

# Full wwPDB X-ray Structure Validation Report (i)

#### May 13, 2020 – 02:28 am BST

PDB ID 6Q5P

> Title Crystal structure of a CC-Hex mutant that forms a parallel six-helix coiled

> > coil CC-Hex\*-II

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2018-12-09 Deposited on

1.44 Å(reported) Resolution

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 following versions of software and data (see references (1)) were used in the production of this report:

MolProbity 4.02b-467

> 1.8.5 (274361), CSD as541be (2020) Mogul

Xtriage (Phenix) 1.13 EDS 2.11

Percentile statistics 20191225.v01 (using entries in the PDB archive December 25th 2019)

> Refmac 5.8.0158

7.0.044 (Gargrove) CCP4 Engh & Huber (2001)

Ideal geometry (proteins) Ideal geometry (DNA, RNA) Parkinson et al. (1996)

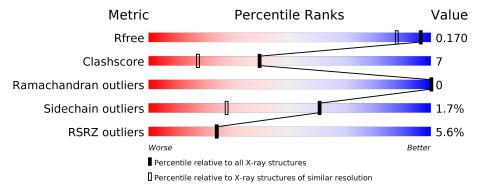
Validation Pipeline (wwPDB-VP) 2.11

# 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 1.44 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	$\begin{array}{c} \text{Whole archive} \\ (\#\text{Entries}) \end{array}$	$\begin{array}{c} {\rm Similar \; resolution} \\ (\#{\rm Entries, \; resolution \; range(\AA)}) \end{array}$
$R_{free}$	130704	2021 (1.46-1.42)
Clashscore	141614	2086 (1.46-1.42)
Ramachandran outliers	138981	2047 (1.46-1.42)
Sidechain outliers	138945	2047 (1.46-1.42)
RSRZ outliers	127900	1993 (1.46-1.42)

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 >=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 electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain		
1	A	32	88%	9%	<del>-</del>
1	В	32	91%	6%	-
1	С	32	6% 88%	9%	-
1	D	32	6%       78%       199	<b>%</b>	-
1	Е	32	75% 19%		<del>.</del>
1	F	32	91%	9%	6



The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
2	PO4	Ε	101	_	_	X	-



# 2 Entry composition (i)

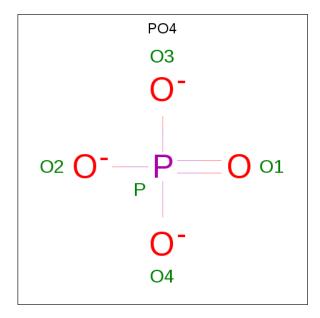
There are 4 unique types of molecules in this entry. The entry contains 1680 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 CC-Hex\*-II.

Mol	Chain	Residues	$\mathbf{At}$	oms		ZeroOcc	AltConf	Trace	
1	A	31	Total C	N	О	0	0	1	
		01	226   14	7 39	40		Ů,		
1	В	31	Total (	N	O	0	1	1 1	
1	Б	31	235   15	3 41	41	U	1	1	
1	С	32	Total C	N	О	0	0	2	1
1		32	247   16	0   43	44		2	1	
1	D	31	Total C	N	О	0	0	0	
1	ע	31	228   14	9 38	41	U	U	0	
1	Е	31	Total C	N	О	0	5	0	
1	<u> </u>	91	278   18	1  45	52	U	9		
1	r.	32	Total C	N	О	0	4	1	
1	F	32	265 17	0 45	50	0	4	1	

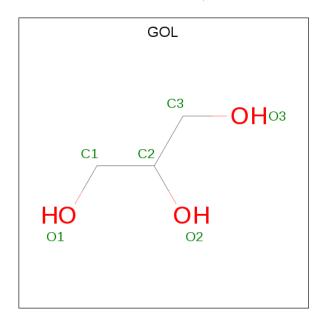
• Molecule 2 is PHOSPHATE ION (three-letter code: PO4) (formula: O<sub>4</sub>P).





