%)	3 (3%)	0	100	100
1	D	93/114 (82%)	91 (98%)	2 (2%)	0	100	100
2	I	2/5 (40%)	2 (100%)	0	0	100	100
2	J	2/5 (40%)	2 (100%)	0	0	100	100
2	K	2/5 (40%)	2 (100%)	0	0	100	100
2	L	2/5 (40%)	1 (50%)	1 (50%)	0	100	100
All	All	386/476 (81%)	375 (97%)	10 (3%)	1 (0%)	41	55

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	59	PRO

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	84/102 (82%)	83 (99%)	1 (1%)	71	85
1	B	87/102 (85%)	85 (98%)	2 (2%)	50	70
1	C	87/102 (85%)	86 (99%)	1 (1%)	73	87
1	D	84/102 (82%)	82 (98%)	2 (2%)	49	68
2	I	3/3 (100%)	3 (100%)	0	100	100
2	J	3/3 (100%)	3 (100%)	0	100	100
2	K	3/3 (100%)	3 (100%)	0	100	100
2	L	3/3 (100%)	3 (100%)	0	100	100
All	All	354/420 (84%)	348 (98%)	6 (2%)	60	78

All (6) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	129	ASN
1	B	56	LYS
1	B	73	MET
1	C	150	ASP
1	D	129	ASN
1	D	142	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (9) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	79	HIS
1	A	135	HIS
1	B	129	ASN
1	C	129	ASN
1	C	135	HIS
1	C	143	ASN
1	D	58	HIS
1	D	126	ASN
1	D	129	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)

4 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	PTR	K	0	2	15,16,17	0.87	1 (6%)	19,22,24	0.59	0
2	PTR	J	0	2	15,16,17	1.43	2 (13%)	19,22,24	0.75	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\| > 2$	Counts	RMSZ	$\#\|Z\| > 2$
2	PTR	L	0	2	15,16,17	1.44	1 (6%)	19,22,24	0.81	0
2	PTR	I	0	2	15,16,17	0.90	1 (6%)	19,22,24	0.68	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	PTR	K	0	2	-	0/10/11/13	0/1/1/1
2	PTR	J	0	2	-	0/10/11/13	0/1/1/1
2	PTR	L	0	2	-	1/10/11/13	0/1/1/1
2	PTR	I	0	2	-	1/10/11/13	0/1/1/1

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	L	0	PTR	P-OH	-4.78	1.51	1.59
2	J	0	PTR	P-OH	-4.14	1.52	1.59
2	I	0	PTR	P-OH	-2.26	1.55	1.59
2	K	0	PTR	P-OH	-2.24	1.55	1.59
2	J	0	PTR	P-O2P	-2.04	1.47	1.54

There are no bond angle outliers.

There are no chirality outliers.

All (2) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	I	0	PTR	CZ-OH-P-O1P
2	L	0	PTR	CZ-OH-P-O1P

There are no ring outliers.

No monomer is involved in short contacts.

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 (i)

6.1 Protein, DNA and RNA chains (i)

EDS was not executed - this section is therefore empty.

6.2 Non-standard residues in protein, DNA, RNA chains (i)

EDS was not executed - this section is therefore empty.

6.3 Carbohydrates (i)

EDS was not executed - this section is therefore empty.

6.4 Ligands (i)

EDS was not executed - this section is therefore empty.

6.5 Other polymers (i)

EDS was not executed - this section is therefore empty.