$\mathbf{Mol}$	Chain	Residues	${f Atoms}$	ZeroOcc	AltConf
2	A	1	Total O P 5 4 1	0	0
2	E	1	Total O P 5 4 1	0	0

 $\bullet$  Molecule 3 is GLYCEROL (three-letter code: GOL) (formula:  $\mathrm{C_3H_8O_3}).$ 



$\mathbf{Mol}$	Chain	Residues	Atoms	ZeroOcc	AltConf
3	В	1	Total C O 6 3 3	0	0

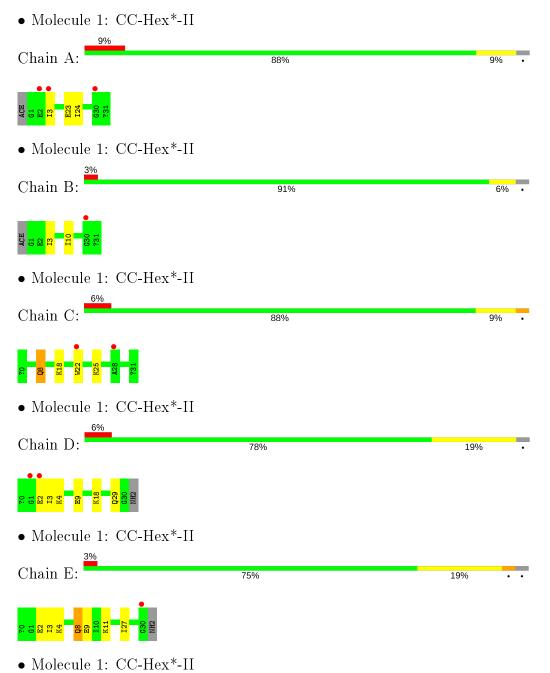
• Molecule 4 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	19	Total O 19 19	0	0
4	В	33	Total O 33 33	0	0
4	С	32	Total O 32 32	0	0
4	D	35	Total O 35 35	0	0
4	E	34	Total O 34 34	0	0
4	F	32	Total O 32 32	0	0

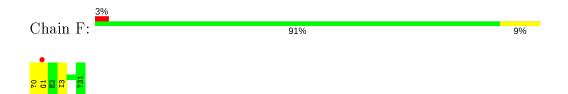


# 3 Residue-property plots (i)

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.









# 4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 63	Depositor
Cell constants	62.76	Domositon
a, b, c, $\alpha$ , $\beta$ , $\gamma$	$90.00^{\circ}$ $90.00^{\circ}$ $120.00^{\circ}$	Depositor
Resolution (Å)	54.41 - 1.44	Depositor
Resolution (A)	54.35 - 1.44	EDS
% Data completeness	99.9 (54.41-1.44)	Depositor
(in resolution range)	99.9 (54.35-1.44)	EDS
$R_{merge}$	0.14	Depositor
$R_{sym}$	(Not available)	Depositor
$< I/\sigma(I) > 1$	1.40 (at 1.44Å)	Xtriage
Refinement program	REFMAC 5.8.0238	Depositor
D D.	0.164 , 0.171	Depositor
$R, R_{free}$	0.166 , $0.170$	DCC
$R_{free}$ test set	1680 reflections $(5.03\%)$	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	18.2	Xtriage
Anisotropy	0.190	Xtriage
Bulk solvent $k_{sol}(e/Å^3)$ , $B_{sol}(Å^2)$	0.36 , 42.8	EDS
L-test for twinning <sup>2</sup>	$< L >=0.50, < L^2>=0.33$	Xtriage
Estimated twinning fraction	0.052 for h,-h-k,-l	Xtriage
$F_o, F_c$ correlation	0.97	EDS
Total number of atoms	1680	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	25.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: The largest off-origin peak in the Patterson function is 10.22% of the height of the origin peak. No significant pseudotranslation is detected.

<sup>&</sup>lt;sup>2</sup>Theoretical values of <|L|>,  $< L^2>$  for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.



<sup>&</sup>lt;sup>1</sup>Intensities estimated from amplitudes.

# 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: GOL, PO4, ACE, NH2

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	Boı	nd lengths	Bond angles		
IVIOI		RMSZ	# Z  > 5	RMSZ	# Z  > 5	
1	A	0.75	$1/226 \ (0.4\%)$	0.67	0/301	
1	В	0.74	0/235	0.60	0/312	
1	С	0.73	0/245	0.67	0/326	
1	D	0.74	0/227	0.55	0/303	
1	Е	0.69	0/279	0.64	0/373	
1	F	0.72	0/263	0.72	0/350	
All	All	0.73	1/1475~(0.1%)	0.65	0/1965	

All (1) bond length outliers are listed below:

$\mathbf{Mol}$	Chain	${f Res}$	Type	${f Atoms}$	$\mathbf{Z}$	$\operatorname{Observed}(\operatorname{\AA})$	$oxed{Ideal(A)}$
1	A	23	GLU	CD-OE2	-5.13	1.20	1.25

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	226	0	251	5	0
1	В	235	0	263	3	0
1	С	247	0	271	3	0
1	D	228	0	252	11	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	Ε	278	0	289	11	0
1	F	265	0	282	2	0
2	A	5	0	0	0	0
2	Ε	5	0	0	2	0
3	В	6	0	8	0	0
4	A	19	0	0	0	0
4	В	33	0	0	0	0
4	С	32	0	0	0	0
4	D	35	0	0	1	0
4	Ε	34	0	0	2	0
4	F	32	0	0	0	0
All	All	1680	0	1616	23	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 7.

All (23) 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:E:11[A]:LYS:NZ	2:E:101:PO4:O2	2.17	0.77
1:E:9[A]:GLU:HG3	4:E:219:HOH:O	1.90	0.71
1:B:3:ILE:HG22	1:D:2:GLU:HB3	1.79	0.64
1:C:8[A]:GLN:HE21	1:C:8[A]:GLN:HA	1.65	0.61
1:A:3:ILE:HD11	1:D:3:ILE:HD11	1.83	0.61
1:F:0:ACE:O	1:F:1:GLY:C	2.43	0.56
1:A:3:ILE:HD11	1:D:3:ILE:CD1	2.36	0.56
1:D:29:GLN:HG3	1:E:27:ILE:HD13	1.88	0.56
1:E:4:LYS:HA	1:F:3:ILE:CD1	2.40	0.51
1:E:8:GLN:HE21	1:E:8:GLN:HA	1.75	0.51
1:E:8:GLN:NE2	1:E:11[B]:LYS:HE2	2.28	0.49
1:D:4:LYS:HB2	1:E:3:ILE:HD11	1.94	0.49
1:E:11[A]:LYS:HE3	2:E:101:PO4:O3	2.13	0.48
1:E:9[A]:GLU:CG	4:E:219:HOH:O	2.54	0.47
1:A:3:ILE:CG1	1:D:3:ILE:HD11	2.45	0.47
1:A:3:ILE:CD1	1:D:3:ILE:HD11	2.45	0.44
1:D:4:LYS:HD3	1:E:2:GLU:CD	2.38	0.44
1:B:3:ILE:CG2	1:D:2:GLU:HB3	2.46	0.42
1:C:22:TRP:HA	1:C:25[B]:LYS:HE3	2.02	0.42
1:D:18:LYS:NZ	4:D:103:HOH:O	2.52	0.41
1:B:10:ILE:HG22	1:D:9:GLU:HB3	2.03	0.41
1:A:24:ILE:HG12	1:C:18:LYS:HA	2.02	0.40

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Atom-1	1100111 1		$egin{aligned}  ext{Clash} \  ext{overlap } ( ext{Å}) \end{aligned}$
1:E:8:GLN:HE22	1:E:11[B]:LYS:NZ	2.20	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	${f Analysed}$	Favoured	Allowed	Outliers	Perce	$\mathbf{ntiles}$
1	A	$29/32 \; (91\%)$	29 (100%)	0	0	100	100
1	В	$30/32 \; (94\%)$	30 (100%)	0	0	100	100
1	$^{\mathrm{C}}$	$32/32 \; (100\%)$	32 (100%)	0	0	100	100
1	D	$29/32 \; (91\%)$	29 (100%)	0	0	100	100
1	E	$34/32 \; (106\%)$	34 (100%)	0	0	100	100
1	F	$34/32 \; (106\%)$	34 (100%)	0	0	100	100
All	All	$188/192\ (98\%)$	188 (100%)	0	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	Perce	${f ntiles}$
1	A	20/20 (100%)	20 (100%)	0	100	100
1	В	21/20 (105%)	21 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
1	С	22/20 (110%)	20 (91%)	2 (9%)	9 0
1	D	$20/20 \; (100\%)$	20 (100%)	0	100 100
1	E	25/20  (125%)	24 (96%)	1 (4%)	31 4
1	F	$24/20 \ (120\%)$	24 (100%)	0	100 100
All	All	132/120 (110%)	129 (98%)	3 (2%)	60 16

All (3) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	С	8[A]	GLN
1	С	8[B]	GLN
1	E	8	GLN

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (1) such sidechains are listed below:

Mol	Chain	Chain Res	
1	Е	8	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 carbohydrates in this entry.

## 5.6 Ligand geometry (i)

3 ligands 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	B	ond leng	${ m gths}$	В	ond ang	gles
MIOI	Type	Chain	Chain Ites	LIIIK	Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
3	GOL	В	101	_	5,5,5	0.10	0	5,5,5	0.30	0
2	PO4	E	101	-	4,4,4	0.74	0	6,6,6	0.43	0
2	PO4	A	101	-	4,4,4	0.67	0	6,6,6	0.43	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
3	GOL	В	101	-	-	2/4/4/4	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (2) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	В	101	GOL	O1-C1-C2-C3
3	В	101	GOL	O1-C1-C2-O2

There are no ring outliers.

1 monomer is involved in 2 short contacts:

$\mathbf{Mol}$	Chain	${ m Res}$	$\mathbf{Type}$	Clashes	Symm-Clashes
2	Ε	101	PO4	2	0

## 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,  $95^{th}$  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	$\langle { m RSRZ} \rangle$	$\#\mathrm{RSRZ}{>}2$	$OWAB(Å^2)$	Q < 0.9
1	A	$30/32 \ (93\%)$	0.23	3 (10%) 7 7	13, 19, 44, 70	0
1	В	30/32 (93%)	-0.03	1 (3%) 46 47	16, 23, 52, 54	0
1	С	30/32 (93%)	0.05	2 (6%) 17 17	13, 19, 31, 38	0
1	D	30/32 (93%)	0.06	2 (6%) 17 17	15, 20, 51, 62	0
1	E	$30/32 \; (93\%)$	-0.01	1 (3%) 46 47	14, 20, 37, 50	0
1	F	30/32 (93%)	0.28	1 (3%) 46 47	15, 23, 44, 54	0
All	All	180/192 (93%)	0.10	10 (5%) 24 24	13, 21, 51, 70	0

All (10) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	F	1	GLY	4.0
1	D	1	GLY	2.9
1	A	2	GLU	2.8
1	A	3	ILE	2.7
1	С	22	TRP	2.5
1	A	30	GLY	2.5
1	В	30	GLY	2.5
1	С	28	ALA	2.4
1	E	30	GLY	2.1
1	D	2	GLU	2.0

## 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 carbohydrates 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,  $95^{th}$  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	${f Res}$	Atoms	RSCC	RSR	${f B-factors(\AA^2)}$	Q<0.9
2	PO4	E	101	5/5	0.79	0.17	29,31,39,44	5
3	GOL	В	101	6/6	0.82	0.17	40,46,47,48	0
2	PO4	A	101	5/5	0.93	0.10	54,66,66,68	5

### 6.5 Other polymers (i)

There are no such residues in this entry.

